Modeling and Simulation of Neocortical Micro- and Mesocircuitry. Part II: Physiology and Experimentation

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Summary

Cortical dynamics underlie many cognitive processes and emerge from complex multiscale interactions, which are challenging to study *in vivo*. Large-scale, biophysically detailed models offer a tool which can complement laboratory approaches. We present a model comprising eight somatosensory cortex subregions, 4.2 million morphological and electrically-detailed neurons, and 13.2 billion local and mid-range synapses. *In silico* tools enabled reproduction and extension of complex laboratory experiments under a single parameterization, providing strong validation. The model reproduced millisecond-precise stimulus-responses, stimulus-encoding under targeted optogenetic activation, and selective propagation of stimulus-evoked activity to downstream areas. The model's direct correspondence with biology generated predictions about how multiscale organization shapes activity; for example, how cortical activity is shaped by high-dimensional connectivity motifs in local and mid-range connectivity, and spatial targeting rules by inhibitory subpopulations. The latter was facilitated using a rewired connectome which included specific targeting rules observed for different inhibitory neuron types in electron microscopy. The model also predicted the role of inhibitory interneuron types and different layers in stimulus encoding. Simulation tools and a large subvolume of the model are made available to enable further community-driven improvement, validation and investigation.

1 Introduction

Neuroscience aims to characterize the dynamics of the brain and understand how they emerge as a product of anatomy and physiology. This is challenging however, due to the complexity of the brain's multi-scale organization and its study *in situ*. *Large-scale, data-driven, biophysically-detailed* models (Markram et al., 2015; Billeh et al., 2020) offer a tool which can complement laboratory investigation. This "bottom-up" approach combines detailed constituent models into a 3D model of a given brain volume, thus consolidating disparate, multi-scale data sources. Such models aim to provide a general tool for multi-scale investigation; access and manipulation of any model component enables predictions about how these components combine to shape emergent dynamics. With increasing biological data, model refinement and validation must be continuous. This necessitates 1) open sourcing of models with high quality software tools for iterative, community-driven refinement and validation, and 2) rigorous methodology for model parameterization and validation, such that model iterations can be meaningfully compared. Here and in our companion paper (Reimann et al., 2024) we present our methodology for parameterizing the anatomy and physiology of a cortical model, and validating its emergent dynamics. This enabled predictions about how cortical activity is shaped by high-dimensional connectivity motifs in local and mid-range connectivity, and spatial targeting rules by inhibitory subpopulations. Elsewhere, this has allowed the presented model to be used to study the formation of cell assemblies (Ecker et al., 2024b), functional synaptic plasticity (Ecker et al., 2024a), propagation of activity between cortical areas (Bolaños-Puchet and Reimann, 2024) the role of non-random connectivity motifs on network activity (Pokorny et al., 2024) and reliability (Egas Santander et al., 2024), the composition of high-level electrical signals such as the EEG (Tharayil et al., 2024), and how spike sorting biases population codes (Laquitaine et al., 2024).

Specifically, we built and validated a model of the entire non-barrel primary somatosensory cortex (nbS1) comprising eight subregions. Whilst our previous data-driven, biophysically detailed model (Markram et al., 2015) provided insights at the scale of a single cortical column (Reimann et al., 2013, 2017, 2022; Nolte et al., 2019, 2020; Newton et al., 2021), the new model is ∼140 times larger and to our knowledge offers the first simulations of *in vivo*-like spontaneous and stimulus-evoked activity in a biophysically detailed cortical model with interregion connectivity. In the companion paper, we introduce the anatomical model (Fig. 1, Step 1), describing how neuron morphologies were placed within an atlas-based geometry and connected through local and mid-range synapses. Here, we describe our improved techniques to model and validate the electrical properties of neurons and synapses (Figure 1, Steps 2 & 3 (Reva et al., 2023; Barros-Zulaica et al., 2019)), and to compensate for input from missing brain areas (Figure 1, Steps 4). These improvements enabled enhanced validation of emerging *in vivo*-like activity (Figure 1, Steps 5), including the reproduction and extension of five published studies in rodent sensory cortex under a single *in vivo*-like regime (Figure 1, Steps 6).

Validating that network activity emerges from the same interactions driving *in vivo* dynamics, requires 1) an approach to tackle the large parameter space without overfitting and 2) comparison of emerging dynamics with laboratory experiments. With respect to 1), we strongly prefer parameterization with directly measured quantities over fitting parameters to yield the correct emerging activity. Additionally, where fitting is applied, we adhere to a principle of *compartmentalization* of parameters. That is, once a parameter

has been parameterized at one biological level, it is no longer a free parameter at a higher level. For example, the maximal conductance of a synapse is fit to biological amplitudes of postsynaptic potentials, but is then never updated in the process of reaching in-vivo like population activity. If a connection is valid on the single-cell level, its contribution at the population level should be equally valid. As a result, the emerging in-vivo like activity is the consequence of only 10 free parameters representing the strength of extrinsic input from other brain regions into 9 layer-specific excitatory and inhibitory populations, and a parameter controlling the noise structure of this extrinsic input. These parameters were fitted using a novel methodology presented here and were in accordance with the mean number of missing synapses for each population (Felleman and Van Essen, 1991; Harris et al., 2019; Gao et al., 2022).

With respect to 2), we conducted the following validations: Spontaneous activity reproduced layer-wise *in vivo* firing rates (or a specified proportion of *in vivo* firing rates to account for *in vivo* recording bias (Wohrer et al., 2013)), varied along a spectrum of asynchronous to synchronous activity, exhibited spatially structured fluctuations and produced long-tailed firing rate distributions with sub 1 Hz peaks as *in vivo* (Wohrer et al., 2013; Buzsáki and Mizuseki, 2014). Under the same parameterization, the model reproduced precise millisecond dynamics of layer-wise populations in response to simple stimuli. These initial validations demonstrated that the model was in a more accurate regime compared to Markram et al. (2015) – an essential step before testing more complex or larger-scale validations. For example, under the same parameterization we then observed selective propagation of stimulus-evoked activity to downstream areas, and reproduced and extended more complex experiments through accurate modeling of targeted optogenetic stimulation and lesions. Importantly, we highlight where emergent activity shows discrepancies with *in vivo* activity, to guide future data-driven model refinement.

The model generated a number of predictions (Table S1), including about the role of different layers in driving layer 2/3 stimulus responses and how inhibitory interneuron types encode contrast, synchronous and rate-coded information. Additionally, with access to the full structural connectome and tools for precisely editing it (Pokorny et al., 2024), we were able to make predictions about the relationship between structure and function. For example, we predict that an increase in the prevalence of non-random connectivity motifs towards deeper layers leads to a matched increase in spiking correlations, and that subregions more strongly innervated by mid-range connectivity have higher correlated activity locally. Additionally, we generated a new connectome which captured recently characterized spatially-specific targeting rules for different inhibitory neuron types (Schneider-Mizell et al., 2023) in the MICrONS electron microscopy dataset (MICrONS-Consortium et al., 2021), such as increased perisomatic targeting by PV+ neurons, and increased targeting of inhibitory populations by VIP+ neurons. Comparing activity to the original connectome gave predictions about the role of these additional targeting rules. For example, inhibitory populations were more strongly inhibited (increasingly towards central layers) and required more non-local drive to reach the firing rates observed *in vivo*. Evoked responses increased and decreased in superficial and deeper excitatory populations respectively, suggesting layer-specific roles of the more specific inhibitory targeting.

To provide a framework for further studies and integration of experimental data, the full model is made available with simulation tools, as well as a smaller subvolume with the

optional new connectome capturing inhibitory targeting rules from electron microscopy. (Figure 1, Step 7). The detailed modeling approach provides a one-to-one correspondence with most types of experimental data, allowing different datasets to be readily integrated. Due to the incredible speed of discovery in neuroscience an integrative model will always be lagging behind the latest available data. We believe the solution is to provide a scientifically solid, validated model with clearly characterized strengths and weaknesses, along with the tools to advance or customize it for individual projects. We have therefore also made our tools for building and improving the model openly available: `www.github.com/BlueBrain`.

2 Results

The companion paper describes the full anatomical nbS1 model containing 4.2M morphological neuron models, connected through 9.1B local synapses and 4.1B mid-range synapses (Reimann et al., 2024). Each neuron is modeled as a multi-compartmental model belonging to one of 60 morphological types (m-types; Figure 2A1), and is either an instance or statistical variant of an exemplar in a pool of 1,017 morphological reconstructions. Neurons were placed (orientated towards the surface) within an atlas-based geometry (Figure 2A2) based on estimated layer-wise density profiles of different morphological types. Local connectivity is based on axo-dendritic overlap with neighbouring neurons, whilst mid-range connectivity combines data on interregion connectivity and laminar innervation profiles. Thalamocortical afferents were also modeled based on laminar innervation to the barrel cortex. To simulate emergent activity it is necessary to model and validate the electrical properties of these neurons and synapses (Figure 1 Steps 2 & 3). These modeling steps are based on published methods and data sources (Table 1), and are summarized first. The method for compensating for missing synapses and the remaining results are then described (Figure 1 Steps 4-6).

2.1 Improved modeling and validation of neuron physiology

Similarly to Markram et al. (2015), electrical properties of single neurons were modeled by optimizing ion channel densities in specific compartment-types (soma, axon initial segment (AIS), basal dendrite, and apical dendrite) (Figure 2B) using an evolutionary algorithm (IBEA; Van Geit et al., 2016) so that each neuron recreates electrical features of its corresponding electrical type (e-type) under multiple standardized protocols. Compared to Markram et al. (2015), electrical models were optimized and validated using 1) additional *in vitro* data, features and protocols, 2) ion channel and electrophysiological data corrected for the liquid junction potential, and 3) stochastic channels (StochKv3) now including inactivation profiles. The methodology and resulting electrical models are described in Reva et al. (2023) (see Methods), and generated quantitatively more accurate electrical activity, including improved attenuation of excitatory postsynaptic potentials (EPSPs) and back-propagating action potentials. Electrical features included firing properties (e.g. spike frequency, inter-spike interval), action potential waveforms (e.g. fall and rise time, width) and passive properties (e.g. input resistance). The optimization was performed for a subset of neuron models. The resulting ion channel densities were generalized to other neuron models of the same e-type. For excitatory neurons such generalization was only made to neurons within the same layer. The resulting electrical activity of each neuron was validated against the corresponding electrical features, including the *charac-*

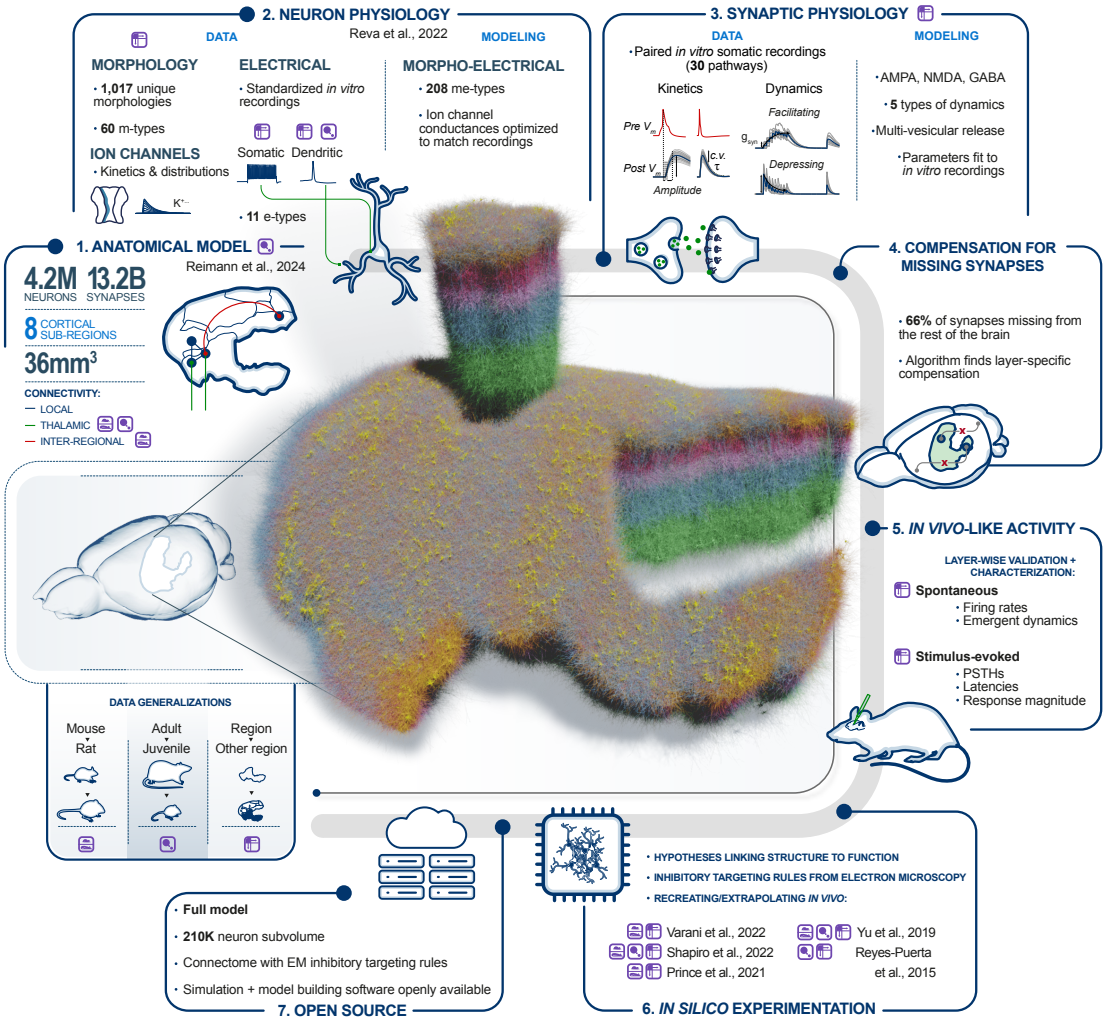

Figure 1: Overview of the physiology and simulation workflow. 1. Anatomical model: Summary of the anatomical nbS1 model described in the companion paper. **2. Neuron physiology:** Neurons were modeled as multi-compartment models with ion channel densities optimised using previously established methods and data from somatic and dendritic recordings of membrane potentials *in vitro*. **3. Synaptic physiology:** Models of synapses were built using previously established methods and data from paired recordings *in vitro*. **4. Compensation for missing synapses:** Excitatory synapses originating from outside nbS1 were compensated with noisy somatic conductance injection, parameterized by a novel algorithm. **5. *In vivo*-like activity:** We calibrated an *in silico* activity regime compatible with *in vivo* spontaneous and stimulus-evoked activity. **6. *In silico* experimentation:** Five laboratory experiments were recreated. Two were used for calibration and three of them were extended beyond their original scope. **7. Open Source:** Simulation software and a seven column subvolume of the model are available on Zenodo (see data availability statement). **Data generalisations:** Three data generalisation strategies were employed to obtain the required data. Left: Mouse to rat, middle: Adult to juvenile (P14) rat, right: Hindlimb (S1HL) and barrel field (S1BF) subregions to the whole nbS1. Throughout the figure, the corresponding purple icons show where these strategies were used.

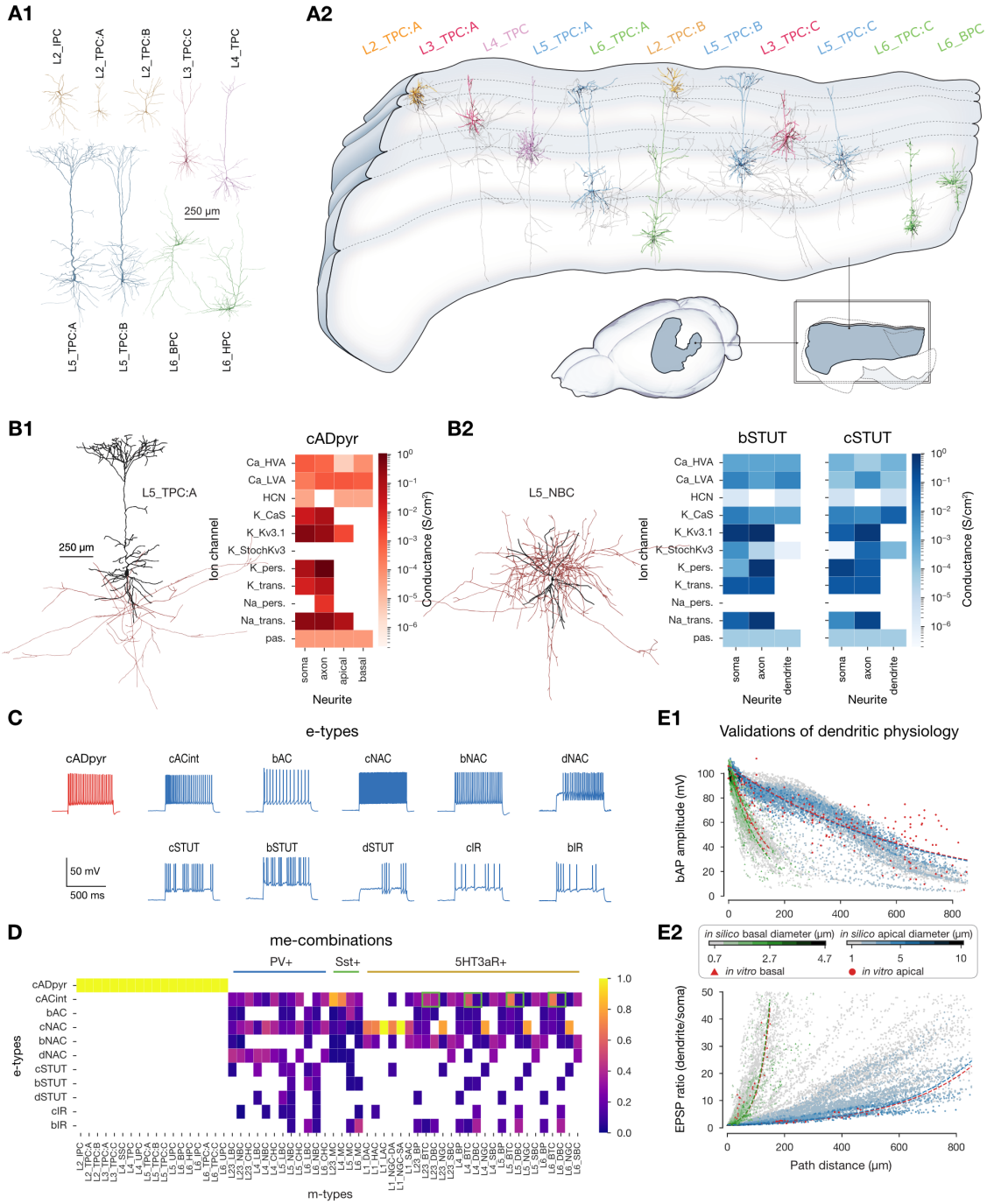

Figure 2: Modeling and validation of neuron physiology. **A1:** Example excitatory neuron morphologies. See companion paper for exemplar morphologies of all morphological types. **A2:** Example morphologies placed within the atlas-based volume. Axons shown in grey. **B**: Optimized conductance densities for two exemplary e-types. **B1**: cADpyr e-type on L5_TPC:A m-type, **B2**: bSTUT and cSTUT e-types on L5_NBC m-type. (The L5_NBC m-type is combined with more e-types than the two shown, see panel D.) Morphologies were visualized with NeuroMorphoVis (Abdellah et al., 2018). Neurite diameters are enlarged (x3) for visibility. Soma and dendrites in black, axon in red. **C:** e-types used in the model. As used in Markram et al. (2015) and similar to the Petilla terminology (Ascoli et al., 2008)).

Table 1: Previously published modeling techniques and data to parameterize them that were combined in this work to model the physiology of nbS1 and conduct *in silico* experimentation.

	Data	
Stage	**Topic**	**Reference**
Neuron physiology	E-type composition	Markram et al. (2004, 2015)
	Electrophysiological recordings	Markram et al. (2015)
		Larkum et al. (2001)
		Nevian et al. (2007)
	Ion-channel models	Reva et al. (2023)
Synaptic physiology	Synaptic pathway physiology	Markram et al. (2015)
		Barros-Zulaica et al. (2019)
		Gupta et al. (2000)
		13 additional sources in Tables S5, S6, S7
In vivo-like activity	*In vivo* spont. firing rates	Reyes-Puerta et al. (2015b)
		De Kock et al. (2007)
	In vivo evoked responses	Reyes-Puerta et al. (2015b)
		Yu et al. (2019)
	In vivo thalamic spiking	Diamond et al. (1992)
		Yu et al. (2019)
In silico experimentation	L4 - L2/3 pathway	Varani et al. (2022)
	Visual contrast	Shapiro et al. (2022)
	Coding in inhibitory subpopulations	Prince et al. (2021)
	Modeling methods	
Stage	**Topic**	**Reference**
Neuron physiology	E-model building	Van Geit et al. (2016)
		Reva et al. (2023)
Synaptic physiology	Synapse model building	Ecker et al. (2020)
	Model of multi-vesicular release	Barros-Zulaica et al. (2019)
In vivo-like activity	Missing input compensation	*New, original methods based on Destexhe et al. (2001)
In silico experimentation		*New, original methods

teristic firing properties of the 11 e-types (Figure 2C). Model neurons with a mean zscore (over the electrical features) further than two standard deviations from the experimental mean were discarded. The new neuron models saw a 5-fold improvement in generalizability compared to Markram et al. (2015) (Reva et al., 2023).

For each of the 60 morphological types (m-types), the corresponding fractions of e-types were determined from experimental data as in Markram et al. (2015), resulting in 208 morpho-electrical types (me-types; Figure 2D). Correspondence with predominant expression of biological markers PV (parvalbumin), Sst (somatostatin) or 5HT3aR (serotonin receptor 3A) was determined based on me-type, as previously done in Markram et al. (2015) (Figure 2D). Finally, for layer five thick-tufted pyramidal cell (L5 TTPC) morphologies, we found that dendritic electrical features, namely the attenuation of back propagating action potentials and EPSPs, reproduced experimental measurements (Figure 2E, Reva et al., 2023).

The required data to constrain region-specific me-type distributions was not available when building the model; to our knowledge Yao et al. (2023) is the first study that explored

D: me-type composition. Heatmap shows the proportion of e-types for each m-type. Each me-type is assigned to one of the three I subpopulations. Assignments depending not only on m-type are highlighted by a green box. Particularly, for BTC and DBC m-types, the cACint e-type belongs to the Sst+ subpopulation. **E**: Validation of dendritic physiology of all L5 TTPCs. Panel reproduced from Reva et al. (2023). **E1**: Validation of back-propagating action potential (bAP) amplitude (i.e., the dependence of bAP amplitude on distance from the soma) for basal (green) and apical (blue) dendrites. Reference data (in red) comes from Stuart and Sakmann (1994); Larkum et al. (2001) (apical) and Nevian et al. (2007) (basal). Lines show exponential fits for the *in silico* (green and blue) and *in vitro* (red) data. Color bar indicates dendritic diameter. **E2:** Validation of EPSP attenuation. Reference data (in red) comes from Berger et al. (2001) (apical) and Nevian et al. (2007) (basal). Lines and colorbar same as in E1.

the question systematically (in mouse cortex). The atlas-based geometry does however impose heterogeneity in morphologies that e-types are paired with: only morphologies that are in line with the region-specific local curvature of the region are used throughout the volume. We demonstrate the effect of geometry on morphological composition in the companion paper.

2.2 Improved modeling and validation of synaptic physiology

The biological realism of synaptic physiology was improved relative to Markram et al. (2015) using additional data sources and by extending the stochastic version of the Tsodyks-Markram model (Tsodyks and Markram, 1997; Markram et al., 1998; Fuhrmann et al., 2002; Loebel et al., 2009) to feature multi-vesicular release, which in turn improved the accuracy of the coefficient of variations (CV; std/mean) of postsynaptic potentials (PSPs) as described in Barros-Zulaica et al. (2019) and Ecker et al. (2020). The model assumes a pool of available vesicles that is utilized by a presynaptic action potential, with a release probability dependent on the extracellular calcium concentration ($[Ca^{2+}]_o$; Ohana and Sakmann, 1998; Rozov et al., 2001; Borst, 2010). Additionally, single vesicles spontaneously release as an additional source of variability with a low frequency (with improved calibration relative to Markram et al. (2015)). The utilization of vesicles leads to a postsynaptic conductance with bi-exponential kinetics. Short-term plasticity (STP) dynamics in response to sustained presynaptic activation are either facilitating (E1/I1), depressing (E2/I2), or pseudo-linear (I3). E synaptic currents consist of both AMPA and NMDA components, whilst I currents consist of a single $GABA_A$ component, except for neurogliaform cells, whose synapses also feature a slow $GABA_B$ component. The NMDA component of E synaptic currents depends on the state of the Mg^{2+} block (Jahr and Stevens, 1990), with the improved fitting of parameters to cortical recordings from Vargas-Caballero and Robinson (2003) by Chindemi et al. (2022).

The workflow for determining a dense parameter set for all synaptic pathways, starting with sparse data from the literature, is described for the use case of hippocampal CA1 in Ecker et al. (2020) and briefly in the Methods. We combined data sources used in Markram et al. (2015), with a large number of recent data sources (Qi and Feldmeyer, 2016; Barros-Zulaica et al., 2019; Yang et al., 2020, 2022). The resulting pathway-specific parameters are listed in Tables S2, S3, S4, the most common short-term dynamics are depicted in Figure 3A1-2, and the assignment of STP profiles to different pathways are shown in Figure 3A3. Postsynaptic potential amplitudes and their CV closely matched their biological counterparts ($r = 0.99$, $n = 27$; Figure 3B1; Table S5 and $r = 0.63$, $n = 10$; Figure 3C1; Table S6, respectively). The dense parameter set also allowed prediction of

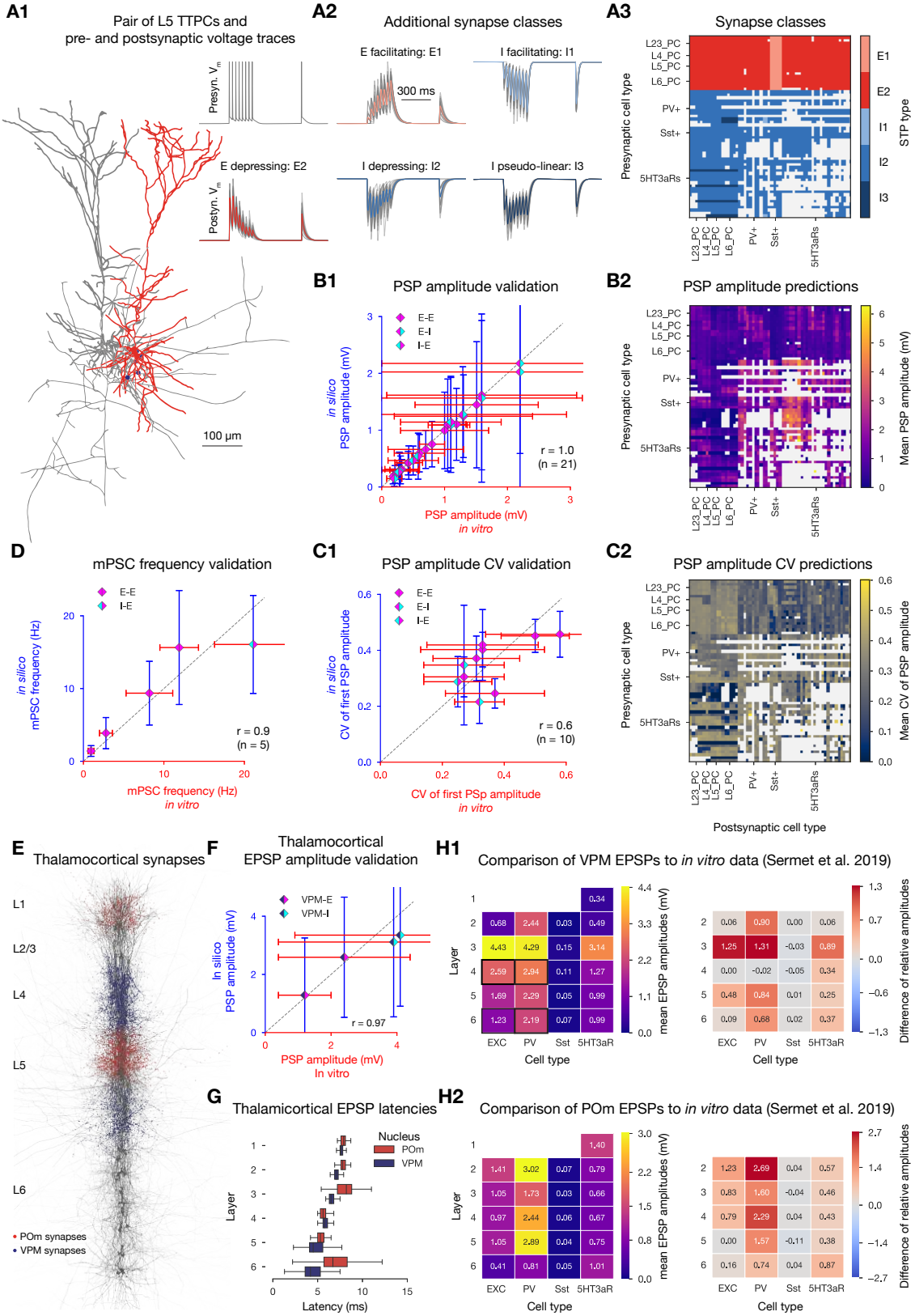

Figure 3: Modeling and validation of synaptic physiology. Caption on the following page.

A1: Exemplary pair of L5 TTPCs (visualized with NeuroMorphoVis (Abdellah et al., 2018)). Presynaptic cell in gray, postsynaptic cell in red, synapses between them in purple. Neurite diameters are enlarged (x3) for visibility and axons were cut to fit into the figure. Pre- and postsynaptic voltage traces on the top right. **A2:** Exemplary postsynaptic traces with different STP profiles. **A3:** Assignment of STP profiles to viable pathways. (Pathways were considered viable if there were at least 10 connections in all eight subregions of the model.) **B1:** Validation of first PSP amplitudes (see also Table S5). Dashed gray line represents perfect correlation between experimental and model values. Error bars show one standard deviation (also for C1, D and F). **B2:** Predicted PSP amplitudes of all viable pathways in the circuit. Postsynaptic cells were held at -70 mV using an *in silico* voltage-clamp. Means were calculated over 100 pairs of neurons with 35 repetitions each. **C1** and **C2**: same as B1 and B2, but showing the CV of the first PSP amplitude (corresponding Table is S6). **D:** Validation of mPSC frequencies (see also Table S7). **E:** Location of synapses from VPM fibers (purple) and POm fibers (red) on 38 neurons (dark gray) in a 5 μm radius column (visualized with `BioExplorer`). **F:** Validation of thalamocortical EPSP amplitudes as in B1. The four pathways used for the validation are marked with a black rectangle on H1 to its right. **G**: EPSP latencies (time from presynaptic spike to the rise to 5% of peak EPSP amplitude in the postsynaptic trace). **H1** Left: mean VPM evoked EPSP amplitudes on postsynaptic cell types (over 50 pairs). Right: Comparison of normalized *in silico* amplitudes (normalized by L4 E as in Sermet et al., 2019) to *in vitro* reference data from Sermet et al. (2019). Heatmap shows model minus reference values, thus positive values indicate a higher normalized EPSP amplitude in our model than in the reference experimental dataset. **H2**: same as H1 but for POm (normalized by L5 E as in Sermet et al., 2019).

PSP amplitudes and CVs for all cortical pathways (Figure 3B2, C2). The frequency of miniature postsynaptic currents (mPSCs) were also in line with *in vitro* measurements ($r = 0.92$, $n = 5$; Figure 3D; Table S7).

Improved modeling and validation of thalamocortical projections

The anatomical model includes fibers from the thalamus, based on fibers projecting to the barrel cortex from the ventral posteriomedial (VPM) and posteriormedial (POm) thalamic nuclei. These fibers make synaptic contacts within a radius of the fiber probabilistically based on laminar innervation profiles (see Reimann et al., 2024; Figure 3E). Compared to the previous model (Markram et al., 2015), POm projections are added and the physiology of synapses from VPM improved (see Methods; Figure 3E, F). Latencies of layer-wise EPSPs increase with distance from the thalamus (Figure 3G). Additionally, thalamocortical EPSP amplitudes normalized relative to a single population were compared to normalized EPSPs in response to optogenetic stimulation targeting bundles of thalamic fibers (Sermet et al., 2019). This provided contrasting insights, however. For example, whilst VPM to L6 I EPSPs match the initial validation data (Figure 3F), VPM to L6 PV+ responses appear too strong relative to other populations (Figure 3H1). The results suggest that the model's POm to L5 E pathway is too weak, when compared to other POm to E and all POm to PV+ pathways (Figure 3H2, right).

2.3 Defining subvolumes and populations

To enable smaller simulations and targeted analyses, we defined standardized partitions comprising all neurons (and their connections) contained in a *subvolume* of the full nbS1 model. We decomposed the model into full-depth hexagonal prisms of a certain diameter that we call *hexagonal subvolumes*. These are slightly curved, following the geometry of

the cortex, and have an intact layer structure. When the diameter of the hexagons is $520\,\mu m$, comparable to the size of the single cortical column model from (Markram et al., 2015), we call these subvolumes *columns*. Taken together, a *central column* and the six columns surrounding it define a *seven column subvolume* (Figure 4A). Additionally, when we separately analyze the E and I neurons in different layers, we refer to them as neuron *populations* of the model or a subvolume. Groups of I neurons that predominantly express either PV, Sst or 5HT3aR markers, are referred to as *inhibitory subpopulations*.

2.4 Compensating for non-modeled brain regions

Algorithm efficiently finds spectrum of network regimes compatible with *in vivo* whilst accounting for unknown *in vivo* recording bias

Initial simulations produced no activity, and it was necessary to compensate for missing excitatory input from neurons external to the model. We estimated that the number of missing synapses for the full nbS1 and seven hexagon subvolume as $\sim$ two and seven times the number of internal synapses, based on Oh et al. (2014). We model the effect of these missing synaptic inputs explicitly as time-varying and statistically independent somatic conductance injections, using Ornstein-Uhlenbeck (OU) processes that mimic aggregated random background synaptic inputs (Destexhe et al., 2001; Figure 4B1; see also Discussion). The mean (OU_μ) and standard deviation (OU_σ) are defined as a percentage of an individual cell's input conductance at its resting membrane potential. The choice of OU_μ and OU_σ for different populations and $[Ca^{2+}]_o$ (Figure 4B2), determine the model's emergent dynamics and mean firing rates (Figure 4B3). Initial simulations showed that using the same value of OU_μ and OU_σ for all neurons makes some populations highly active whilst others are silent, or produces network-wide bursts. Finding population-specific OU parameters which produce stable *in vivo*-like activity is challenging, however, due to the non-linearity and computational cost of simulations.

We developed an algorithm that efficiently calibrates population-specific OU parameters, for different values of $[Ca^{2+}]_o$, which affects the strength and reliability of synaptic transmission (see "Synaptic Physiology"). Additionally, it fixes the ratio OU_σ/OU_μ, denoted R_{OU}, across all neurons to specific values representing the amount of noise in the extrinsic inputs (Figure 4B2). As extracellularly-derived firing rates are known to be severely overestimated to an unknown degree (Olshausen and Field, 2006; Wohrer et al., 2013; Buzsáki and Mizuseki, 2014), the algorithm finds parameters which produce realistic inter-population firing rate ratios at different global levels of activity (Figure 4B3). Specifically, to account for uncertainty in the firing rate bias during spontaneous activity from extracellular spike sorted recordings it targets mean spontaneous firing rates of neuron populations that are a constant fraction P_{FR} of *in vivo* reference values, for 10 P_{FR} values between 0.1 and 1. We refer to $[Ca^{2+}]_o$, R_{OU} and P_{FR} as *meta-parameters*. The initial calibration was made for the seven hexagonal subvolume, and later generalised to the full nbS1 model.

The algorithm was first run for $[Ca^{2+}]_o = 1.1\,\text{mM}$, $R_{OU} = 0.4$. Target firing rates for the 10 P_{FR} values were reached (Figure 4C) after five iterations of 10 simulations of 6.5 seconds (Figure 4D, left upper). Only three iterations were needed when calibration began using previously calibrated parameters for different R_{OU} and $[Ca^{2+}]_o$ (Figure 4D, right upper). This allowed us to parameterize extrinsic input for a range of combinations of the three *meta-parameters* (Figure 4D, lower & 4E, left) within biologically relevant ranges

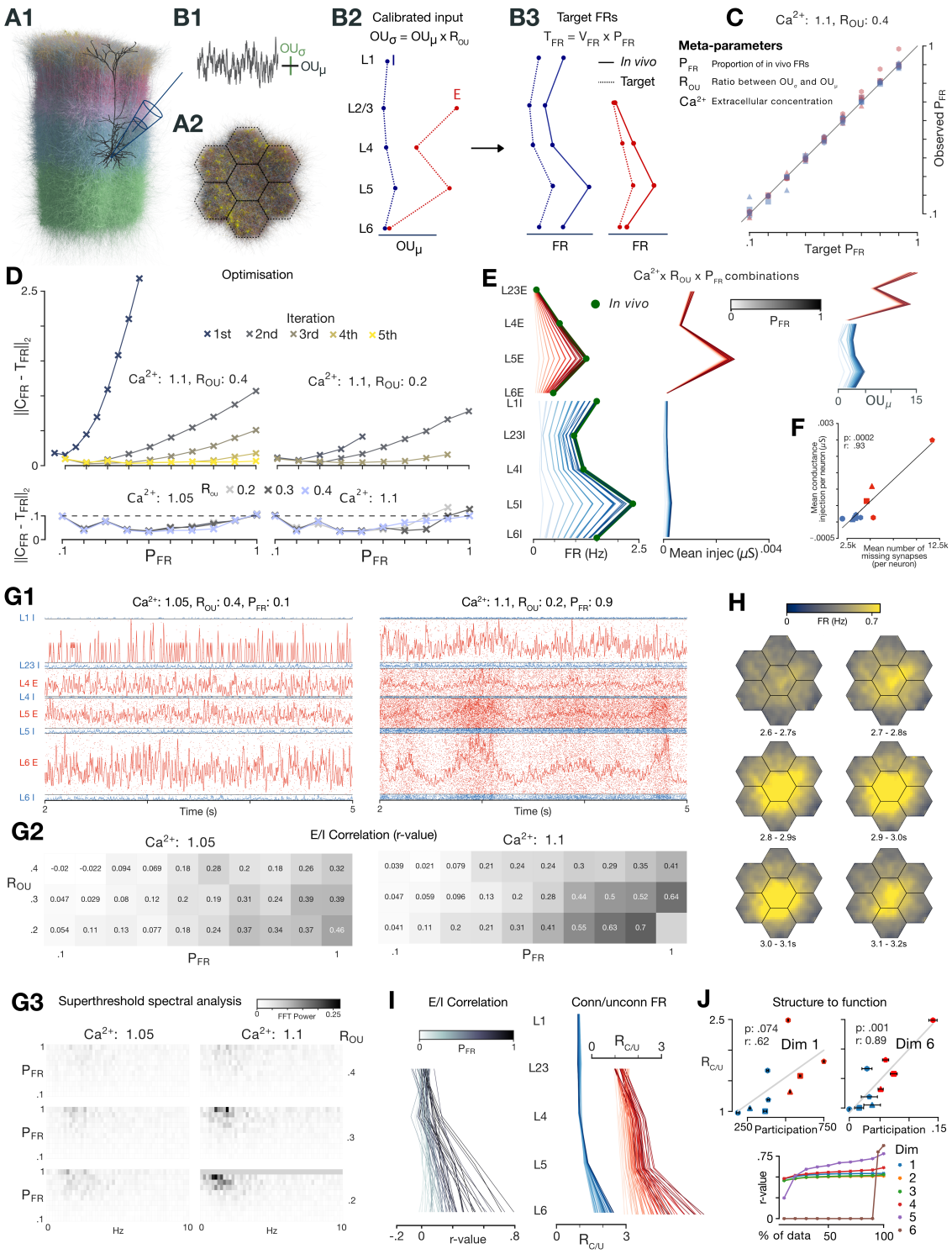
A1
B1
A2
B2 Calibrated input
OUσ = OUμ x ROU
L1
L2/3
L4
L5
L6
OUμ
B3 Target FRs
TFR = VFR x PFR
In vivo
Target
FR
C
Ca2+: 1.1, ROU: 0.4
Meta-parameters
PFR Proportion of in vivo FRs
ROU Ratio between OUσ and OUμ
Ca2+ Extracellular concentration
Observed PFR
Target PFR
D
Optimisation
Iteration
1st 2nd 3rd 4th 5th
Ca2+: 1.1, ROU: 0.4
Ca2+: 1.1, ROU: 0.2
Ca2+: 1.05
ROU 0.2 0.3 0.4
Ca2+: 1.1
PFR
E
Ca2+x ROU x PFR combinations
In vivo
L23E
L4E
L5E
L6E
L1I
L23I
L4I
L5I
L6I
FR (Hz)
Mean injec (μS)
OUμ
F
p: .0002
r: .93
Mean conductance injection per neuron (μS)
Mean number of missing synapses (per neuron)
G1
Ca2+: 1.05, ROU: 0.4, PFR: 0.1
Ca2+: 1.1, ROU: 0.2, PFR: 0.9
L1 I
L23 I
L4 E
L4 I
L5 E
L5 I
L6 E
L6 I
Time (s)
H
FR (Hz)
2.6 - 2.7s
2.7 - 2.8s
2.8 - 2.9s
2.9 - 3.0s
3.0 - 3.1s
3.1 - 3.2s
G2
Ca2+: 1.05
E/I Correlation (r-value)
Ca2+: 1.1
ROU
PFR
G3
Superthreshold spectral analysis
FFT Power
Ca2+: 1.05
Ca2+: 1.1
Hz
I
E/I Correlation
PFR
r-value
Conn/unconn FR
RC/U
J
Structure to function
p: .074
r: .62
Dim 1
p: .001
r: 0.89
Dim 6
Participation
r-value
% of data
Dim

Figure 4

Spontaneous activity: calibration, *in vivo*-like dynamics, linking structure to function. **A:** Seven column subvolume. **B:** OU_μ and OU_σ of somatic conductance injection (B1) parameterized by population (B2) determine FRs (B3). Target FRs equal to *in vivo* firing rates multiplied by P_{FR}. Inset: Table summarising meta-parameters. **C:** Target P_{FR} (x-axis) plotted against the observed P_{FR} (y-axis) for each E (red) and I (blue) population after calibration. The number of sides of the shape indicates the layer (triangle used for L2/3). **D:** Euclidean distance between target and observed P_{FR} values (over populations) decreases over iterations for two meta-parameter combinations (upper). Values after final iteration shown for all meta-parameter combinations (lower; dashed line shows termination condition). **E:** (left) Firing rates, (centre) mean conductance injection and (right) OU_μ by population for the non-bursting simulations (1 line per simulation; E and I values separated). **F:** Estimated mean number of missing number synapses per neuron by population vs. the mean conductance injection, averaged over all combinations, for each population. Markers as in C. **G1:** Max normalised histograms for two meta-parameter combinations (5 ms bin size, 1σ Gaussian smoothing). **G2:** Effect of meta-parameters on correlation between E and I histograms (5 ms bin size, 1σ Gaussian smoothing; central column). **G3:** Fourier analysis of spontaneous activity for the 59 non-bursting simulations. **H:** Activity in flat space over seven consecutive 100 ms windows. Activity smoothed (Gaussian kernel, $\sigma = 1pixel$). **I:** Left: Correlation r-value between the histograms of layer-wise E and I populations for the 59 non-bursting simulations. Right: $R_{C/U}$ by population for the 59 non-bursting simulations. **J:** Top: The mean *node participation* of E and I populations in each layer for dimension one (left) and six (right) vs. $R_{C/U}$ for the parameter combination $[Ca^{2+}]_o = 1.05\,\text{mM}$, $R_{OU} = 0.4$ and $P_{FR} = 0.3$. Markers as in C. Line shows linear fit. Bottom: Correlation r-values between mean node participation and $R_{C/U}$ when neurons with highest node participation are not included in the calculation of mean node participation (via a sliding threshold).

($[Ca^{2+}]_o$: 1.05 mM - 1.1 mM (Jones and Keep, 1988; Massimini and Amzica, 2001; Amzica et al., 2002; Gonzalez et al., 2022); P_{FR}: 0.1 - 1.0; R_{OU}: 0.2 - 0.4 (Destexhe et al., 2001)). We found that the resulting mean conductance injections were highly population-specific (Figure 4E, centre). The range of OU_μ values between populations was on average 5.2 times higher than the range of OU_μ values for a single population across meta-parameter combinations (Figure 4E, right). This was expected, as the missing mid-range innervation is known to have specific and heterogeneous laminar profiles (Felleman and Van Essen, 1991; Harris et al., 2019; Gao et al., 2022).

Population-wise input compensation correlates with estimated number of missing synapses

We estimated the number of missing synapses per neuron assuming a total density of E synapses of 1.1 synapses/μm, based on mean spine densities (Larkman, 1991; Datwani et al., 2002; Kawaguchi et al., 2006), and subtracting the number of synapses present in the model (Figure S3). We confirmed a strong correlation between this measure and required conductance injection (Figure 4F). Heterogeneity in synaptic density within and across neuron classes and sections makes estimating the number of missing synapses challenging (DeFelipe and Fariñas, 1992). Changing the assumed synaptic density value of 1.1 synapses/μm would only change the slope of the relationship, however. Estimates of mean number of existing and missing synapses per population were within reasonable ranges; even the larger estimate for L5 E (due to higher dendritic length; Figure S3) was within biological estimates of 13,000 $\pm$ 3,500 total afferent synapses (DeFelipe and Fariñas, 1992).

2.5 *In vivo*-like spontaneous activity

P_{FR}, R_{OU} and $[Ca^{2+}]_o$ determine the properties of correlative spontaneous activity

Rasters and histograms of spontaneous activity for two meta-parameter combinations are shown in Figure 4G1 (and for all combinations in Video 1). The first simulation uses a higher R_{OU}, lower P_{FR} and lower synaptic transmission reliability ($[Ca^{2+}]_o$). In the second simulation, we found larger fluctuations, correlated between E and I populations across layers. Overall, increasing $[Ca^{2+}]_o$ and P_{FR}, and decreasing R_{OU}, increases the amplitude of correlated fluctuations (Video 1; Figure 4G2) and increases power at lower frequencies (Figure 4G3). This supports the notion that decreasing R_{OU} or increasing $[Ca^{2+}]_o$ shifts the model along a spectrum from externally (noise) driven to internally driven correlated activity. Note that the most correlated meta-parameter combination $[Ca^{2+}]_o$: 1.1mM, R_{OU}: 0.2, P_{FR}: 1.0 produced network-wide "bursting" activity, which we define as highly synchronous all or nothing events (Video 1). Such activity, which may be characteristic of epileptic activity, can be studied with the model but is not the focus of this study.

We reemphasize that the $[Ca^{2+}]_o$, R_{OU} and P_{FR} meta-parameters account for uncertainty of *in vivo* extracellular calcium concentration, the nature of inputs from other brain regions and the bias of extracellularly recorded firing rates. Whilst estimates for $[Ca^{2+}]_o$ are between 1.0 - 1.1mM (Jones and Keep, 1988; Massimini and Amzica, 2001; Amzica et al., 2002; Gonzalez et al., 2022) and estimates for P_{FR} are in the range of 0.1 - 0.3 (Olshausen and Field, 2006), combinations of these parameters supporting *in vivo*-like stimulus responses in later sections will offer a prediction for the true values of these parameters. Both these later results and our recent analysis of spike sorting bias using this model (Laquitaine et al., 2024) predict a spike sorting bias corresponding to $P_{FR} \sim 0.3$, confirming the prediction of Olshausen and Field (2006).

Long-tailed population firing rate distributions with means $\sim 1\,Hz$

To study the firing rate distributions of different subpopulations and m-types, we ran 50s simulations for the meta-parameter combinations: $[Ca^{2+}]_o$: 1.05 mM, R_{OU}: 0.4, P_{FR}: 0.3, 0.7 (Figure S4). Different subpopulations showed different sparsity levels (proportion of neurons spiking at least once) ranging from 6.6 to 42.5%. Wohrer et al. (2013) considered in detail the biases and challenges in obtaining ground truth firing rate distributions *in vivo*, and discuss the wide heterogeneity of reports in different modalities using different recording techniques. They conclude that most evidence points towards long-tailed distributions with peaks just below $1Hz$. We confirmed that spontaneous firing rate distributions were long-tailed (approximately lognormally distributed) with means on the order of $1\,Hz$ for most subpopulations. Importantly the layer-wise means were just below $1\,Hz$ in all layers for the $P_{FR} = 0.3$ meta-parameter combination. Moreover, our recent work applying spike sorting to extracellular activity using this meta-parameter combination found spike sorted firing rate distributions to be lognormally distributed and very similar to *in vivo* distributions obtained using the same probe geometry and spike sorter (Laquitaine et al., 2024).

Spatially-coordinated fluctuations and increase in correlative and recurrent activity from supra- to infragranular layers

In the horizontal dimensions, under higher correlation regimes, fluctuations are spatially coordinated and global within the central hexagon of the simulated subvolume (Figure 4H; Video 2). In depth, the size of fluctuations and level of correlated activity increases from supragranular to infragranular layers (Figure 4G1, I, left; Video 1), suggesting that activity in deeper layers of the model is more internally driven. We characterized the effect of recurrent connectivity by measuring the layer-specific decrease in firing rates when neurons in the model are disconnected from each other. As expected, we found that the effect (quantified by the ratio between connected and disconnected firing rates: $R_{C/U}$) increased from supra- to infragranular layers (Figure 4I, right).

High-dimensional connectivity motifs predict layer-wise spontaneous activity

By analysing the underlying network structure, we observed a corresponding gradient in the topology of intra-layer synaptic connectivity from supra- to infragranular layers. We calculated the mean *node participation* of neuron populations in various dimensions (see Methods; Figure 4J, top). For dimension one, this is simply the degree of a neuron; for dimensions above one, this generalizes the notion to counting participation in dense, directed motifs of increasing size (*directed simplices*; Reimann et al., 2017). We found that correlations of this measure with the ratio of connected and disconnected firing rates increased with dimension (Figure 4J, bottom, 100% of data), indicating the importance of large directed simplices in shaping activity. Curiously, the correlations for higher dimensions were driven by a small number of neurons with very high node participation. This was indicated by a sharp drop in correlation when neurons above a given value were excluded (Figure 4J, bottom). Additionally, we studied the structural effect on the firing rate (here measured as the inverse of the inter-spike interval, ISI, which can be thought of as a proxy of non-zero firing rate). We found that for the connected circuit, the firing rate increases with simplex dimension; in contrast with the disconnected circuit, where this relationship remains flat (see Figure S6 red vs. blue curves and Methods).

This also demonstrates high variability between neurons, in line with biology, both structurally (Towlson et al., 2013; Nigam et al., 2016) and functionally (Wohrer et al., 2013; Buzsáki and Mizuseki, 2014). We next identified the cell types that are overexpressed in the group of neurons that have the 5% highest values of node participation across dimensions (Figure S7). This could inform theoretical point neuron models with cell-type specificity, for example. We found that while in dimension one (i.e., node degree) this consists mostly of inhibitory cells, in higher dimensions the cell types concentrate in layers 4, 5 and 6, especially for TPC neurons. This is in line with our structural layer-wise findings in Figure 8B in Reimann et al. (2024).

2.6 Stimulus-responses reproduce *in vivo* dynamics with millisecond-scale precision

Recreating simple whisker deflection experiments

We compared stimulus-responses with *in vivo* barrel cortex responses to both *single whisker deflections* and *active whisker touches* under anaesthetized (Reyes-Puerta et al., 2015b) and awake states (Yu et al., 2019) respectively. While the model is of non-barrel somatosensory regions, this nevertheless provides validations of overall excitability and the laminar structure of responses reflecting general trends of cortical processing. We ac-

tivated a percentage (F_P) of the VPM fibers projecting to the central column of the seven column subvolume (Figure 5A1). For each selected thalamic fiber, spike times were drawn from VPM PSTHs (peristimulus time histogram) recorded *in vivo* for the two stimulus types (Figure 5A2; Methods). For both stimulus types, a single thalamic stimulus was presented 10 times at 1 s intervals at three intensities ($F_P : 5\%, 10\%, 15\%$).

Validation of millisecond precise *in vivo* population responses and corresponding prediction of *in vivo* spontaneous firing rates

For the parameter combination $[Ca^{2+}]_o = 1.05\,\text{mM}$, $R_{OU} = 0.4$, $P_{FR} = 0.3$ and $F_P = 10\%$, E and I populations in each layer show clear responses on each trial (Figure 5B; three trials shown), except for L1. Videos 3 and 4 show all simulated combinations of the four meta-parameters. Out of 72 parameter combinations, 21 passed an initial assessment of *in vivo* similarity to the *in vivo* data based on latencies and decays (see Methods, Figure 5C, S5). Responses remained localized to within $600\,\mu m$ of the stimulus location (Figure 5D, Video 5). *In vivo*, layer-wise I populations precede the corresponding E populations and response latencies increase with distance from thalamus, except for the fast response of L4 I. The latencies and decays are matched by criteria passing simulations (Figure 5C, E, left), except for a longer L4 I latency, and shorter and longer sustained responses of L2/3 E and L4 E. PV+ and Sst+ subpopulations respond reliably in layers 2-6, but the 5HT3aR+ subpopulation responses are weaker and less reliable (Figure S5). Under the active whisker touch paradigm, PV+ latencies precede Sst+ latencies *in vivo*, and either precede or are simultaneous with Sst+ latencies *in silico* (Figure 5E, right).

The passing parameter combinations form a contiguous region in the parameter space (Figure 5F), characterized by combinations of low P_{FR}, $[Ca^{2+}]_o$ and F_P with higher R_{OU}, which displayed weakly correlated spontaneous activity (compare Figure 5F with Figure 4G2). This offers a prediction that true *in vivo* firing rates are within the range of these lower FRs. Specifically, simulations with P_{FR} from 0.1 to 0.5 robustly support realistic stimulus responses, with the middle of this range (0.3) corresponding with estimates of *in vivo* recording bias; both the previous estimates of Olshausen and Field (2006) and from a spike sorting study using this model (Laquitaine et al., 2024). The remaining results apply to the criteria passing simulations. We characterized the magnitude of responses by R_E, the ratio between the peak of the evoked response and the pre-stimulus baseline activity level. Assuming that extracellular sampling biases are similar during spontaneous and evoked activity, R_E provides a bias-free metric for comparing response magnitude with *in vivo*. Decreasing R_{OU} and P_{FR}, and increasing $[Ca^{2+}]_o$ and F_P led to a global increase of R_E, and results matched *in vivo* closely for a large part of the parameter space (Figure 5F).

Interestingly, the parameter combination closest to *in vivo* was central in the parameter space of criteria passing simulations (Figure 5G, left). Values of R_E, normalized by the mean R_E across populations, were remarkably constant (Figure 5G, right), indicating that variation of the parameters provides a global scaling of response magnitude. Moreover, I populations matched the *in vivo* reference closely, while the responses of L2/3 E were slightly greater, and for L4 E and L5 E slightly weaker. The region of the parameter space where responses match *in vivo* for the active whisker touch stimulus was the same as for single whisker deflections (Figure S8). Latencies were also similar to *in vivo*, with the main discrepancy being slower responses in L4 (E and I). With respect to the meta-

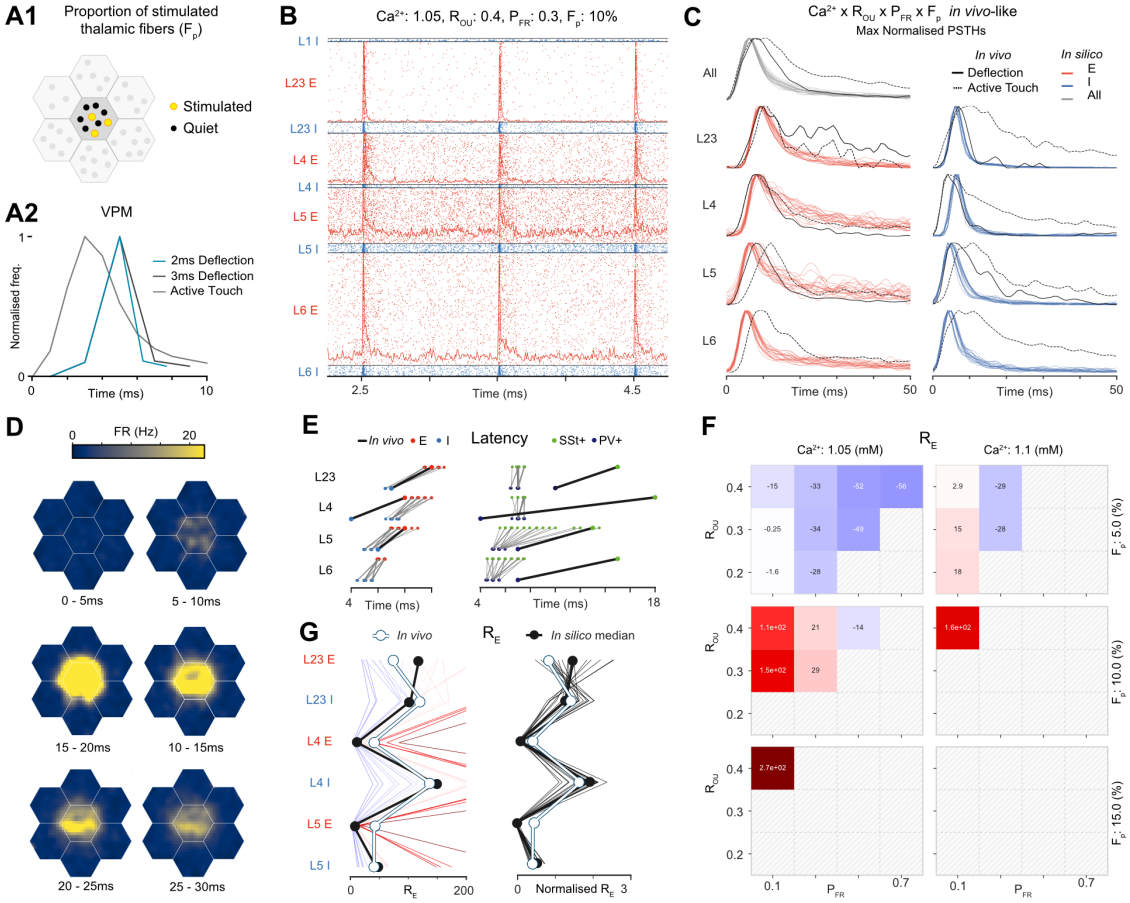

Figure 5: Layer-wise population responses to single whisker deflection and active whisker touch stimuli closely match *in vivo* millisecond dynamics and response amplitudes. A1: Stimuli are simulated by activating a proportion (F_P) of fibers projecting to the central hexagon of the seven column subvolumne. **A2:** Each fiber is assigned a spike time from a PSTH of VPM activity recorded *in vivo* for either a single whisker deflection or active whisker touch paradigm. **B:** Spiking activity and histograms (baseline and max normalised) for each layer-wise E and I population for the parameter combination $[Ca^{2+}]_o = 1.05\,\text{mM}$, $R_{OU} = 0.4$, $P_{FR} = 0.3$ and $F_P = 10\%$ for a 2.5s section of the 10 whisker deflection test protocol. **C:** Trial-averaged PSTHs (baseline and max normalised) in response to the single whisker deflection stimulus for all of the parameter combinations which passed the initial criteria, and the *in vivo* references. **D:** Spatiotemporal evolution of the trial-averaged stimulus response in flat space for the same parameter combination in B. **E:** Left: Latencies of different layer-wise E and I populations for all criteria passing combinations in response to single whisker deflection stimuli. Right: Latencies for inhibitory interneuron subpopulations in response to active whisker touch stimuli. Correponding *in vivo* references are shown. **F:** Heatmap showing the effect of the meta-parameters on the difference of R_E for the entire central column from the corresponding *in vivo* reference. Parameter combinations which failed the criteria tests are masked. **G:** Left: Ratio R_E between maximum evoked response and spontaneous baseline activity by population. One line per simulation. Simulation line colour shows the difference of R_E for the entire central column from the corresponding *in vivo* reference (color values shown in G). Thick black line shows median of *in silico* values. White shows *in vivo* reference. Right: Normalised ratios of each simulation by dividing by R_E for the entire central column.

parameters, we found that the best match for the anesthetized state was characterized by lower firing rates (P_{FR}) and reduced external noise levels (lower R_{OU}) compared to the awake active whisker touch paradigm (white areas in Figures 5F and S8B). These results

fit expectation for anaesthetized and awake states respectively, and provide predictions of their spontaneous firing rates, noise levels and corresponding *in silico* regimes.

Prediction of 2-9% population response sparsity

Response sparsity (i.e. the proportion of neurons spiking at least once following a stimulus) varied across populations and meta-parameter combinations, but was around the range of 10-20% reported *in vivo* in the barrel cortex (Barth and Poulet (2012); Figure S5D). Interestingly, excitatory population responses were sparser than the corresponding inhibitory layer-wise populations across layers. The observed heterogeneous layer-wise population sparsities offer a prediction for *in vivo*. Moreover, the majority of responding cells spike only once to single whisker whisker deflections (Figure S5E), as reported *in vivo* (Isbister et al., 2021).

2.7 Validation and prediction through reproduction and extension of complex laboratory experiments using a single model parameterization

Building upon the *in vivo*-like activity states, we combined various simulation techniques to recreate laboratory experiments from the literature (see Methods). For these experiments, we use the parameter combination: $[Ca^{2+}]_o = 1.05\,\text{mM}$, $R_{OU} = 0.4$ and $P_{FR} = 0.3$, as this combination supports realistic *in vivo*-like responses to the two stimulus types over a range of fiber percentages (F_P).

2.7.1 Exploring the canonical model: layer-wise contributions to L2/3 stimulus-responses

In the canonical model of the cortex (reviewed e.g., in Lübke and Feldmeyer, 2007; Feldmeyer, 2012) information from the thalamus arrives to L4, then propagates to L2/3, from there to L5 (which serves as the main cortico-cortical output layer) and lastly to L6 (which projects back to the thalamus). The coordinated action of all layers of S1 is required for high-level behavioral tasks (Park et al., 2020). As the canonical model is based on the highest layer-wise density of axons, it cannot describe all interactions in the cortex. For example VPM does not only innervate L4, but also the border of L5 and L6, as well as the bottom of L2/3 (Meyer et al., 2010; Constantinople and Bruno, 2013; Sermet et al., 2019).

Recreating modulation of L2/3 PCs during optogenetic inactivation of L4 PCs during whisker deflection

To study how L4 contributes to the stimulus preference of L2/3 PCs, Varani et al. (2022) used optogenetic inactivation of L4 PCs during whisker stimulation and quantified the changes in the subthreshold response of L2/3 PCs. They found, that the early phase of the subthreshold response significantly differed from the control condition, if the whisker was deflected in either the most or the least preferred direction (see the top and bottom rows of their Figure 5B, C). From this they concluded that both L4 and VPM contribute to the direction tuning of L2/3 PCs. After reproducing their experimental conditions *in silico* (Figure 6A,B; Figure S9; see Methods) we confirmed that we can reproduce their results, i.e., subthreshold responses of L2/3 PCs decreased, when L4 PCs were inhibited (Figure 6C for preferred direction whisker stimulation; see Methods).

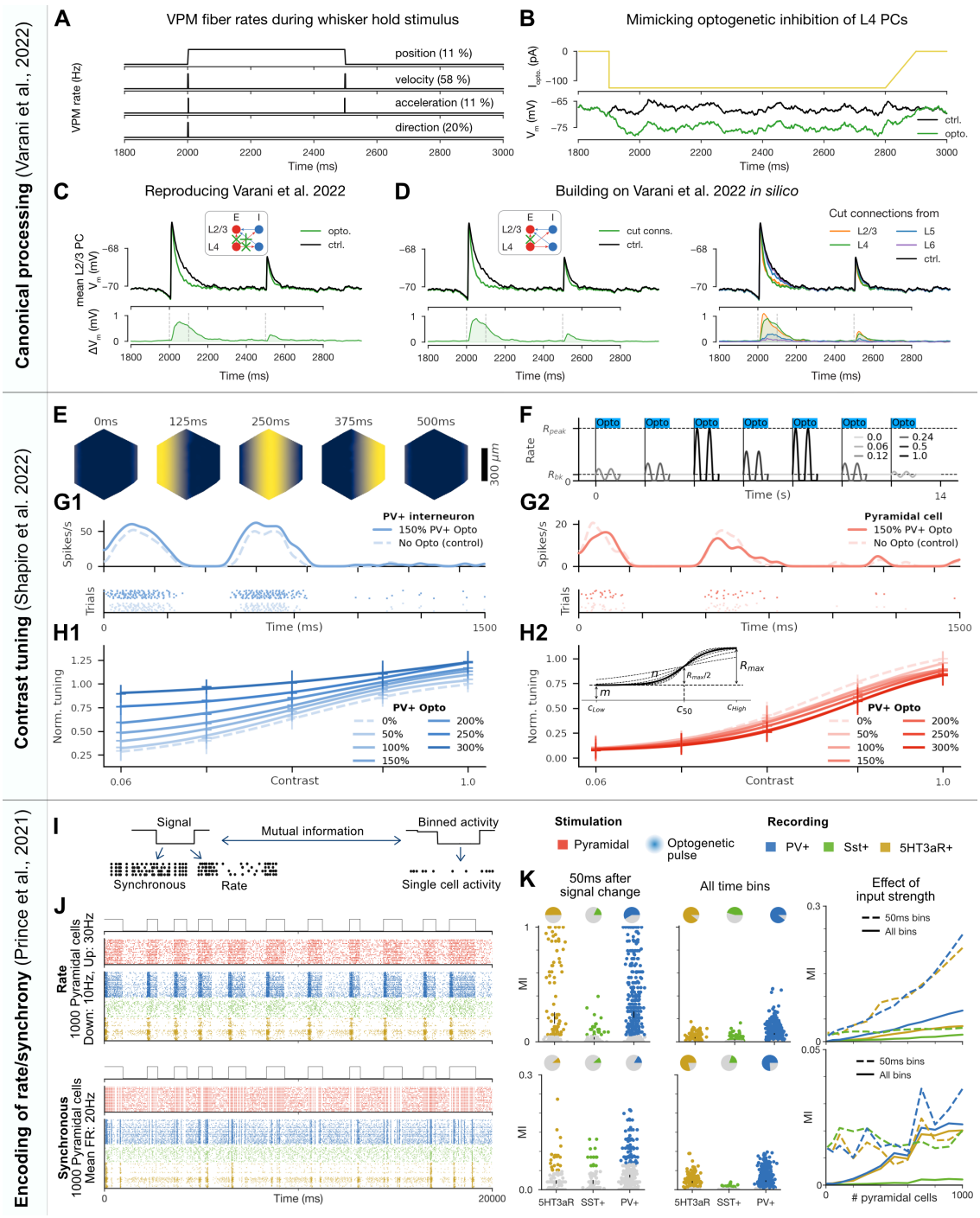

Figure 6: Reproducing and extending detailed experiments exploring the canonical model and encoding of contrast, rate-coded and synchronous information.
First experiment: Reproducing the effect of optogenetic inactivation of L4 pyramidal cells on L2/3 stimulus responses and predicting the role of other pathways through circuit lesions. **A:** Schematics of whisker kinetics and VPM fiber rates during 500 ms long whisker hold stimulus. Fraction of VPM fibers coding for each kinetic feature are taken from Petersen et al. (2008). **B:** Mimicking the effect of activation of the Halo inhibitory opsin *in silico*. Injected somatic hyperpolarizing current mimicking opsin activation (top), and the resulting somatic voltage trace from a combination of injected conductance, current, and synaptic PSPs from the network (bottom).

C: Comparison of average traces from selected L2/3 PCs (see Methods) in control (black) and optogenetically inhibited (green) conditions. **D:** Same as C, but instead of mimicking the optogenetic inhibition of L4 PCs, only the connections to L2/3 PCs are "cut" (compare inset with the one in C). The right part depicts connections systematically cut from PCs in all layers, while the left shows L4 only for a better visual comparison with the conditions of Varani et al. (2022) in C.
Second experiment: Contrast tuning modulation by optogenetic activation of PV+ interneurons. **E:** Spatial distribution of firing rates of VPM fibers projecting to a single simulated column at different points in time, corresponding to linear drifting gratings with a temporal frequency of $f_{temp} = 2\,\text{Hz}$ and a spatial frequency of $f_{spat} = 0.001\,\text{cycles}/\mu\text{m}$. **F:** Firing rate signal of a single VPM fiber corresponding to a random sequence of drifting grating patterns with different contrast levels C, as indicated by the legend. All optogenetic stimuli targeting PV+ (or Sst+) interneurons were completely overlapping with the grating stimulus intervals, as indicated by the blue bars. **G1:** Spiking activity and PSTH of an exemplary PV+ interneuron over 10 repetitions (trials) in response to a grating stimulus at maximum contrast ($C = 1.0$) without (control) and with medium strength (150%) optogenetic stimululation. **H1:** Contrast tuning modulation of an exemplary PV+ interneuron by different levels of PV+ optogenetic stimulation, ranging from 0% (control) to 300%. The individual markers denote actual data points (mean ± SD over 10 repetitions, normalized to baseline response at maximum contrast) while curves illustrate sigmoidal fits to these data points. **G2/H2:** Same as C1/D1, but for exemplary PCs. **H2 inset:** Illustration of sigmoidal parameters m, n, R_{max}, and c_{50}.
Third experiment: Encoding of synchronous and rate-coded signals by interneuron subtypes. **I:** A binary signal is encoded either through changes in the rate or synchronicity of optogenetic pulses applied to a set of PCs. We define a direct correspondence between single optogenetic pulses and single spikes. Spiking activity is measured in PV+, Sst+ and 5HT3aR+ cells, and the mutual information between the binned activity of individual cells and the original binary signal is measured. **J:** Visualization of the rate (upper) and synchronous (lower) coded stimulus experiments stimulating 1000 PCs, showing the binary signal (top), input neuron spike trains for 40 neurons (middle), and responses of the three L2/3 neuron types (bottom). **K: Upper:** Results for the rate coded stimulus experiment. Left: Mutual information between spiking activity and the binary signal (one point for each cell that spiked at least once). Only activity in the 50 ms following the change of the binary signal is considered. Cells with mutual information not significantly different from that of a shuffled control are coloured grey. Centre: Same as left but considering all time bins. Right: The effect of the number of stimulus neurons on the mean single cell mutual information for each subpopulation. **Lower:** The same as upper but for the synchronous stimulus type.

Prediction that L4 PCs enhance L2/3 PC responses directly, not through disynaptic inhibition

We then leveraged our *in silico* setup to study what Varani et al. (2022) could not, because of methodological limitations. In our reading, the authors aimed to test how direct E connections from L4 PCs to L2/3 PCs influence the stimulus representation in L2/3. This connection can not specifically be blocked *in vivo*, instead (95% of) the L4 PC population is inhibited (as well as some lower L3 PCs). In our setup we could selectively block the connection and found almost the same result (compare Figure 6C and D, left). This extends the conclusion of Varani et al. (2022): L4 PCs contribute to the stimulus preference of L2/3 PCs via direct E connections, and not via disynaptic inhibition.

Prediction of the contribution of different layer-wise populations to L2/3 PC response

The authors also discussed studying L5 PCs' contribution to L2/3 responses (as a large fraction of L5 PC axons terminate in L2/3), but this is infeasible with current mouse lines. Leveraging our model, we found that L5 contributes much less to subthreshold

L2/3 traces than L4 (Figure 6D, right). Extending to other presynaptic layers, we found that the contribution of L2/3 is similar to that of L4, whereas inputs from L6 are negligible (Figure 6D, right). Whilst mouse lines targeting L5 PCs might arrive soon (which could validate our prediction), blocking L2/3 connections between L2/3 cells without hyperpolarizing the same L2/3 population seems only achievable *in silico*.

2.7.2 Recreation of contrast tuning modulation by optogenetic activation of PV+ interneurons

Shapiro et al. (2022) compared the modulatory effects of optogenetic activation of interneuron subtypes on contrast tuning of neurons in V1. Whilst visual regions differ from somatosensory regions, the study provided an opportunity to explore the generality of interactions between E and I subpopulations. We therefore created a version of the study *in silico*, presenting spatio-temporally modulated patterns with various contrast levels through the VPM inputs (Figure 6E,F; see Methods).

Overall, we found within the single simulated column 228 PCs and 259 PV+ interneurons with robust contrast tuning of their responses (see Methods). Within spike detection range of a vertically penetrating extracellular electrode (50 μm; Henze et al. (2000); Buzsáki (2004)), we found 15 PCs and 13 PV+ interneurons with robust tuning, which is roughly comparable to the original study (average of 8.2 tuned PCs and 3.0 PV+ neurons per mouse Shapiro et al., 2022). Unlike the original study we found no Sst+ neurons with robust tuning.

Additionally, we found the following results, all in line with (Shapiro et al., 2022): The firing rates of both PCs and PV+ neurons were affected by optogenetic activation of the PV+ subpopulation (Figure 6G), resulting in changes to the contrast tuning curves of these populations (Figure 6H, S12A). The main effect of the optogenetic manipulation was an increase in contrast tuning for PV+ and a decrease for PCs. However, at high contrasts, we observed a paradoxical effect of the optogenetic stimulation on L6 PV+ neurons, reducing their activity with increasing stimulation strength (Figure S12B; cf. Mahrach et al. (2020)). This effect did not occur under grey screen conditions (i.e., at contrast 0.0) with a constant background firing rate of 0.2 Hz or 5 Hz respectively (not shown). The individual tuning curves could be accurately fit by sigmoidal functions ($r^2_{PV+} = 0.995 \pm 0.008$; $r^2_{PC} = 0.990 \pm 0.012$), and consequently the effect of optogenetic activation could be quantified in terms of changes to the fitted parameters (Figure 6H2 inset, S13; Methods). We found great variability between neurons with increasing trends for parameter m in PV+ and c_{50} in PCs, and decreasing trends for R_{max} in PV+ and both m and R_{max} in PCs. Unlike in (Shapiro et al., 2022), we found in addition an increasing trend of c_{50} also in PV+ interneurons (Figure S13).

Comparing three abstract mathematical models (Shapiro et al., 2022; Methods), we found that the saturation additive model best captured the effect of the optogenetic manipulation for PV+ neurons (Figure S14A, B1), as in the reference study. The relative contributions of saturation and addition varied strongly between individual neurons (Figure S14C1). At low intensities of the optogenetic manipulation, this distribution matched qualitatively the results of Shapiro et al. (2022), but at higher intensities we observed a shift towards stronger saturation. Combining the saturation additive model with a simpli-

fied, population-level model of PC firing (Shapiro et al., 2022; Methods) provided a good description of the observations (Figure S14B2) with relative contributions of saturation and addition that qualitatively match the reference (Figure S14C2).

2.7.3 Encoding of synchronous and rate-coded signals by inhibitory subpopulations

Prince et al. (2021) studied how different I subpopulations represent signals that are encoded as changes in the firing rate or synchronicity of PCs (Figure 6I). We repeated their study *in silico* (Figure 6J), but using *in vivo*-like conditions as the authors have suggested in their Discussion. The original study pointed out the importance of membrane properties and short-term dynamics of synaptic inputs onto the subpopulations in shaping the results. Note, that the lower synaptic reliability *in vivo* weakens synaptic depression (Borst, 2010), and the ongoing background input leads to higher membrane conductance (Destexhe et al., 2001); therefore our results are expected to differ substantially, and provide an independent prediction for a different dynamic state. While in the original *in vitro* study stimulation of 10 PCs was sufficient to find a decodable signal, we expected a larger number to be required under our *in vivo*-like conditions, due to the lower $[Ca^{2+}]_o$, and the higher level of noise (see Methods).

Indeed, we found little discernible mutual information in I spiking for the activation of 10 PCs, but that mutual information increased with the number of activated neurons (Figure 6K, right). For 1000 activated neurons each of the three I subpopulations in L2/3 showed clear but qualitatively unique modulation for both encoding schemes (Figure 6J). As in (Prince et al., 2021) we found differences in the encoding capabilities of the I subpopulations (Figure 6K). We found strongest encoding in PV+ neurons for both schemes, and overall low encoding strength in Sst+ neurons. Further, we found overall low amounts of mutual information for the synchronous stimulus, which is in line with Prince et al. (2021), as they linked encoding of that stimulus to depressing synaptic dynamics, which would be weakened *in vivo*.

2.8 Exploring the effect of inhibitory targeting trends observed in electron microscopy (EM)

Additional targeting rules recreate quantitative EM-connectivity trends

We next explored how certain trends in inhibitory targeting observed in a recent mouse electron microscopic connectome (Schneider-Mizell et al., 2023; Figure 7A) affect spontaneous and evoked activity. Consequently, an alternative connectome which quantitatively recreates these trends has been built (Reimann et al., 2024). We refer to this as the Schneider-Mizell compatible connectome (SM-connectome). It ensures that PV+ neurons target the perisomatic region, VIP+ neurons target other inhibitory neurons, and cells in L1 connect predominantly monosynaptically. Consequently, inhibition onto E neurons is sparser and closer to the soma (Figure 7A2). After validating the presence of these trends, we characterized how this affects the dynamics of the spontaneous and evoked states (Figure 7A3). Note, that individual synapses were recalibrated to preserve the pathway specific reference PSP amplitudes. As expected, the largest change was for PV+ neurons where the average number of vesicles in the release-ready pool N_{RRP} was increased by 2.4 times.

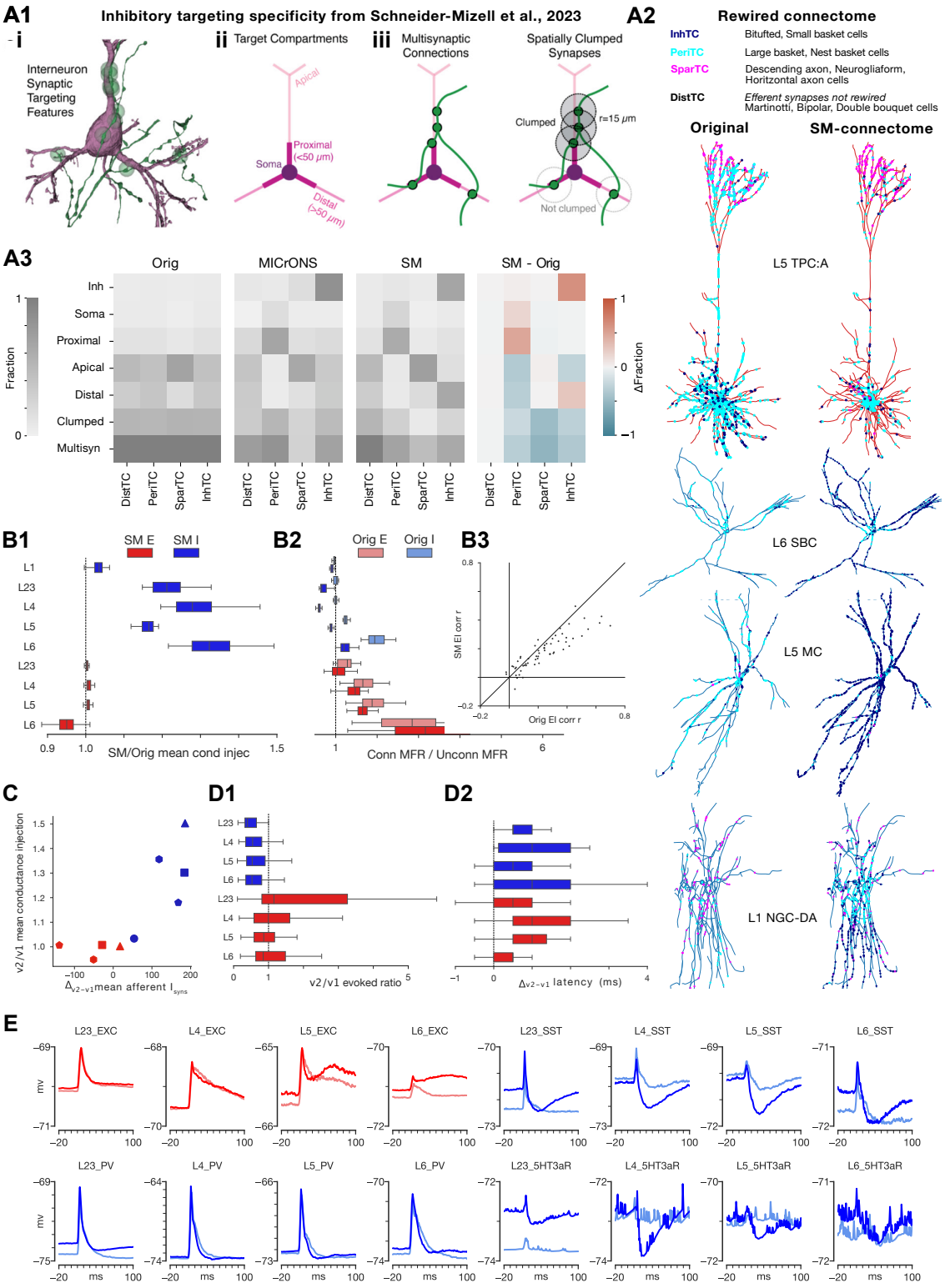

Figure 7: The effect of inhibitory targeting trends observed in electron microscopy on spontaneous and stimulus-evoked activity. A1: Panel illustrating interneuron synaptic targeting features and caption taken from Schneider-Mizell et al. (2023) (under CC-BY 4.0 license). i) For determining inhibitory cell subclasses, connectivity properties were used such as an axon

(green) making synapses (green dots) the perisomatic region of a target pyramidal cell (purple). ii) Dendritic compartment definitions for excitatory neurons. iii) Cartoon of a multisynaptic connection (left) and the synapses within the multisynaptic connection considered "clumped" along the presynaptic axon (right). **A2:** Exemplar neurons showing the synapse locations from different inhibitory m-type groupings in the original and SM connectome respectively: Distal targeting (DistTC: martinotti, bipolar, double bouquet cells), Perisomatic targeting (PeriTC: large basket, nest basket cells), Sparse targeting (SparTC: descending axon, neurogliaform, horitzontal axon cells), Inhibitory targeting (InhTC: bitufted, small basket cells). **A3:** Heatmaps showing the mean fraction of efferent synapses from the inhibitory m-type groupings onto inhibitory neurons, somas, proximal dendrites, apical dendrites, distal dendrites, or that are part of clumped or multisynaptic connections. Heatmaps show mean fractions (left to right) for the original, Schneider-Mizell et al. (2023) characterization of the MICrONS dataset ((MICrONS-Consortium et al., 2021)), SM-connectome, and the change between the original and SM-connectome. **B1:** Proportional change in mean conductance injection between original and SM-connectome by population. **B2:** Distribution of ratios between connected and disconnected firing rates ($R_{C/U}$) by population over non-bursting meta-parameter combinations for original and SM-connectome. **B3:** Comparison of correlation (r-values) between E and I histograms (5 ms bin size, 1σ Gaussian smoothing; central column) between original and SM-connectome (each point represents a specific meta-parameter combination). **C:** Scatter plot showing the change in the mean number of afferent inhibitory synapses onto each E (red) and I (blue) population after calibration versus the proportional change in mean conductance injection. The number of sides of the shape indicates the layer (triangle used for L2/3). **D1:** Proportional change in the the ratio between the peak of the evoked response and the pre-stimulus baseline activity level (R_E) between the original and SM-connectome. Plot shows distribution over meta-parameter combinations which passed the the initial assessment of *in vivo* similarity to the in vivo data based on latencies and decays (see Methods). **D2:** Change in the latencies of populations peak responses between original and SM-connectome (distribution over same meta-parameter combinations shown in D1). **E:** Mean membrane potential responses for layer-wise subpopulations for the meta-parameter combination $[Ca^{2+}]_o = 1.05\,\text{mM}$, $R_{OU} = 0.4$, $P_{FR} = 0.3$ and $F_P = 10\%$. Responses averaged over 20 stimulus repetitions with an inter-trial-interval of 500ms.

EM targeting trends increase inhibition of inhibitory populations enabling increased long-range excitation

Inspite of this, the change in connectivity affected the activity sufficiently that recalibration of missing synaptic compensation was needed to attain the target firing rates for the original meta-parameter combinations (Figure S15). Mean conductances onto I neurons had to be increased, indicating the efficacy of the newly introduced I-I targeting by VIP+ neurons (Figure 7B1). On the other hand, conductances for E neurons remained roughly the same, except for L6. Curiously, we found that the firing rates of I populations were reduced when the internal connectivity was activated compared to when it was inactive, further highlighting the efficacy of the I-I targeting (Figure 7B2, S15). For E neurons in L2-5, activating internal connectivity increased firing rates, but less than in the original connectome. As the number of inhibitory synapses innervating them decreased (Figure 7A2), this indicates that the placement of PV+ synapses closer to the soma increased the efficacy of inhibitory as expected. Taken together, this indicates that in the SM-connectome, I populations are more externally driven and more internally inhibited (as a function of proximity to L4), and L6 E more internally driven during spontaneous activity. Over the different meta-parameter combinations, correlation in the network decreased relative to the original circuit with some exceptions (Figure 7B3, S15). This indicates, that activity in the SM-connectome is shifted slightly towards a more asynchronous state.

By correlating the structural and functional changes we concluded that the increased conductance injection into the I populations can be explained by the increased inhibitory synapse count (Figure 7C). Conversely, the mostly decreased synapse counts for E populations did not lead to a decrease of conductance injection, further indicating that the more perisomatic positioning of PV+ synapses compensates for the reduced synapse counts.

EM targeting trends affect population-wise stimulus-evoked response magnitudes and latencies

The lack of effect onto most of the E populations disappeared in the evoked state (Figure 7D). Overall, responses increase strongly in L23 and slightly decreased in L5 and L6 (Figure 7D1), while latencies of responses increased in every layer (Figure 7D2), suggesting different roles of the more specific inhibitory targeting in different layers.

EM targeting trends hyperpolarize Sst+ and HT3aR+ late response, and disinhibit L5/6 E

Studying somatic membrane potentials for different subpopulations in response to whisker deflections shows that PV+, L23E and L4E subpopulations are largely unaffected in the SM-connectome (Figure 7E). Interestingly, Sst+ and 5HT3aR+ subpopulations show a strong hyperpolarization in the late response that isn't present in the original connectome. Interestingly, this corresponds with a stronger late response in L5/6 E populations, which could be caused by disinhibition due to the Sst+ and 5HT3aR+ hyperpolarization. This could be explored further in follow up studies using our connectome manipulator tool (Pokorny et al., 2024).

2.9 Mid-range connectivity determines independent functional units and selective propagation of stimulus-responses at larger spatial scales

Stable spontaneous activity only emerges in nbS1 at predicted *in vivo* firing rates

After calibrating the model of extrinsic synaptic input for the seven column subvolume, we tested to what degree the calibration generalizes to the entire nbS1. Notably, this included the addition of mid-range connectivity (Reimann et al., 2024). The total number of local and mid-range synapses in the model was 9138 billion and 4075 billion, i.e., on average full model simulations increased the number of intrinsic synapses onto a neuron by 45%. Particularly, we ran simulations for $P_{FR} \in [0.1, 0.15, ..., 0.3]$ using the OU paramaters calibrated for the seven column subvolume for $[Ca^{2+}]_o = 1.05\,\text{mM}$ and $R_{OU} = 0.4$. Each of these full nbS1 simulations produced stable non-bursting activity (Figure 8A), except for the simulation for $P_{FR} = 0.3$, which produced network-wide bursting activity (Video 6). Activity levels in the simulations of spontaneous activity were heterogeneous (Figure 8B, Video 7). In some areas, firing rates were equal to the target P_{FR}, whilst in others they increased above the target (Figure 8C). In the more active regions, mean firing rates (averaged over layers) were on the order of 30-35% of the *in vivo* references for the maximum non-bursting P_{FR} simulation (target P_{FR} : 0.25). This range of firing rates again fits with the estimate of firing rate bias from our paper studying spike sorting bias (Laquitaine et al., 2024) and the meta-parameter range supporting realistic stimulus responses in the seven column subvolume. This also predicts that the nbS1 cannot sustain higher firing rates without entering a bursting regime.

Independent functional subunits emerge during spontaneous activity with accurate layer and distance-dependence of noise correlations

The subregion with consistently higher firing rates was the upper-limb representation (S1ULp), separated from subregions of lower activity by the dysgranular zones (S1DZ, S1DZO). This demonstrates that the larger spatial scale of the model supports several independently acting functional units. Locations with higher firing rates were accompanied by higher spiking correlations of the local population (Figure 8B2, Video 7), indicating activity that was more driven by intrinsic excitation. Unlike in the simulations of smaller volumes, the correlation emerged mostly from short, transient packets of activity in L6 (Figure 8A). Consequently, deviation from the target P_{FR} in those cases was largest in L6 (Figure 8C). Taken together, it appears as if the additional synapses from mid-range connectivity moved the model along the spectrum from extrinsically vs. intrinsically driven, but further for some regions than for others. We confirmed a divergence into two populations: one with correlation slightly increased from the simulations of smaller volumes, and one with almost maximal correlations (Figure 8D). This distinction was determined mostly in L6 with increases of correlations in other layers remaining small.

The distance dependence of correlations followed a similar profile to that observed in a dataset characterizing spontaneous activity in the somatosensory cortex (Reyes-Puerta et al., 2015a) (compare red line in Figure 8I with Figure S16). In the *in vivo* dataset spiking correlation was also low but highest in lower layers, with short "up-states" in spiking activity constrained to L5 & 6 (see Figure 1E,F in (Reyes-Puerta et al., 2015a)). In the model, they are constrained to L6.

Stable propagation of evoked activity through mid-range connectivity only emerges in nbS1 at predicted *in vivo* firing rates

We repeated the previous single whisker deflection evoked activity experiment in the full model, providing a synchronous thalamic input into the forelimb sub-region (S1FL; Figure 8E; Video 8 & 9). Responses in S1FL were remarkably similar to the ones in the seven column subvolume, including the delays and decays of activity (Figure 8F). However, in addition to a localized primary response in S1FL within 350 μm of the stimulus, we found several secondary responses at distal locations (Figure 8E; Video 9), which was suggestive of selective propagation of the stimulus-evoked signal to downstream areas efferently connected by mid-range connectivity. The response of the main activated downstream area (visible in Figure 8E) was confined to L6 (Figure 8G). In a follow up study using the model to explore the propagation of activity between cortical regions (Bolaños-Puchet and Reimann, 2024), it is described how the model contains both a feedforward projection pattern, which projects to principally to synapses in L1 & L23, and a feedback type pattern, which principally projects to synapses in L1 & L6. On visualizing the innervation profile from the stimulated hexagon to the downstream hexagon we can see that we have stimulated a feedback pathway (Figure S16).

Membership in mid-range connectivity rich club predicts correlation of spontaneous activity

As the model is homogeneous across the different subregions in terms of neuronal morphologies and physiology, we expected the differences in spontaneous and evoked activity

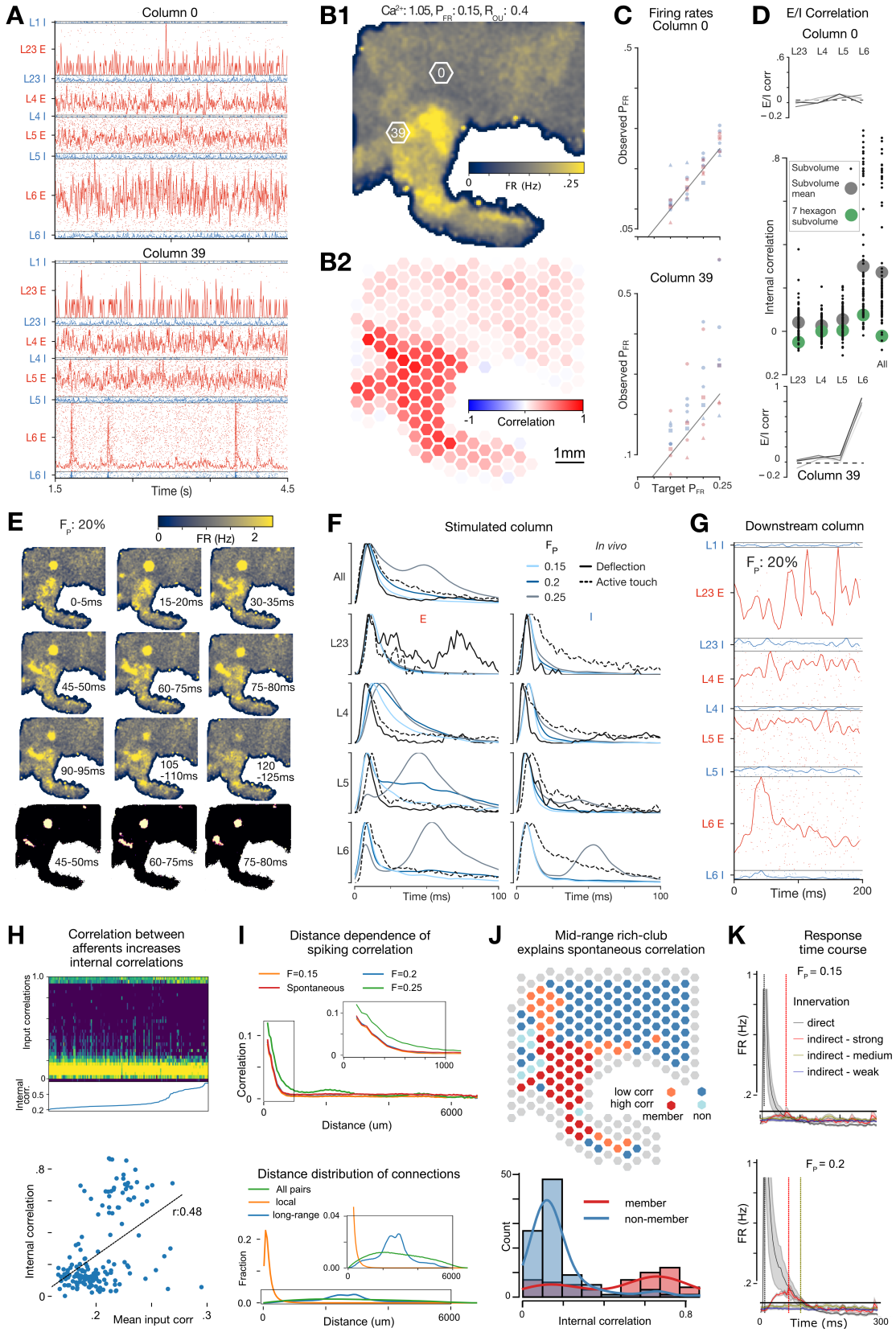

Figure 8: Full nbS1 simulations: independent functional units, millisecond-precise stimulus-responses, selective propagation of stimulus-evoked activity through mid-range connectivity, linking structure to function. Caption on following page.

A: Spiking activity and max normalised histograms for layer-wise E and I populations for the meta-parameter combination $[Ca^{2+}]_o$: 1.05 mM, R_{OU}: 0.4, P_{FR}: 0.15, and the 0th (upper) and 39th (lower) hexagonal subvolumes (shown in B). **B1:** Mean FRs across the model. Columns 0 and 39 (subsequently used) are highlighted. **B2:** Spiking correlations of E/I populations in 240 hexagonal subvolumes (diameter: $\approx 460\,\mu m$). **C:** Target vs. observed P_{FR} values for the four non-bursting simulations. The number of sides of each marker corresponds to the layer (triangle represents L2/3). Red: E, blue: I.. **D:** Correlations between E and I populations by layer for the four non-bursting simulations for the two hexagons (top and bottom). Color of line from light to dark represents P_{FR}. Middle: Distributions of spiking correlations of layer-specific populations in columns ($520\,\mu m$) of the nbS1 model (black dots; mean values: grey). Compared to the central column when the seven column subvolume is simulated in isolation (green). **E:** Trial-averaged activity in flatspace following single whisker deflections. Lower: Subset of time windows shown with only the top 2% of bins for each time window after baseline activity level subtracted. **F:** Trial-averaged PSTHs (baseline and max normalised) for column 0. For $F_P = 15\%$ and $F_P = 25\%$ respectively, the evoked responses passed and failed the latency and decay-based criteria tests for similarity to *in vivo*. Response for $F_P = 20\%$ passed the tests for all populations except L5 E which showed a more sustained response. **G:** Trial-averaged response of column 39. **H:** Correlations of mid-range inputs. Upper: Distribution of spiking correlations of inputs into 240 subvolumes. Calculated at reduced spatial resolution, based on connection counts and correlations between the subvolumes (see Methods). Subvolumes are sorted by the E/I correlation of neurons within them. Lower: Mean of the correlations of inputs into 240 subvolumes vs internal spiking correlation for all subvolumes during spontaneous activity. Black line: linear fit. Calculated based on connection counts and correlations between $50\,\mu m$ hexagonal subvolumes (see Methods). Data for evoked activity is shown in Figure S16. **I**: Upper: Spiking correlations of subvolumes against their distances in spontaneous (red) and evoked (orange: $F_p = 0.15\%$, blue: $F_p = 0.2\%$, green: $F_p = 0.25$) activity. For increased spatial resolution, smaller ($58\,\mu m$) subvolumes were used, hence correlation values are not comparable to values in B. Lower: Distribution of soma distances of neuron pairs connected by local (orange) or mid-range (blue) connectivity. Green: distances of all pairs, independent of connectivity. **J:** Upper: Classification of subvolumes based on low or high internal correlation and membership in mid-range rich club Data for evoked activity shown in Figure S16. Lower: E/I correlation of subvolumes for members of the rich club (red) and non-members (blue). **K:** FRs of subvolumes following a stimulus with $F_P = 0.15\%$ (top) and $F_P = 0.2\%$ (bottom). Mean (lines) and SEM (shaded area) over 10 repetitions shown for subvolumes directly innervated by the VPM stimulus (black), strongly innervated by directly innervated subvolumes (with over 10^6 synapses, red), or by medium strength (over 10^5 synapses, yellow) or weak (over 10^4 synapses) indirect innervation. Dashed lines indicate locations of peaks.

across the model to be explained by the topology of synaptic connectivity (Reimann et al., 2024). While the extrinsic input from the OU injections was uncorrelated by design, synaptic input from local connectivity would feature at least some degree of correlation. This led to asking, how correlated was the input from mid-range connections? We estimated for each pair of mid-range connections innervating a $460\,\mu m$ hexagonal subvolume its spiking correlation and compared the resulting distribution to the correlation within the subvolume itself (see Methods; Figure 8H, upper). We found low correlations for most pairs, but with a significant number of high-correlation outliers for subvolumes with high internal correlations. Moreover, when we considered the mean of the measure, we found that it explains most of the variability in internal correlations, for both spontaneous (Figure 8H, lower) and evoked states (Figure S16).

This led to the following tentative explanation: Local connectivity provides inputs from within $500\,\mu m$, which is virtually guaranteed to be correlated to some degree (Figure 8I upper vs. lower, orange). This is a result of connections being *locally dense*, as

they are concentrated within a small neighborhood (Figure 8 lower, green vs. orange). mid-range connectivity originates from further away, sampling from different functional units that may or may not be correlated, and being more diluted (Figure 8I lower, green vs. blue). Consequently, mid-range inputs are likely to act not much different from the uncorrelated OU process, unless this is overcome by a non-random topology of mid-range connectivity.

Specifically, we considered the mid-range connectivity at meso-scale in terms of the graph of synapse counts between 460 μm subvolumes. When the graph was thresholded at eight million synapses, most subvolumes lacked connections at that strength completely, but others formed a single connected component, indicating the formation of a *rich club* (Colizza et al., 2006; Figure 8J, upper, red and orange). We found that subvolumes with high internal correlation were part of the rich club, or directly adjacent to one of its members (Figure 8J). In the presence of strong thalamic inputs, this could be overcome, as the increased activity level spread along sufficiently strong mid-range connections (Figure 8K), albeit with substantial delays between 60 and 100 ms. This could induce high correlations in strongly connected parts of the model, outside the rich club as well (Figure S16) and shows that the model supports selective propagation of activity to areas efferently connected with mid-range connectivity.

3 Discussion

We presented novel methods to build, simulate and validate models of cortical tissue that correspond directly with 3D digitised brain atlases. As demonstrated, this enables laboratory experiments to have a simulatable *in silico* counterpart, and vice versa: predictions made by the model automatically have a precise correspondence in biology. By recreating and extending five laboratory experiments under a single model parameterization, we provided strong model validation and demonstrated the model's natural versatility. To our knowledge the simulations of the full nbS1 represent the first simulations of stable *in vivo*-like spontaneous and stimulus-evoked activity in a large-scale biophysically detailed model of multiple cortical subregions connected through local and mid-range connectivity. The model generated an initial set of predictions about the relationship between cortical structure and function, and provides a basis for future studies and predictions. Table S1 describes each quantitative prediction made in this manuscript, and how it might be tested *in vivo*. Additionally, all assumptions are listed in Table S8. We made the model and simulation tools available for use, enabling community driven testing, exploration and refinement.

Excitation from non-modeled brain regions is modeled by injecting somatic conductances and is calibrated for specific populations. For the purpose of calibration, we presented a novel technique, which allows rapid and methodical characterisation and validation of emergent model activity. The efficiency of the technique allows rapid recalibration after changes to the model such as adding new brain regions or changing anatomical details. Connected divided by unconnected firing rates measured during the process are also a prediction of the degree to which the activity of a population is determined by incoming connections from local vs extrinsic sources. We found an increase of the importance of local connectivity from superficial to deeper layers, in line with the canonical view of the cortex (Lübke and Feldmeyer, 2007; Feldmeyer, 2012), which places layers 5 and 6 at the

end of local information flow.

Although abstract relative to the model, the injection amplitudes could be predicted from the number of missing synapses, suggesting it provides a functional representation of their anatomical counterparts. The modular model of extrinsic connectivity can be refined or replaced in the future, or when larger fractions of the brain are modeled. The calibration framework could optimize per population parameters for other compensation methods, whilst still offering an interpretable spectrum of firing rate regimes at different levels of P_{FR}. For example, more realistic compensation schemes could be explored which introduce a) correlations between the inputs received by different neurons and b) compensation distributed across dendrites, as well as at the soma. We predict that such changes would make spontaneous activity more correlated at the lower spontaneous firing rates which supported in vivo like responses ($P_{FR} : 0.1 - 0.5$), which would in turn make stimulus-responses more noise correlated.

Our approach to obtaining *in vivo*-like activity contrasts with a recent approach in a large-scale biophysical model of primary visual cortex of similar scale to our smaller subvolume (Billeh et al., 2020). There, extrinsic inputs were delivered through dendritic synapses instead of somatic injection, which is more anatomically realistic, and intrinsic recurrent weights were adjusted to match extracellularly recorded firing rates. They find a single activity state, instead of the *in vivo*-compatible spectrum here that allowed us to contrast anesthetized and awake states. The model in general differs from hybrid models, which jointly use biologically-detailed models and point neuron models (Billeh et al., 2020; Dura-Bernal et al., 2023), and also from the work of Egger et al. (2020) who modeled activation of L5 pyramidal cells by constraining patterns of synaptic input based on receptive fields and predicted anatomical innervation.

Given the complexity of the model, how can we be confident that its activity is *in vivo*-like? First, we demonstrated correlated spontaneous dynamics in the form of global and local fluctuations and dynamic E-I balance, as found experimentally (Renart et al., 2010). Second, population firing rate distributions were long-tailed with sub 1 Hz peaks, and were similar for spontaneous and stimulus-evoked activity, as reported (Wohrer et al., 2013). Moreover, mean firing rates below 1 Hz are required by metabolic constraints (Attwell and Laughlin, 2001; Lennie, 2003). In response to simple whisker stimuli, response sparsity, spike counts, and the temporal profile and amplitudes of layer-wise populations were similar to *in vivo* under anesthetized and awake conditions, for different regions of the meta-parameter space. The effect of the spontaneous meta-parameters on evoked responses, also shows that the networks spontaneous state affects stimulus-responses, as observed *in vivo* (Isbister et al., 2021). Although from the barrel system, these stimuli offer some of the simplest stimulus-response paradigms, enabling principles of neural dynamics and information processing to be studied; in particular, the correspondence between atomic units of sensory information and neural representations. The model also predicts the number of thalamic fibers stimulated for whisker-flick stimuli. Such validations are crucial for complex models, as they provide context for more complex validations. Moreover, in a rich and complex nonlinear system, the source of discrepancies with *in vivo* activity are simpler to ascertain under simpler protocols.

For more complex validations, we reproduced protocols from three laboratory experiments. These experiments used a wide array of techniques, which could be accurately

recreated due to the model's close correspondence with biological tissue. Additionally, we could go beyond the original experiments. For example, we predicted an increased number of neurons would be required to have a decodable effect on postsynaptic activity under *in vivo* conditions over the *in vitro* conditions of the original experiment. This can be explained by lower synaptic reliability under *in vivo* conditions. Also, we predicted a paradoxical effect of optogenetic stimulation on L6 PV+ interneurons, namely a decrease in firing with increased stimulus strength. This is reminiscent of the paradoxical responses found by Mahrach et al. (2020) in the mouse anterior lateral motor cortex (in L5, but not in L2/3) and barrel cortex (no layer distinction) respectively. While Mahrach et al. (2020) conducted their recordings in awake mice not engaged in any behavior, we observed this effect only when drifting grating patterns with high contrast were presented. Nevertheless, consistent with their findings, we found the effect only in deep but not in superficial layers, and only for PV+ interneurons but not for PCs. Our model could therefore be used to improve the understanding of this paradoxical effect in follow up studies. These examples demonstrate that the approach of modeling entire brain regions can be used to further probe the topics of the original articles and cortical processing. This could be continued in the future using paradigms that take advantage of the multiple regions offered by the model to study processing in cortical hierarchies.

Responses to whisker flick stimuli were closer to biology for values of the P_{FR} metaparameter between 0.1 and 0.5, according with the known inflation of mean firing rates stemming from the bias of extracellular spike sorting techniques towards larger and more active neurons (Olshausen and Field, 2006). Supporting our estimates, patch-clamp experiments show ubiquitous neuronal silence (Crochet and Petersen, 2006), and spontaneous and stimulus-evoked barrel cortex firing rates as much as 10 times lower than for extracellular recordings (0.05-0.15 Hz vs. 0.8-1.5 Hz; Olshausen and Field, 2006). This is also inline with our recent work using the model, which estimated a spike sorting bias corresponding to $P_{FR} = 0.3$ using virtual extracellular electrodes (Laquitaine et al., 2024). Each recording technique comes with challenges and biases (Shoham et al., 2006; Olshausen and Field, 2006; Barth and Poulet, 2012; Wohrer et al., 2013). Calcium imaging and patch-clamp experiments are less biased towards frequently spiking neurons (Wohrer et al., 2013), yet the former can only infer spiking activity and may be biased towards neurons that favor marker expression. Patch-clamp techniques can reduce firing rates, be biased towards larger or more active neurons (Olshausen and Field, 2006); and are limited to recording a few neurons simultaneously, preventing characterizations of single trial population dynamics. An earlier version of the model has been used to simulate cortical extracellular potentials (Reimann et al., 2013). We can now simulate modern extracellular electrodes and compare multi-unit activity and spike sorting results to the *in vivo*-like ground truth to gain further insights into the potential over-estimation of mean firing rates.

During simulations of the entire nbS1, we found emerging spatial inhomogeneities in network activity. Specifically, we observed sharp transitions in firing rates and pairwise correlations at disgranular zones. This highlights that the model supports several, independently acting functional units. Analysis of spatial correlations suggests a radius of approximately $400\,\mu m$ for a single unit. This property was not present in the previous intra-regional scale model (Markram et al., 2015), but is rather an emergent property of the interregional scale, demonstrating that we achieved our goal of building a model that can be used to study mid-range interactions between regions. Analyzing the source of

the inhomogeneities suggested a prominent role of a non-random rich-club structure of mid-range connections at the meso-scale. Within functional units, we found that inhomogeneous increases of spiking correlations were confined to spontaneous packets of L6 activity.

In keeping with the philosophy of compartmentalization of parameters and continuous model refinement (see Introduction), it was essential to improve validity at the columnar scale (relative to Markram et al. (2015)) as part of demonstrating validity of the full nbS1. Indeed, improved parametrization and validation at smaller scales was essential to parameterizing background input which generated robust nbS1 activity within realistic $[Ca^{2+}]_o$ and firing rate ranges. We view this as a major achievement, as it was unknown whether the model would achieve a stable and meaningful regime at the start of our investigation. Whilst we would have liked to go further, our primary goal was to publish a well characterized model as an open resource that others could use to undertake further in-depth studies. In this regard, we are pleased that the parametrization of the nbS1 model has already been used to study EEG signals (Tharayil et al., 2024), as well as propagation of activity between two subregions (Bolaños-Puchet and Reimann, 2024). Investigation, improvement and validation must be continued at all spatial scales in follow up papers with detailed description, figures and analysis, which cannot be covered in this manuscript. Each new study increases the scope and validity of future investigations. In this way, this model and paper act as a stepping stone towards more complex questions of interest to the community such as perception, task performance, predictive coding and dendritic processing. This was similar for Markram et al. (2015) where the initial paper was followed by more detailed studies. Unlike the Markram et al. (2015) model, the new model can also be exploited by the community and has already been used in a number of follow up papers studying (Ecker et al., 2024a,b; Bolaños-Puchet and Reimann, 2024; Pokorny et al., 2024; Egas Santander et al., 2024; Tharayil et al., 2024; Laquitaine et al., 2024). We believe that the number of use cases for such a general model is vast, and is made larger by the increased size of the model.

It is important to highlight where the model deviates from biological data. First, the model omits several known anatomical elements, such as glia and the presence of gap junctions between certain neuron-types, but the model's spatial context provides a natural scaffold for them. Our modeling techniques assume generality of rules and parameters, unless indicated by the data. Therefore, violations indicate that biological rules and data may be more specific. For example, model thalamic inputs innervate any dendrite placed in the targeted layers equally, but this did not reproduce the timing of inhibitory subpopulation responses. Stronger innervation of PV+ neurons than other inhibitory neurons may rectify this. However, it is unclear whether innervation should be anatomically or physiologically stronger, as the best available data mixes structural and physiological strength (Sermet et al., 2019).

In our previous work (Roussel et al., 2023) we linked mouse inhibitory me-models to transcriptomic types (t-types) in a whole mouse cortex transcriptomic dataset (Gouwens et al., 2019). This can provide a direct correspondence in future large-scale mouse models. As we model only a single electrical type for pyramidal cells there is no one-to-one correspondence between our me-models and the 10 different pyramidal cell types identified there. We are not currently aware of any method which can recreate the electrical features of different types of pyramidal cells using only generic ion channel models. To

achieve the firing pattern behavior of more specific electrical types, usually ion channel kinetics are tweaked, and this would violate the compartmentalization of parameters. In future we hope to build morpho-electric-transcriptomic type (met-type) models by selecting gene-specific ion channel models (Ranjan et al., 2019, 2024) based on the met-type's gene expression. Data specific to different neuron sections (i.e. soma, AIS, apical/basel dendrites) of different met-types, such as gene expression, distribution of ion channels, and voltage recordings under standard single cell protocols would be particularly useful.

Finally, when required, we generalized data from different animals and brain regions to build our rat nbS1 model. This is the accepted state-of-the-art in computational neuroscience, e.g., all 19 data-driven models of rodent microcircuitry listed in Figure 2 of the recent review of Ramaswamy (2024) conduct some sort of mixing, including the advanced mouse V1 model of the Allen Institute (Billeh et al., 2020). Whilst a first truly single species model would be a great advance, it is not required to be the basis of *in silico* research. Our model (and previous ones) can be used to study the many cortical mechanisms that are common to the closely related organisms rat and mouse. This paper and its companion paper serve to present a methodology for modeling micro- and mesoscale anatomy and physiology, which can be applied for other cortical regions and species. With the rapid increase in openly available data, efforts are already in progress to build models of mouse brain regions with reduced reliance on data mixing thanks to much larger quantities of available atlas-based data. This also includes data for the validation of emergent network level activity. Here we chose to compare network-level activity to data mostly from the barrel cortex, as well as a single study from primary visual cortex. Whilst a lot of the data used to build the model was from the barrel cortex, the barrel cortex also represents a very well characterized model of cortical processing for simple and controlled sensory stimuli. The initial comparison of population-wise responses in response to accurate thalamic input for single whisker deflections was essential to demonstrating that the model was closer to *in vivo*, and we were unaware of similar data for non-barrel somatosensory regions. Moreover, our optogenetic & lesion study demonstrated the capacity to compare and extend studies of canonical cortical processing in the whisker system.

However, we cannot always predict the effect caused by mixing data sources. An interesting example of this is described in the companion paper (Reimann et al., 2024), stating that certain rules of inhibitory connectivity found in a mouse electron-microscopic (EM) connectome (Schneider-Mizell et al., 2023) cannot be explained by an non-selective pruning axo-dendritic appositions. We demonstrated the utility of the model to explore the effect of any connectivity rule, using the example of a mouse EM-compatible "SM-connectome". After rewiring, and refitting synaptic, and conductance injection parameters, we found that the purely perisomatic targeting by PV+ neurons and the increased inhibitory targeting by VIP+ neurons shifted how much individual layers were driven by intrinsic and extrinsic excitation. This could not be explored with current techniques *in vivo* and highlights a strength of *in silico* experimentation. On the other hand, this data source contradicts some of our rat nbS1 parameters, e.g., the number of synapses per connection from light microscopy (Markram et al., 2015) do not match with the ones obtained from mouse V1 EM. Thus we used the rat data sources for building our baseline model, but make both models available in a simulatable format (see Data Availability).

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Declaration of interests

The authors declare no competing interests.

4 Methods

Key resources table

REAGENT or RESOURCE	SOURCE	LOCATION
Final simulatable models		
Anatomical and physiological model (Full model)	This paper	doi.org/10.7910/DVN/HISHXN
Anatomical and physiological model (7 column subvolume)	This paper	doi.org/10.5281/zenodo.7930276
SM-connectome reproducing inhibitory trends from MICrONS (7 column subvolume)	This paper	doi.org/10.5281/zenodo.10677883
Deposited data		
Raw neuron recordings	Reva et al., 2023	bbp.epfl.ch/nmc-portal/downloads.html
Neuron morphology reconstructions	Reimann et al., 2024	doi.org/10.5281/zenodo.6906785
Raw paired recordings	Markram et al., 2015	bbp.epfl.ch/nmc-portal/downloads.html
PSP amplitudes	Sources as listed in	Table S5
CV of PSP amplitudes	Sources as listed in	Table S6
mPSC frequencies	Sources as listed in	Table S7
Spont. and evoked spiking freq.	Reyes-Puerta et al., 2015b	From original authors on request
VPM spike trains	Diamond et al., 1992	Digitized from Figure 8
	Yu et al., 2019	From original authors on request
Volumetric atlases	Bolaños-Puchet et al., 2024	doi.org/10.5281/zenodo.7930276
Ion channel models	Reva et al., 2023	doi.org/10.5281/zenodo.7930276
Anatomical model	Reimann et al., 2024	doi.org/10.5281/zenodo.6906785
Models of neuron electrical types	Reva et al., 2023	doi.org/10.5281/zenodo.7930276
Software and algorithms		
Electrical model optimization	Reva et al., 2023	github.com/BlueBrain/singlecell-emodel-suite
Simulation software	This paper	doi.org/10.5281/zenodo.8075202
Model loading and interaction	This paper	doi.org/10.5281/zenodo.8026852
Model and simulation analysis	This paper	doi.org/10.5281/zenodo.8016989
Specific simulation configurations	This paper	doi.org/10.5281/zenodo.7930276
Connectome-Manipulator	Pokorny et al., 2024	github.com/BlueBrain/connectome-manipulator

Resource availability

Lead contact

Further information and requests for data and code should be directed to and will be fulfilled by the lead contact: Michael W. Reimann (sscx@reimann.science)

Materials availability

No materials were used in this computational work.

Data and code availability

- Both the full nbS1 model and smaller seven hexagon subvolume are available on Harvard Dataverse and Zenodo respectively in SONATA format (Dai et al., 2020) with simulation code. DOIs are listed under the heading “Final simulatable models”

in the Key resources table. An additional link is provided to the SM-Connectome with instructions on how to use it with the seven hexagon subvolume model.

- Neuron morphology reconstructions, ion channel models, neuron electrical models, volumetric atlases have been deposited at Zenodo and are publicly available as of the date of the publication. The DOI is listed in the key resources table. Raw single cell recordings and paired synaptic recordings have been deposited in the Blue Brain portal and are publicly available as of the date of publication. The links are listed in the key resources table.
- All original code has been deposited at Zenodo and is publicly available as of the date of publication. DOIs are listed in the key resources table.
- Any additional information required to reanalyze the data reported in this paper is available from the lead contact upon request.

4.1 Method details

4.1.1 Optimisation of ion channel conductance densities

Neuron models from Reva et al. (2023) were made as follows. Ion channel conductance densities were optimised for a pool of reconstructed neurons, for which *in vitro* recordings had previously been made. Ion channel densities were then generalised to other neuron models of the same e-type. Resulting neuron models were only used in the construction of the model if the value of the cost function was within 5 standard deviations of the experimental mean.

4.1.2 AIS Adjustment

For some electrical models, further adjustments were made to AIS sections to handle the large input currents present under conditions of high network activity. In short, for certain pyramidal cell morphologies, the AIS was replaced by a cylinder with a length of $60\,\mu m$. Its diameter was manually calibrated such that the ratio of the AIS input resistance over the input resistance of somato-dendritic compartments was equal to 2. Afterwards, it was confirmed that the cost function of their electrical models remained below the threshold.

4.1.3 Parametrization of synaptic physiology

The Tsodyks-Markram synaptic model (Tsodyks and Markram, 1997; Markram et al., 1998; Fuhrmann et al., 2002; Loebel et al., 2009), upgraded to feature multi-vesicular release (Barros-Zulaica et al., 2019; Ecker et al., 2020) comprises the following parameters: peak conductance $\hat{g}$, depression and facilitation time constants D, F, the decay time constant of the PSC τ_{decay}, the release probability U_{SE}, the average number of vesicles in the release-ready pool N_{RRP}, the Hill coefficient of the nonlinear $[Ca^{2+}]_o$ dependent scaling of release probability U_{Hill}, and finally $\hat{g}_{ratio}$: the NMDA/AMPA ratio for excitatory synapses, and the $GABA_B/GABA_A$ ratio for inhibitory synapses. Where possible, pathway and synapse-type specific parameter values were taken from the literature, and after eventual corrections (for differences in the temperature and solutions used in the experiments), were put directly into the model using the technique described for the use case of hippocampal CA1 in Ecker et al. (2020). For example, parameters U_{SE}, D, F,

and U_{Hill} have previously been fitted for a number of pathways using data acquired from paired-recording experiments. Furthermore, $\hat{g}_{ratio}$ parameter has been previously determined from outside-out patch recording experiments.

The remaining parameters ($\hat{g}$ and N_{RRP}) were iteratively calibrated using an *in silico* setup reproducing the paired-recordings experiments detailed below. For this parameterization, all paired-recording data sources from Markram et al. (2015) were re-used. To further constrain the variance of EPSP amplitudes in L5 TTPCs, fitted parameters from Barros-Zulaica et al. (2019) were used. The dataset was also enriched with recent recordings from L6 (Qi and Feldmeyer, 2016; Yang et al., 2020, 2022). Instead of generalizing L4 E peak synaptic conductances for all thalamic fibers (as in Markram et al., 2015), synaptic conductances were constrained using EPSP amplitude measurements from thalamocortical slices (Beierlein and Connors, 2002; Beierlein et al., 2003). Fibers originating from POm were not present in Markram et al. (2015). Due to the lack of *in vitro* measurements, physiological parameters from VPM synapses were generalized to describe POm synapses.

Not all synaptic peak conductances can be measured with paired recordings due to the space-clamp artifact (Markram et al., 2015; Ecker et al., 2020), and estimating the number of release-ready vesicles is also challenging experimentally (Loebel et al., 2009; Barros-Zulaica et al., 2019). Thus, for synaptic pathways for which there was *in vitro* reference data, these two parameters were determined in a simulation-driven iterative process. Firstly, 50 pairs of *in silico* neurons were randomly sampled. Second, the postsynaptic cell was current-clamped, and the PSP at the soma of the postsynaptic cell in response to a presynaptic action potential was measured. This was repeated 35 times for each pair as in Ecker et al. (2020). Thridly, the mean and the CV of these amplitudes were extracted and compared with reference *in vitro* data. Finally, peak conductance ($\hat{g}$), and the average number of vesicles in the release-ready pool (N_{RRP}) were adjusted to match the amplitude and CV of the *in vitro* reference (Ecker et al., 2020). In some cases, this resulted in reaching the lower bound of univesicular release (Barros-Zulaica et al., 2019).

Where experimental data was not available, mean synaptic physiology parameters from similar pathways were used (Markram et al., 2015; Ecker et al., 2020). For the VPM to L5 E pathway, the maximum of VPM to L4 E and VPM to L6 E conductances (instead of the mean) were used, based on resulting evoked firing rates found in a later modeling step (Figure S5C). To calibrate the mPSC frequencies of different pathways, single cell simulations with different values of the spontaneous release frequency for all synapses of a set of 1000 cells in a given pathway were run. In these simulations, *in silico* voltage-clamp recordings were performed to measure the resulting mPSC frequency at the soma. This data was then fitted with a logarithmic function and the value of the spontaneous release frequency matching the *in vitro* reference value for the mPSC frequency was interpolated. As *in vitro* paired recording data is sparse, all available sources to determine synaptic parameters were re-used for validation.

4.1.4 Datasets used for validation of *in vivo*-like dynamics

Activity in the model is compared with spike-sorted extracellular recordings from the barrel cortex of anaesthetised rats (Reyes-Puerta et al., 2015b). The dataset contains single unit spike times for both spontaneous activity and responses to single whisker deflections,

across 6 layer-wise neuron populations (L2/3 E, L2/3 I, L4 E, L4 I, L5 E & L5 I). We extend the dataset using the average of L2/3 I, L4 I and L5 I as a reference for L1 I and L6 I, and an alternative reference for L6 E (De Kock et al., 2007). The spontaneous firing rates of the 9 neuron populations are collected in the vector of reference firing rates, $\boldsymbol{V_{FR}}$.

As a secondary comparison, we use a dataset of *in vivo* juxtacellular and whole-cell recordings of barrel cortex responses in awake mice during an active whisker touch paradigm (Yu et al., 2019). While the animal model is different, using this data enables comparison to awake responses of layer-wise E populations and I subpopulations (VIP+ (vasoactive intestinal peptide, a part of our 5HT3aR+ subpopulation), Sst+, FS (fast spiking, corresponding to our PV+ subpopulation)). Moreover, this allows validating the model against properties of cortical responses across similar but different paradigms, reducing the risk of over fitting.

4.1.5 Somatic conductance injection

Random background synaptic inputs, representing uncorrelated inputs from other brain regions not present in the model, are modelled as a conductance-based somatic injection (Figure 4B1). Specifically, we inject conductance signals described by an Ornstein-Uhlenbeck (OU) process (similar to Destexhe et al. (2001)), given by the following equation:

$$\frac{dg(t)}{dt} = -\frac{1}{\tau}[g(t) - g_0] + \sqrt{D} \tag{1}$$

where $g(t)$ is the conductance signal, g_0 its mean value, τ is the decay time constant, D is the diffusion coefficient, and $\chi(t)$ is a Gaussian white noise process. The diffusion coefficient can also be expressed in terms of the standard deviation σ of the signal: $D = \frac{2\sigma^2}{\tau}$. Note that we only consider an excitatory conductance signal representing mid-range excitatory drive, whereas local inhibitory input is deemed sufficient within the circuit model. As we are modeling a non-specific random background noise, we use a different, uncorrelated OU process for each cell.

Given the diversity of morphologies and electrical behaviors of cells in our circuit, we scale the mean and standard deviation of the injected signal based on individual cell properties. Specifically, we compute the input resistance R_{in} of each cell at its resting potential, then take its reciprocal value $G_{in} = 1/R_{in}$ (units of conductance). The mean g_0 and standard deviation σ of the injected conductance signal are then expressed as percentages OU_μ and OU_σ of this input conductance G_{in}:

$$g_0 = \frac{OU_\mu}{100} * G_{in} \tag{2}$$

$$\sigma = \frac{OU_\sigma}{100} * G_{in} \tag{3}$$

The OU_μ and OU_σ percentage values are used in the calibration technique described in the following sections. To reiterate, OU_μ and OU_σ scale the mean of the injected conductance and the size its fluctuations respectively.

4.1.6 Details of spontaneous activity calibration

OU_μ and OU_σ are parameterised separately for each of 9 populations (layer-wise E and I combinations; Figure 4B2), leading to 18 parameters, grouped into two 9-dimensional vectors $\boldsymbol{OU_\mu}$ and $\boldsymbol{OU_\sigma}$. Spontaneous firing rates across populations, denoted by the vector $\boldsymbol{C_{FR}}$, are then determined by the vectors $\boldsymbol{OU_\mu}$ and $\boldsymbol{OU_\sigma}$, and $[Ca^{2+}]_o$. The objective of the calibration procedure is to determine a mapping that outputs the $\boldsymbol{OU_\mu}$ and $\boldsymbol{OU_\sigma}$ required to achieve a particular set of firing rates $\boldsymbol{C_{FR}}$, for a given $[Ca^{2+}]_o$.

This requires two simplifications: First, we reduce the space of possible $\boldsymbol{OU_\mu}$ and $\boldsymbol{OU_\sigma}$ values by fixing $\boldsymbol{OU_\sigma} = \boldsymbol{OU_\mu} * R_{OU}$, where R_{OU} is a pre-specified constant that controls the level of noise assumed to be present in the external synaptic input. Second, we learn the mapping only for dynamical states where the firing rates of the 9 populations are a proportion of reference *in vivo* firing rates, i.e. $\boldsymbol{C_{FR}} = P_{FR} * \boldsymbol{V_{FR}}$, with $P_{FR} \in [0, 1]$ (Figure 4B2). This is based on the assumption that extracellular spike detection sampling biases (Olshausen and Field, 2006; Wohrer et al., 2013) affect all populations equally.

The mapping can be written as $\Psi_{Ca^{2+},R_{OU}} : \boldsymbol{C_{FR}} \mapsto \boldsymbol{OU_\mu}$ and is simplified into two separate mappings which are determined separately and then combined (Figure S1). The first mapping finds values of the 9 output parameters $\boldsymbol{OU_\mu}$, for a given R_{OU}, which produce particular *unconnected firing rates* $\boldsymbol{U_{FR}}$ (i.e., where the neurons in the network are not connected to each other). The second then maps between $\boldsymbol{U_{FR}}$ and $\boldsymbol{C_{FR}}$.

The first mapping $\chi : (R_{OU}, \boldsymbol{U_{FR}}) \mapsto \boldsymbol{OU_\mu}$, is attained by running 1 second simulations over various combinations of OU_μ and OU_σ (Figure S1). R_{OU} constrains OU_μ and OU_σ to a line of possible combinations in the 2D space. We generate an approximation of χ based on linear interpolation between the results of simulations along the line. Note in particular, that χ is independent of $[Ca^{2+}]_o$.

Given the mapping χ, the remaining problem is to determine the values of $\boldsymbol{U_{FR}}$ that achieve certain target firing rates given by $P_{FR} * \boldsymbol{V_{FR}}$, for $P_{FR} \in [0, P_{max}]$ and each combination of $[Ca^{2+}]_o$ and R_{OU}, i.e., to determine the mapping $\phi_{Ca^{2+},R_{OU}} : \boldsymbol{U_{FR}} \mapsto \boldsymbol{C_{FR}}$. This is done by measuring values of $\boldsymbol{C_{FR}}$ produced for given values of $\boldsymbol{U_{FR}}$ in a number of simulations. However, instead of exploring the whole parameter space of possible $\boldsymbol{U_{FR}}$ values, we only explore a small number of values of $\boldsymbol{U_{FR}}$ which we expect to produce the target $\boldsymbol{C_{FR}}$ values. This is done by iteratively learning the mapping $\phi_{Ca^{2+},R_{OU}} : \boldsymbol{U_{FR}} \mapsto \boldsymbol{C_{FR}}$ and in each iteration using ϕ to predict $\boldsymbol{U_{FR}}$ values that bring the dynamics closer to the target firing rate, i.e., by sampling values given by $\boldsymbol{U_{FR}} = \phi^{-1}(C_{FR}) = \phi^{-1}(P_{FR} * \boldsymbol{V_{FR}})$ for 10 equidistant values of $P_{FR} \in [0, P_{max}]$. The initial guess of ϕ is simply the identity, i.e., assuming no effect of connecting the network, with $P_{max} = 0.5$. All other iterations use $P_{max} = 1.0$.

We update ϕ by fitting an exponential: $\boldsymbol{C_{FR}} = \alpha * e^{\beta \boldsymbol{U_{FR}}} + \kappa$ to the values of $\boldsymbol{U_{FR}}$, $\boldsymbol{C_{FR}}$ measured on the latest iteration (Figure S1). In a recurrently connected network such as our model, the connected firing rate of a population depends on the firing rates of all other populations in complex and nonlinear ways. This is addressed by our simplification to restrict the compatible dynamic states, where by definition the target firing rate of one population determines the target firing rates of all others.

The firing rates of the L2/3 I, and L4 I and L6 I populations could not be sufficiently

lowered for $P_{FR} < 0.2$ and $P_{FR} < 0.1$ respectively, as they spontaneously fired even at their resting potentials (Figure S1D).

4.1.7 Generalization to other network states

We first approximated ϕ for $[Ca^{2+}]_o = 1.1\,\text{mM}$ and $R_{OU} = 0.4$. To reduce the number of iterations steps needed for other combinations of $[Ca^{2+}]_o$ and R_{OU}, we initialized the optimization process with the mapping ϕ obtained for this parameter pair instead of basing it on the identity (Figure S1D, lower; Figure S1). Only for P_{FR} above 0.8 and $[Ca^{2+}]_o = 1.1\,\text{mM}$ did we have to slightly relax our acceptance criteria (Figure 4D, lower). Additionally $[Ca^{2+}]_o = 1.1\,\text{mM}$, $P_{FR} = 1.0$, and $R_{OU} = 0.2$ led to bursting activity uncharacteristic of *in vivo* activity and was excluded from further study.

4.1.8 Evoked activity comparison and validation

The spike times of single whisker deflection stimuli were drawn from a PSTH of VPM neurons in response to 3 ms mechanical single whisker deflections made at 1 Hz in urethane anesthetized rats (Diamond et al., 1992; Figure 5A2). Since the *in vivo* data for cortical responses to single whisker deflections was from responses to 2 ms mechanical whisker deflections, we compressed the tail of the VPM PSTH to allow a direct comparison with *in silico* responses (Figure 5A2). A VPM PSTH for the active whisker touch stimulus was used from the same dataset as the corresponding cortical responses (Yu et al., 2019).

Firstly, *in silico* responses were compared to data from the C2 barrel of the anaesthetized rat in response to single whisker deflections made at < 1Hz. For the active whisker touch stimulus, *in vivo* activity was used from aggregated over principal barrels corresponding to the untrimmed whisker.

As an initial test of similarity with the corresponding *in vivo* dataset, trial-averaged PSTHs were first calculated for each parameter combination, both for all neurons, and for each of the layer-wise E and I populations. We then tested whether the latencies, 50% and 25%-decay points of the trial-averaged PSTHs were respectively no more than 10 ms, 10 ms and 40 ms later than those of the corresponding *in vivo* populations, and that there was no secondary rise in the PSTHs after the initial decay (by testing that none of the PSTHs for individual populations were more than 35% above baseline after 75 ms). L1 I was excluded from these tests, as it showed little or no response to the stimulus and we had no *in vivo* reference. These tests allowed us to split the 4D parameter space into two regions, one where *in silico* responses are consistent with *in vivo* responses, and another where they are not (see Results).

4.1.9 In-silico experimental methods

Simulation of a morphologically detailed model first requires specifying the conditions (parameters and inputs) under which to perform the simulation. Given the correspondence between variables in the model and properties of biological systems, we are able to mimic to a certain extent the conditions and protocols of experimental studies. These are combinations of existing techniques, or even techniques that cannot or have not yet been performed experimentally. On top of the compensation for missing external input

and different $[Ca^{2+}]_o$, we implemented further mechanisms to simulate specific experimental conditions. On a technical level, these comprise somatic current or conductance injections, adjustment of synaptic connectivity parameters, and selective activation of thalamic fibers. These are static conditions, however, in that their time course must be determined before the simulation is run. Somatic injections and connectivity adjustments can be targeted with single neuron or single pair resolution, respectively. To each thalamic fiber or neuron in the model, we can assign an arbitrary spike train, triggering synaptic release from all of its synapses with anatomically determined delays (from axonal conduction speed and path length). These mechanisms can target specific groups of neurons, e.g. based on neuron properties, such as location, layer, m-type or e-type, or inhibitory subpopulation (determined based on me-type as in Markram et al. (2015); Figure 2B). We combined mechanisms to simulate various *in vitro* or *in vivo* experimental paradigms. Pathway lesions, for example, are simulated by selecting sets of pre- and postsynaptic neurons and removing all synaptic connections between them (Figure S2A). Simulated optogenetic stimulation, in addition to being targeted at specific groups of neurons, took into account the attenuation of light with depth for the wavelength being used. Neurons were then inhibited or excited according to the intensity of light reaching them (Figure S2B). Finally, sensory stimuli were simulated by generating instances of stimulus-specific stochastic spike trains activating the thalamic input fibers (Figure S2C).

4.1.10 Optogenetic inhibition or activation

We model optogenetic inhibition or activation of a neuron population through a current injection at the soma of each cell in the population, with an intensity proportional to the cell's threshold current (see Reva et al. (2023); but with the technical caveat that we did not apply a hyperpolarizing holding current at the same time). To mimic the conditions of surface illumination, we considered the dependence of effective depolarization strength on cortical depth using a modified Beer-Lambert law approximation for the exponential attenuation of light intensity through scattering tissue (Al-Juboori et al., 2013; Azimipour et al., 2014, Figure S2B):

$$I(d) = I_0 \exp(-\mu_{eff}\, d) \tag{4}$$

where $I(d)$ describes the light intensity at depth d (in mm), with a maximum light intensity I_0 (on the surface of the cortex) and an effective attenuation coefficient given by:

$$\mu_{eff} = \sqrt{3\mu_a(\mu_a + \mu_s')} \tag{5}$$

Values for the absorption coefficient μ_a and the reduced scattering coefficient μ_s' were interpolated for the chosen wavelength from Mesradi et al. (2013). For implementation reasons, the targeted cells were grouped into depth bins and for each group the intensity at the center of the bin was used. Bins were equally distributed in terms of the injected current, and not in terms of depth. The value of I_0 was calibrated independently for each experimental paradigm.

4.1.11 Modeling sensory inputs

Sensory inputs were simulated using a three step procedure (Figure S2C2): First, a time series representing sensory stimulation is assigned to each selected thalamic fiber; second, the time series is optionally transformed with a fiber-dependent transfer function;

third, a spike train is generated from the time series through a stochastic spiking process. Thalamic input fibers were associated with roughly columnar, overlapping volumes of the model that they formed synaptic connections in (Reimann et al., 2024). Their centers were projected into the plane using a flat map of the model (Bolaños-Puchet et al., 2024), yielding $[x_\zeta, y_\zeta]$, the *flat locations* of each fiber ζ. A sensory stimulus was defined based on fiber location as $\rho_\zeta(t) = \rho(x_\zeta, y_\zeta, t)$. The stimulus function could be partially stochastic and its value was evaluated for each time bin of the simulation (Figure S2C1). Next, a fiber could be associated with a transfer function υ_ζ that transforms the results of ρ. If none is mentioned, identity was used as transfer function. Finally, a spiking process ψ was used to instantiate a spike train for each fiber, based on its transformed time series. That is, the spike train associated with ζ was $\Gamma_\zeta = \psi(\upsilon_\zeta(\rho_\zeta))$. The processes used were stochastic, leading to different spike trains for fibers associated with the same time series. Different, specific ρ, υ and ψ were used for different experimental paradigms that will be further described below.

4.1.12 Recreating Varani et al., 2022

To study how input from L4 contributes to L2/3 subthreshold responses Varani et al. (2022) used a 500 ms long whisker hold paradigm, while patch-clamping PCs in L2/3 in anesthetized and awake mice. We encoded the whisker hold stimulus as a step function ($\rho_\zeta(t) = 1$, if 2000 ms $\leq$ t $<$ 2500 ms, 0 otherwise) in 10% of the VPM fibers within the seven column subvolume. One of four transfer functions were assigned to each fiber, based on the types of kinetic response properties of thalamic neurons identified in (Petersen et al., 2008). The types were selective for whisker position (υ_{pos}), velocity (υ_{vel}), acceleration (υ_{acc}), or direction (υ_{dir}), and were implemented as:

$$\begin{aligned}
\upsilon_{pos}(t) &= r_{max} \cdot \rho(t) \\
\upsilon_{vel}(t) &= r_{max} \cdot (\rho(t+1) - \rho(t)) \\
\upsilon_{acc}(t) &= r_{max} \cdot (\rho(t+1) - 2\rho(t) + \rho(t-1)) \\
\upsilon_{dir}(t) &= r_{max} \cdot |\rho(t+1) - \rho(t)|_+
\end{aligned}$$

where $r_{max} = 150$ Hz denotes the firing rate of a thalamic fiber when its associated feature property is at the fiber's preferred value. Transfer functions were randomly assigned to fibers with the fractions identified in Petersen et al. (2008) (Figure 6A, 11% coding for position and acceleration, 58% for velocity and 20% for direction). The spiking process ψ was an adapting Markov process (Muller et al., 2007) with an adaptation time constant of 100 ms. As the whisker movements were short lasting, rates were evaluated at submillisecond (0.1) resolution.

Similarly to before, only the seven column subvolume (210k neurons) was used for the simulations, and the *in vivo*-like state was realized as $Ca^{2+} = 1.05$ mM, $R_{OU} = 0.4$, and $P_{FR} = 0.3$.

The optogenetic inhibition in this experiment targeted 95% (in line with Varani et al. (2022)) of excitatory cells in layer 4. The authors found a few cells which also tested positive for Halo at the bottom of L3 as well, but as they did not quantify it, we decided not to target any lower L3 PCs in the *in silico* version of the experiment. Based on the 595 nm wavelength (yellow light) parameters were set to $\mu_a \approx 0.49\,mm^{-1}$ and $\mu'_s \approx 4.12\,mm^{-1}$. For the depth-based spatial binning of cells, 5 bins were used in L4. After scanning several values, I_0 was set to -200% as that reproduced the ≈ 10 mV hyperpolarization of L4 PCs

observed *in vivo*. In line with the *in vivo* experiment, the optogenetic stimulus ended in a (100 ms long) ramp to avoid rebound spikes (Figure 6B).

When going beyond reproducing the same experimental conditions and instead leveraging the *in silico* nature of our setup, synaptic pathways were lesioned by selecting the excitatory population in a given layer as the pre-synaptic population and the excitatory population in L2/3 as the post-synaptic population and not instantiating the connecting synapses during the simulation.

L2/3 PCs had to meet three criteria to be included in the subsequent analysis. Firstly, their activity was required to remain subthreshold during the 500 ms long whisker hold stimulus and in 200 ms long time windows before and after the stimulus, both in control and *in silico* optogenetic runs. Second, they had to be innervated by at least one (active) VPM fiber. Third, the derivative of their voltage trace had to cross the 1 mV/ms threshold in a 20 ms time window after stimulus onset in the control simulation. The last two were motivated by comparing subthreshold voltages to voltage traces from Varani et al. (2022) that showed large, stimulus evoked EPSPs. Around 8% of L2/3 PCs in the central column met all the above criteria and their voltages were averaged to arrive to the traces shown in Figure 6C-D. Thus, unlike in the original analysis, cells rather than trials were averaged. The motivation for this approach is that while *in vivo* it is easier to repeat the same paradigm after establishing stable recording conditions in a given cell, *in silico* it is quicker to record from all cells in a single simulation, instead of repeating the stimulus several times.

4.1.13 Recreating Shapiro et al., 2022

Since our model comprises the nbS1 and not the V1 brain area, we modelled visual drifting gratings in a more abstract way, without taking specifics of the visual system into account. In particular, we defined $\rho(x_\zeta, y_\zeta, t)$ as a spatio-temporal rate pattern corresponding to linear sinusoidal drifting gratings for a fraction F_P of 937 VPM fibers projecting to a single simulated column (30k neurons, 520 μm diameter). For all other VPM fibers ρ was zero. The gratings had a temporal frequency of $f_{temp} = 2\,\text{Hz}$ and a spatial frequency of 0.03 cycles/degree which we translated to $f_{spat} = 0.001\,\text{cycles}/\mu m$ by assuming a cortical magnification factor in rat of 30 μm/degree (Gias et al., 2005). In Figure 6E, the spatial grating patterns are illustrated at different points in time.

As in Shapiro et al. (2022), we used five contrast levels $C \in [0.06, 0.12, 0.24, 0.5, 1.0]$ which were defined as the Michelson contrast given the minimum and maximum luminance values L_{min} and L_{max}:

$$C(L_{min}, L_{max}) = \frac{L_{min} - L_{max}}{L_{min} + L_{max}} \tag{6}$$

Since the physical quantity of luminance does not have a clear correspondence in our model, we used normalized luminance values L_{min} and L_{max} between 0.0 and 1.0 by computing the inverse Michelson contrast centered around a mean normalized luminance of 0.5. The resulting values of L_{min} and L_{max} where then scaled and shifted to the minimum and maximum rates of the sinusoidal modulation R_{min} and R_{max} respectively such that the peak firing rate at contrast 1.0 was given by R_{peak} and the mean of the

modulation corresponding to the background firing rate at contrast 0.0 was given by R_{bk}. The resulting sinusoidal input rate signal can be written as:

$$\rho_\zeta(t) = R(t, l_\zeta) = R_{min} + 0.5(R_{max} - R_{min})\Big[1 + \sin(2\pi\, f_{temp}\, t - 2\pi\, f_{spat}\, l_\zeta)\Big]\Big|_+ \tag{7}$$

where t is the time in seconds, l_ζ the linear position of ζ within the grating, and $|_+$ denotes that firing rates are truncated to positive values only. Figure 6F illustrates a random series of rate signals corresponding to different contrasts. No transfer function was used, and spiking process ψ was an adapting Markov process (Muller et al., 2007) with an adaptation time constant of 100 ms. Values for F_P, R_{peak}, and R_{bk} were determined beforehand by a parameter optimization so that the resulting grating responses were qualitatively comparable with the ones reported by Shapiro et al. (2022), see next subsection for details.

Calibration of drifting grating stimulus We ran a parameter scan to determine optimal values for F_P (fraction of 937 VPM fibers projecting to the central column of our model to apply grating stimulus to), R_{peak} (peak firing rate at contrast 1.0), and R_{bk} (background firing rate at contrast 0.0). This calibration was done by running 45 simulations using all combinations of parameter values in the ranges $F_P \in [0.5, 0.75, 1.0]$, $R_{peak} \in [5.0, 10.0, 15.0, 20.0, 25.0]$ Hz and $R_{bk} \in [0.05, 0.1, 0.2]$ Hz, and selecting the optimal combination amongst them. Each simulation lasted 40 s during which 20 contrast stimuli were presented for 1 s, followed by a 1 s (blank) inter-stimulus interval. Four contrast levels $C \in [0.06, 0.12, 0.5, 1.0]$ were presented five times each in random order, which was sufficient to fit sigmoidal tuning functions with four parameters (see Eq. 9).

We observed that especially under strong stimulus conditions the response rates of PCs to the first and second cycle of the sinusoidal grating pattern (1 s stimulus at $f_{temp} = 2$ Hz) were quite different, with the second response largely attenuated due to synaptic depletion. Therefore, we extracted first and second peak firing rates r_1 and r_2 respectively from the peristimulus time histograms (PSTHs) computed with 1 ms resolution and 20 ms Gaussian smoothing (Figure S10). We defined a measure of the normalized peak difference as the Michelson contrast of the peak rates r_1 and r_2, given by

$$\hat{r}_{diff} = \frac{r_1 - r_2}{r_1 + r_2} \tag{8}$$

Additionally, we extracted average firing rates for each contrast level of the whole population of PCs within the full (1 s) as well as the first and second halves (0.5 s each) of the stimulation intervals. We then fitted sigmoidal tuning functions with parameters c_{50}, m, n, and R_{max} (see Eq. 9) to these average tuning responses (Figure S11). Finally, as summarized in Figure S10 and S11, we selected the best combination of parameters based on the following selection criteria:

- The peak firing rates in response to the grating stimulus should be sufficiently strong, covering a range of values including the one reported in (Shapiro et al., 2022, cf. Figure 1D). So we imposed the constraint that the maximum peak rates over the whole population of PCs of the first and second peaks r_1 and r_2 respectively should be at least $r_{th} = 30$ Hz at maximum contrast.

- The peak responses to the first and second cycle of the grating stimulus should not be too different. So we aimed for a low peak difference $\hat{r}_{diff}$ at maximum contrast.

- The overall tuning response of the PCs should be in a regime where the tuning curve would have a sigmoidal shape, meaning that it should be increasing but saturating with increasing contrasts. To fulfill this constraint, we aimed for
  - Low c_{50}, i.e., the inflection point of the tuning curve would be at low contrasts
  - High n, i.e., a steep non-linear increase of the tuning curve until saturation

In order to combine these criteria independent of the actual scales of $\hat{r}_{diff}$, c_{50} and n, we computed their individual rank scores in decreasing ($\hat{r}_{diff}$, c_{50}: lower is better) or increasing (n: higher is better) order. We then selected the parameter combination with the highest product of rank scores, excluding the ones with peak firing rates r_1 and r_2 below r_{th} and the ones with c_{50} values close to 1.0 (border cases). We found an optimal parameter combination of $F_P = 1.0$, $R_{peak} = 10.0\,\mathrm{Hz}$, and $R_{bk} = 0.20\,\mathrm{Hz}$ which we used throughout this *in-silico* experiment.

Optogenetic stimulation Optogenetic stimulation was targeted at either 1654 PV+ or 822 Sst+ interneurons in a single column. We used parameters $\mu_a \approx 0.46\,\mathrm{mm}^{-1}$ and $\mu_s' \approx 5.38\,\mathrm{mm}^{-1}$, based on the wavelength of 470 nm (blue light; see Figure S2). I_0 was increased from 0% to 300% in steps of 50%.

Quantification of contrast tuning responses by sigmoidal functions We quantified contrast tuning responses in the same way as described by Shapiro et al. (2022), by least-squares fitting sigmoidal functions to the normalized tuning curves. Normalized tuning curves were obtained by computing the time-averaged firing rates of all 1 s stimulus intervals and dividing them by the mean baseline firing rate (i.e., w/o optogenetic stimulation) at the highest contrast level. The sigmoidal function was given by

$$R(c) = \frac{R_{max}\, c^n}{c^n + c_{50}^n} + m \tag{9}$$

where $R(c)$ describes the response amplitude at contrast c, m is the baseline response at minimum contrast, R_{max} is the maximum increase above baseline, n defines the steepness of the curve, and c_{50} is the contrast at half R_{max}. We used the coefficient of determination (r^2 score) as a measure of the goodness of fit.

Detection of neurons with robust contrast tuning We identified PV+, Sst+, and pyramidal neurons with robust contrast tuning behavior under all conditions. In the experimental study of Shapiro et al. (2022), tetrode recordings were used together with spike sorting. Correspondingly, we only considered neurons firing at rates above 0.5 Hz under all stimulus conditions, meaning they could potentially be detected by spike sorting (Pedreira et al., 2012). In addition, we considered neurons as being robustly tuned if they had strictly monotonically increasing tuning curves.

Modelling the effects of optogenetic stimulation of interneurons Direct photostimulation effects on interneurons were modelled by a divisive scaling model $R_{div}(c)$, a subtractive shifting model $R_{sub}(c)$, or a saturation additive model $R_{sat}(c)$ (Shapiro et al., 2022). For fitting these models, the parameters c_{50}, m, n, and R_{max} of the underlying contrast tuning function $R(c)$ were kept constant at values obtained from baseline fits (i.e., w/o optogenetic stimulation). The divisive scaling model was defined as

$$R_{div}(c) = R(c)/g \tag{10}$$

with a scaling term g. The subtractive shifting model was given by

$$R_{sub}(c) = R(c) - h \Big|_{+} \tag{11}$$

with a shifting term h and rectification to rates equal or above zero. The saturation additive model was defined as

$$R_{sat}(c) = R(c) + \frac{S\, c^{-n}}{c^{-n} + c_{50}^{-n}} + A \tag{12}$$

with a saturation term S and an additive term A. We used the r^2 score to measure the goodness of model fits.

Indirect effects on PCs receiving inhibitory input from optogenetically activated interneurons were modelled by a conductance-based model $R_{cond}(c)$, assuming a saturating additive model description of interneurons (Shapiro et al., 2022). Response rates under this conductance-based model were given by

$$R_{cond}(c) = \Big[\Delta V(c) - V_{th}\Big]^3 \Big|_{+} \tag{13}$$

with a spike threshold $V_{th} = 3.4\,\mathrm{mV}$ and rectification to rates equal or above zero. The membrane potential $\Delta V(c)$ as a function of contrast was given by

$$\Delta V(c) = \frac{g_L\, R_L + g_E(c)\, R_E + g_I(c)\, R_I}{g_L + g_E(c) + g_I(c)} - V_r \tag{14}$$

with values for leak conductance $g_L = 6\,\mathrm{nS}$, leak reversal potential $R_L = -50\,\mathrm{mV}$, excitatory reversal potential $R_E = 0\,\mathrm{mV}$, inhibitory reversal potential $R_I = -65\,\mathrm{mV}$, and resting potential $V_r = -50\,\mathrm{mV}$ as reported by Shapiro et al. (2022). The excitatory synaptic conductance was given by

$$g_E(c) = \frac{g_{E_max}\, c^n}{c^n + c_{50}^n} + g_{E_min} \tag{15}$$

with the excitatory conductances at low/high contrast given by g_{E_min} and g_{E_max} respectively. The inhibitory synaptic conductance was given by

$$g_I(c) = g_E(c) + \frac{S\, c^{-n}}{c^{-n} + c_{50}^{-n}} + \Delta g_{IE_min} + A \tag{16}$$

with an inhibitory conductance offset $\Delta g_{IE_min} = 2\,\mathrm{nS}$ at low contrast relative to g_{E_min}.

In a first step, parameters S and A were set to zero and the model parameters $c50$, g_{E_min}, g_{E_max}, and n were fit to baseline responses of PCs. In a second step, those parameter values were kept constant and the model parameters S and A were fit to PC responses under photostimulation conditions. Again, we used the r^2 score to measure the goodness of model fits.

4.1.14 Recreating Prince et al., 2021

We also compared the *in vivo* state of our model with the results of a recent *in vitro* study (Prince et al., 2021), which explored how neurons with different biophysical properties

encode different types of signals. The *in vitro* study optically activated groups of 10 PCs in slices of L2/3 barrel cortex from mouse lines labelling fast-spiking (FS) and regular-spiking (RS) interneurons. Each PC was targeted individually and a binary signal was encoded either through changes in the rate of optical pulses applied to the 10 stimulus neurons, or through changes in the synchronicity of the pulses. The mutual information shared between the binary signal (when encoded either as changes in firing rate or synchronicity) and the firing rate of different inhibitory sub-types (recorded using whole-cell patch clamping *in vitro*) was analysed.

While the *in vitro* stimuli used optical pulses targeted at single neurons with timings drawn from Poisson processes, it was not necessary to explicitly model such an optical stimulus *in silico*, as we can instead elicit spikes directly in the model. In the original study, the 10 stimulus neurons were uniformly separated in a grid-like pattern at horizontal and vertical distances of $\sim 50\,\mu m$. The binary signal alternated between two states at random intervals of 2-7 s. For the rate coding paradigm, the timings of the optical pulses for the 10 stimulus neurons were drawn from 10 independent inhomogeneous Poisson processes, with the rates of optical activation varying between 5 Hz and 0.5 Hz for the up and down states respectively (average firing rate: 2.7 Hz). For the synchronous case, the timings of the optical pulses for the 10 stimulus neurons were drawn from a single inhomogeneous Poisson process during the up state, or 10 independent inhomogeneous Poisson processes during the down state. For the synchronous case, the firing rates of the up and down state were both 2.7 Hz. We therefore tested stimulus encoding using a range of stimulus neuron counts: from 10 to 1,000.

In our interpretation of the study, mutual information was measured between the binary signal and neural activity during a 0-5 ms and 5-50 ms window following a change in the signal. These represented 'early' and 'late' stimulus encoding windows following the change in the signal, respectively. As the synchronous up state activated synchronous patterns at a rate of 2.7 Hz, we calculated that a synchronous pattern would only be activated during the early and late windows with probability 0.0135 ($= 2.7 * 5/1000$) and 0.1125 ($= 2.7 * 45/1000$) respectively. We therefore chose to use higher FR of 20 Hz for the synchronous up and down states, and to analyse mutual information between the binary signal and all 50 ms bins. To afford comparison with the rate code experiment type, we used 30 Hz and 10 Hz as the FRs of the up and down states respectively. We also compare stimulus coding during the first 50 ms following the stimulus change for both the synchronous and rate stimulus types.

4.1.15 Analyzing mid-range connectivity & correlations

Neurons were split into hexagonal subvolumes of a specified diameter d considering their locations in a flattened view (Bolaños-Puchet et al., 2024).Then, the number of mid-range connections within and between the hexagonal subvolumes were counted, yielding in S, the adjacency matrix of the resulting directed graph. Distances between hexagonal subvolumes were calculated by considering the centers of the hexagons in the flattened view. Furthermore, correlations of spiking activity of pairs of hexagonal subvolumes were also calculated. To that end, all spikes within a hexagonal subvolume were pooled and their number in 5 ms time bins; and lastly the Pearson correlations of the resulting time series were calculated. The correlation within a hexagonal subvolume was calculated

similarly, but using the separate time series of the E and I populations. Together, this yielded F, the matrix of correlations of subvolumes. Based on S and F, the expected correlations of mid-range inputs was calculated as follows: Let i be a hexagonal subvolume and S_i the column of S associated with input counts into i. Then $P = S_i \cdot S_i^\top$ is in the matrix of counts of pairs of inputs for all pairs of hexagonal subvolumes. Combining P and F allows one to estimate the distribution of correlations of mid-range inputs into i, albeit at the population rather than single-cell level. For the correlation in Figure 8A2, H, J1 a hexagon size of $400\mu m$ was used, while in Figure 8I2 a smaller size of only $50\mu m$ was used.

4.1.16 Node participation

Given a connectivity graph G, a directed n-simplex in G is a set of $n+1$ nodes which are all all-to-all connected in G in a feed-forward fashion, i.e., such that any subset of these has a unique source and a unique sink (see Reimann et al. (2017) for more details). The *n-node participation* of a node v in G is the number of directed n-simplices this node is part of. In particular, for $n = 1$, this is the total degree of the node in G. Thus, this can be though of a generalization of the notion of degree that takes into account account higher order interactions and has been shown to strongly correlate with other node centrality metrics Sizemore et al. (2018).

For any numeric property of neurons, e.g., firing rate, we evaluate the effect of dimension on it by taking weighted averages across dimensions. That is for each dimension k, we take the weighted average of the property across neurons where the weights are given by node participation on dimension k. More precisely, let N be the number of neurons and $\overrightarrow{V} \in \mathrm{R}^N$, be a vector of a property on all the neurons e.g., the vector of firing rates. Then in each dimension k we compute

$$\mathbf{mean}_k = \frac{1}{N * \sum(\overrightarrow{Par_k})} \overrightarrow{V} \cdot \overrightarrow{Par_k},$$

where $\overrightarrow{Par_k}$ is the vector of node participation on dimension k for all neurons and $\cdot$ is the dot product.

To measure the over and underexpression of the different m-types among those with the highest 5% of values of node participation, we used the hypergeometric distribution to determine the expected distribution of m-types in a random sample of the same size. More precisely, for each dimension k and m-type m, let N_{total} be the total number of neurons in the circuit, N_m be the number of neurons of m-type m in the circuit, C_{top} be the number of neurons with the highest 5% values of node participation in dimension k, C_m the number of neurons of mtype m among these, and let $P = hypergeom(N_{total}, N_m, C_{top})$ be the hypergeometric distribution.

By definition, $P(x)$ describes the probability of sampling x neurons of m-type m in a random sample of size C_{top}. Therefore, using the cumulative distribution $F(x) = P(\text{Counts} \leq x)$, we can compute the p-values as follows:

underexpression: $P(\text{Counts} \leq C_m) = F(C_m)$,
overexpression: $P(\text{Counts} \geq C_m) = 1 - P(\text{Counts} < C_m - 1) = 1 - F(C_m - 1)$.

Small values indicate under and over representation respectively.

4.2 Quantification and statistical analysis

Details of all statistical analyses can be found in figures and figure legends.

4.3 Additional Resources

No other additional resources.

Videos

1. Layer-wise E and I population rasters and max-normalised histograms of spontaneous activity for the central column of the seven column subvolume for each of the 60 meta-parameter combinations. Meta-parameter values are shown in brackets in the following order: Ca^{2+}, P_{FR}, R_{OU}.

2. Visualisation of spontaneous activity for the seven column subvolume for the parameter combination $Ca^{2+} = 1.1\,\text{mM}$, $P_{FR} = 0.9$, $R_{OU} = 0.2$ after collapsing activity to flatspace (activity binned and smoothed).

3. Layer-wise E and I population rasters and max-normalised histograms of evoked activity during the 10 single whisker deflection protocol for each of the simulated meta-parameter combinations. Meta-parameter values are shown in brackets in the following order: Ca^{2+}, P_{FR}, R_{OU}, F_P.

4. Trial-averaged max-normalised histograms of evoked activity during the 10 single whisker deflection protocol for each of the simulated meta-parameter combinations. Rasters of spiking activity shown for the first of 10 trials activity. Dashed lines show *in vivo* single whisker deflection reference data. Meta-parameter values are shown in brackets in the following order: Ca^{2+}, P_{FR}, R_{OU}, F_P.

5. Visualisation of trial-averaged response of the seven column subvolume over the 10 single whisker deflection protocol for the parameter combination $Ca^{2+} = 1.1\,\text{mM}$, $P_{FR} = 0.3$, $R_{OU} = 0.4$, $F_P = 20\%$ after collapsing activity to flatspace (activity binned and smoothed).

6. Layer-wise E and I population rasters and max-normalised histograms of spontaneous activity for (a) hex0 and (b) hex39 for meta-parameter combinations: $Ca^{2+} = 1.05\,\text{mM}$, $R_{OU} = 0.4$ and $P_{FR} = 0.05 - 0.3$.

7. Visualisation of spontaneous activity for the full nbS1 model for the parameter combination $Ca^{2+} = 1.05\,\text{mM}$, $P_{FR} = 0.15$, $R_{OU} = 0.4$ after collapsing activity to flatspace (activity binned and smoothed).

8. Layer-wise E and I population rasters and max-normalised histograms of stimulus evoked activity for (a) hex0 and (b) hex39 for each meta-parameter combination $Ca^{2+} = 1.05\,\text{mM}$, $R_{OU} = 0.4$, $P_{FR} = 0.15$ and $F_P = 0.1 - 0.25$.

9. Visualisation of trial-averaged response of the full nbS1 model over the 10 single whisker deflection protocol for the parameter combination $Ca^{2+} = 1.1\,\text{mM}$, $P_{FR} = 0.15$, $R_{OU} = 0.4$, $F_P = 20\%$ after collapsing activity to flatspace (activity binned and smoothed).

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Table S1: Predictions

(1)	
Prediction	**Correlation between excitatory and inhibitory populations increases exponentially from supra to infragranular layers; the power of low frequency oscillations also increases towards deeper layers.**
Importance	Charazterizing the correlation between excitatory and inhibitory populations is critical for our understanding of the neural code and is of high interest to theoretical point neuron modellers and experimentalists (Vogels and Abbott, 2009; Vogels et al., 2011). Particularly, such correlations are thought to govern homeostasis ("E/I balance") and in turn the dynamics of populations during resting and evoked activity. Moreover, such correlations can give clues towards the level of recurrent processing within a neural population. Despite its perceived importance in the field, a laminar characterization of such correlations over a full spectrum of temporal frequencies is beyond existing techniques for spiking activity. Spike sorting usually only finds a small handful of neighbouring E and I neurons within each cortical layer, which is insufficient to quantify local intra-layer inter-population correlations. Calcium imaging does not have the required temporal resolution for such a characterization and is limited at deeper layers. Unfortunately, only proxies of such correlated neuronal activity can currently be studied, although this still has high impact appeal, due to the described relevance of this question. For example, a recent study analyzed the local field potential (LFP) to demonstrate "a ubiquitous spectrolaminar motif of local field potential power across the primate cortex" (Mendoza-Halliday et al., 2024). Particularly, the authors found a decrease in the frequency of the dominant LFP power, from supra- to infra-granular layers. Although this piece of evidence was demonstrated only for noise in the extracellular space (LFP), which was generated by neural activity, this piece of evidence excitingly supports the more detailed prediction of our model where we observed an increase in low frequency oscillations towards deeper layers. The presence of such a hetero-laminar effect also demonstrates the utility of our model: point neuron modellers can now explore the role of different neruon types and connectivity motifs in excitatory/inhibitory balance within a calibrated and detailed model.
Novelty	Our model allows access to the spiking activity of all neurons across layers, for a well calibrated activity state. The detail of our model allow us to explore the correlation and interaction between different morphoelectric neuron types with full spatiotemporal resolution.
Experiment	Beyond the recent LFP study, the quantitative predictions which our model makes will be able to be tested once recording techniques provide suffient clarrity of neuronal population activity. For example, the rapid improvement of extracellular recording devices and spike sorting techniques will hopefully make it possible to soon measure sufficient numbers of E and I neurons within each layer.
Extension	1. Fit exponentials to the data in Figure 4I to predict the precise layer dependence. 2. Extend to look at the cortical depth dependence of spiking correlations.

(2)	
Prediction	**Specific spatial targeting rules observed for different inhibitory subpopulations in electron microscopy act to more strongly self-inhibit inhibitory populations and inhibit excitatory populations. This changes E/I balance for inhibitory populations from an excitation dominated state to an inhibition dominated state, whilst overall excitatory populations became less dominated by excitation. Specifically, increased perisomatic targeting by PV+ neurons, increased VIP+ targeting of other inhibitory neurons, neurons in L1 connecting more monosynaptically, and I connections onto E neurons being sparser and closer to the soma. This increased self-inhibition towards central layers with the greatest effect in L4. As a result, inhibitory populations require increased non-local drive.**
Importance	Highly specific targeting rules and self-inhibition by inhibitory populations are likely to play important roles in cortical function. However, it is currently challenging to manipulate the connectivity of inhibitory subpopulations as a way of probing their causal effect. The fact that the firing rates of inhibitory populations increased upon connection of the network in the original connectome but decreased upon connection in the SM-connectome shows that the more specific targeting rules act to make inhibitory populations more inhibited overall by local connectivity, rather than excited.
Novelty	To our knowledge this is the first comparison of two models where one includes spatially specific targeting rules and one that does not. The new calibration technique allowed methodical comparison of the two networks over a 60 different regimes in which the firing rates of the two networks were matched.

(3)	
Prediction	**Quantitative prediction of extracellular recording bias.**
Importance	It has commonly been discussed that extracellular recording and spike sorting are likely to bias our view of in vivo spiking activity (Wohrer et al., 2013). This has serious consequences for our interpretation of sorted spike trains, which we plan to investigate further.
Novelty	Whilst synthetic datasets have been used to benchmark spike sorting algorithms before, this model is the first to capture the variety of M-types and E-types, combined with realistic in vivo dynamics.
Experiment	This would require large-scale unbiased patch-clamping combined with extracellular recording and spike sorting.

(4)

Prediction

The degree of participation in high-dimensional simplices predicts the level of correlation between inhibitory and excitatory populations in a cortical layer.

Importance

Internal "recurrent" processing is of great interest to theoretical modellers because such recurrent processing is thought to underlie many cognitive functions. To study the factors underlying such recurrent processing, theoretical modellers commonly use networks of abstract point neurons with random or all-to-all connectivity. It is important to study how three-dimensional biological design influences the spatiotemproal dynamics of recurrent processing to better understand complex cortical function. Our prediction suggests that pairwise connectivity statistics are insufficient to predict the level of correlation within a cortical layer, and that specific high-dimensional local connectivity motifs drive internal spontaneous activity.

Novelty

Such an analysis is currently unattainable *in vivo* because: 1. consistent electron micropscopy datasets across cortical layers are not available, and 2. the spiking activity over large intra-layer populations is limited (as described for the previous prediction). To our knowledge our analysis represents the most biophysically-constrained *in silico* comparison between high-dimensional connectivity motifs and emergent activity.

Experiment

Larger electron-microscopy datasets which are currently being collected will enable direct comparisons with the dimensionality of the connectivity motifs within a cortical layer. Quantifying E/I spiking correlations at the population level will require better tools for measuring *in vivo* spiking activity, as described for the previous prediction.

(5)

Prediction

Higher order structure has functional implications

Importance

The higher order network metrics that have been found relevant in describing the non-random complexity of the network and detailed in the accompanying manuscript have been linked to function. The importance is two-fold: First, it gives relevance to the many ways in which the structure of connectivity has been characterized as non-random before. We now know that this is no mere epiphenomenon, but a mechanism of cortical processing. Second, it provides useful metrics for the description of how structure shapes function. More specific predictions of the link between higher-order network structure and function:

- E/I correlations can be predicted from higher order centrality metrics.
- The strength of a connection can be predicted from how it is embedded in the whole network in a higher order sense. This finding has been further verified in MICrONS-Consortium et al. (2021) (see Ecker et al. (2024b))
- Higher order interactions shape the correlation of activity. This has also been verified in MICrONS-Consortium et al. (2021) (see Egas Santander et al. (2024)).

Novelty

In all these structure-function predictions highlighted, the use of higher-order structures was crucial.

(6)	
Prediction	**Layer-wise populations receive external drive from non-local connectivity within a precise and specific range. Moreover, input from non-local connectivity is essential for stable non-zero activity at resting.**
Importance	To our knowledge, the amount of conductance that a neuron receives from non-local vs local connectivity is unknown, as it is unknown how a cortical brain region would behave when disconnected from other brain regions. These two factors are important for the constraint of biophysically-detailed models, and the insights they can make. Although it seems trivial that a cortical area should be silent under *in vivo* conditions when disconnected from other areas, we have received questions from experimentalists about whether this is the case, and to our knowledge it is unknown.
Novelty	This was only possible to test with a model at the level of an entire cortical subregion, which incorporated both local and non-local connectivity.
Experiment	This could be estimated *in vivo* by measuring the frequency of synaptic activations across dendrites during resting state activity. To test the need for afferent input from non-local connections for non-zero resting state activity, one would need to ablate incoming connections to a cortical region and measure spiking activity.

(7)	
Prediction	**Cortical curvature does not predict level of correlative activity in a cortical column (negative result not shown).**
Importance	The cortex is a highly and heterogeneously curved structure, especially in humans. To our knowledge there have been no studies of the effect of such curvature on spiking activity, for example in terms of the level of correlated activity. If such an effect exists in rodent, it is likely to play out even stronger in human. Even in our model of a single cortical region we observed high heterogeneity in curvature, which we quantified in the first manuscript. However, we found that activity metrics were remarkably unaffected by the resulting differences in connectivity.
Novelty	We are not aware that this potential aspect of cortical function has been considered before.
Experiment	As with the previous point, this could be confirmed or rejected by specifically generating co-registered connectome and activity dataset for regions with different curvature.

(8)	
Prediction	**Single whisker deflections activate 5-10% of thalamic fibres in a single barreloid. Excitatory populations respond more sparsely to whisker deflections than inhibitory populations. Stimulus response sparsity is heterogeneous across layers.**
Importance	These predictions are about unknowns of cortical processing within the canonical barrel system.
Novelty	This highlights that critical details about basic cortical processing remain unknown but can be predicted by well constrained cortical models.
Experiment	Testing these predictions would require calcium imaging over VPM barreloids and different layers of cortex.

(9)	
Prediction	**L4 PCs contribute to L23 PC response through direct excitatory connections rather than disinhibition. L2/3 PCs and L4 PCs make similar contributions to L2/3 PC responses, L5 PCs have a smaller effect, L6 PCs' have a negligible effect.**
Importance	This relates to the mechanisms underlying canonical cortical processing.
Novelty	This demonstrates the model's capacity for experiments that are currently limited by existing *in vivo* techniques as described in the manuscript.
Experiment	These predictions are grounded in techniques which could become available in the near future (markers for the optogenetic tagging of different cell types).

(10)	
Prediction	**Encoding of synchronous and rate-code signals by inhibitory subpopulations is strongest for PV+, followed by 5HT3aR+, and then SSt+.**
Importance	Encoding by different inhibitory neuron-types is likely to play a key role in how the cortex processes and represents information *in vivo*.
Novelty	The study which inspired this work could only be performed *in vitro*. That is, to our knowledge, stimulating precise multi-neuron patterns of spikes and measuring spiking responses from different inhibitory sub-types would be challenging to perform *in vivo*.
Experiment	Voltage-imaging may soon make such a study simpler to perform *in vivo*.

(11)	
Prediction	**Quantitative predictions about the nature and connectivity underlying correlated activity.** Particularly, we predict 1) that correlations between afferent regions, increases internal correlations, 2) local correlation is predicted by participation in (or vicinity to) a rich club of cortical columns connected by dense non-local connectivity, 3) the distance dependence of spiking correlations.
Importance	The importance, novelty and means of testing predictions about correlated activity have been discussed in other points.

(12)	
Prediction	**Specific targeting rules by inhibitory subpopulations increase stimulus-evoked responses in L23, decrease responses in L5 and L6, and slightly increase stimulus response latencies.**
Importance	As discussed for prediction (2) the role of specific targeting rules are important to understand but difficult to study *in vivo*.

Table S2: Excitatory synaptic pathways. Average class parameters are marked in bold and are used predictively (in lack of reference *in vitro* data) for the remaining pathways belonging to the same class. Physical dimensions are as follows: peak conductance $\hat{g}$: nS, depression and facilitation time constants D, F, and the EPSC τ_{decay}: ms, the Hill coefficient of the nonlinear $[Ca^{2+}]_o$ dependent scaling of release probability U_{Hill}: mM, the release probability U_{SE}, the average number of vesicles in the release-ready pool N_{RRP}, and the NMDA/AMPA ratio $\hat{g}_{ratio}$ are dimensionless.

Pre	**Post**	$\hat{g}$	U_{SE}	D	F	N_{RRP}	τ_{decay}	$\hat{g}_{ratio}$	U_{Hill}
				PC to Sst+IN (E1)					
PC	MC	0.2±0.1	0.09±0.12	138±211	670±830	1.5	1.74±0.18	0.8	2.79
PC	**PT**	**0.6±0.5**	**0.02±0.00**	**194±18**	**507±37**	**4.5**	**1.74±0.18**	**0.8**	**1.09**
PC	**DT**	**0.2±0.1**	**0.02±0.00**	**194±18**	**507±37**	**1.5**	**1.74±0.18**	**0.8**	**2.79**
				PC to PC (E2)					
L23_PC	L23_PC	1.0±0.5	0.46±0.26	671±17	17±5	2.6	1.74±0.18	0.7	2.79
L4_PC	L4_PC	0.6±0.3	0.86±0.09	671±17	17±5	1.0	1.74±0.18	0.9	2.79
L4_SSC	L23_PC	0.2±0.1	0.79±0.04	671±17	17±5	1.8	1.74±0.18	0.5	2.79
L5_STPC	L5_STPC	0.9±0.3	0.39±0.03	690±90	44±21	1.0	1.74±0.18	0.7	2.79
L5_TTPC	L5_TTPC	1.9±1.0	0.38±0.10	365±100	25±45	2.8	1.74±0.18	0.7	2.79
L23_PC	L5_TTPC	0.5±0.2	0.50±0.02	671±17	17±5	1.5	1.74±0.18	0.7	2.79
L4_SSC	L5_STPC	0.6±0.3	0.50±0.02	671±17	17±5	1.2	1.74±0.18	0.7	2.79
L4_SSC	L6_PC	0.4±0.2	0.50±0.02	671±17	17±5	1.0	1.74±0.18	0.7	2.79
L6_TPC:A	L6_TPC:A	1.0±0.5	0.37±0.11	280±90	90±80	1.0	1.74±0.18	0.7	2.79
L6_TPC:C	L6_TPC:C	0.5±0.2	0.23±0.06	420±340	200±130	1.0	1.74±0.18	0.7	2.79
L6_IPC	L6_IPC	0.9±0.3	0.23±0.06	420±340	200±130	1.0	1.74±0.18	0.7	2.79
L6_PC to same L6_PC		**0.8±0.2**	**0.23±0.06**	**420±340**	**200±130**	**1.0**	**1.74±0.18**	**0.7**	**2.79**
L6_TPC:A	L6_TPC:C	1.2±0.5	0.23±0.06	420±340	200±130	1.0	1.74±0.18	0.7	2.79
L6_TPC:A	L6_BPC	0.3±0.1	0.23±0.06	420±340	200±130	1.0	1.74±0.18	0.7	2.79
L6_TPC:C	L6_IPC	0.2±0.1	0.23±0.06	420±340	200±130	1.0	1.74±0.18	0.7	2.79
L6_IPC	L6_BPC	0.4±0.1	0.23±0.06	420±340	200±130	1.0	1.74±0.18	0.7	2.79
L6_BPC	L6_TPC:A	0.2±0.1	0.23±0.06	420±340	200±130	1.0	1.74±0.18	0.7	2.79
L6_PC to diff. L6_PC		**0.5±0.4**	**0.23±0.06**	**420±340**	**200±130**	**1.0**	**1.74±0.18**	**0.7**	**2.79**
PC	**PC**	**0.7±0.4**	**0.50±0.02**	**671±17**	**17±5**	**1.5**	**1.74±0.18**	**0.7**	**2.79**
				PC to Sst-IN (E2)					
PC	NBC	0.6±0.4	0.72±0.12	227±70	13±24	4.5	1.74±0.18	0.8	1.09
PC	**PT**	**0.6±0.5**	**0.50±0.02**	**671±17**	**17±5**	**4.5**	**1.74±0.18**	**0.8**	**1.09**
PC	L1_GABAB-	0.3±0.1	0.50±0.02	671±17	17±5	1.5	1.74±0.18	0.8	1.94
L6_TPC:A	L6_BC	0.4±0.1	0.58±0.13	240±80	70±90	1.5	1.74±0.18	0.8	1.09
L6_TPC:C	L6_BC	0.4±0.1	0.36±0.21	380±310	280±340	1.5	1.74±0.18	0.8	1.09
L6_IPC	L6_BC	0.3±0.1	0.51±0.20	440±300	100±50	1.5	1.74±0.18	0.8	1.09
L6_PC	**L6_BC**	**0.4±0.1**	**0.47±0.21**	**370±290**	**155±215**	**1.5**	**1.74±0.18**	**0.8**	**1.09**
PC	**IN**	**0.4±0.1**	**0.50±0.02**	**671±17**	**17±5**	**1.5**	**1.74±0.18**	**0.8**	**1.94**

Proximal Targeting inhibitory mtypes: N/L/SBC, CHC. N/LBC etypes: cACint, cIR, bAC, bIR, cNAC have E1, while the rest of etypes; and SBC and CHC mtypes have E2 short-term dynamics.
Distal Targeting inhibitory mtypes: BP, DBC, BTC. L1_GABAB- comprise all non NGC mtypes in L1

Table S3: Inhibitory synaptic pathways. Average class parameters are marked in bold and are used predictively (in lack of reference *in vitro* data) for the remaining pathways belonging to the same class. Physical dimensions are as follows: peak conductance $\hat{g}$: nS, depression and facilitation time constants D, F, and the IPSC τ_{decay}: ms, the Hill coefficient of the nonlinear $[Ca^{2+}]_o$ dependent scaling of release probability U_{Hill}: mM, the release probability U_{SE}, the average number of vesicles in the release-ready pool N_{RRP}, and the $GABA_B/GABA_A$ ratio $\hat{g}_{ratio}$ are dimensionless.

Pre	**Post**	$\hat{g}$	U_{SE}	D	F	N_{RRP}	τ_{decay}	$\hat{g}_{ratio}$	U_{Hill}
				IN to PC (I1)					
L6_BC	L6_BC	2.3±0.5	0.16±0.10	45±21	376±253	1.0	10.40±6.20	0.0	1.94
SBC (cACint)	PC	1.9±1.0	0.16±0.10	45±21	376±253	3.3	10.40±6.20	0.0	1.94
				IN to PC and IN (I2)					
MC	PC	3.0±1.5	0.30±0.08	1250±520	2±4	1.0	8.30±2.20	0.0	1.94
DT	**PC**	**3.0±1.5**	**0.25±0.13**	**706±405**	**21±9**	**1.0**	**8.30±2.20**	**0.0**	**1.94**
NBC	PC	1.9±1.0	0.14±0.05	875±285	22±5	3.3	8.30±2.70	0.0	1.94
NGC	PC	0.2±0.1	0.25±0.13	706±405	21±9	1.0	36.50±1.30	0.8	1.94
L1_GABAB-	PC	0.3±0.1	0.25±0.13	706±405	21±9	1.0	8.30±2.20	0.0	1.94
SBC (dNAC)	PC	1.9±1.0	0.25±0.13	706±405	21±9	3.3	8.30±2.20	0.0	1.94
IN	*****	**2.3±0.5**	**0.25±0.13**	**706±405**	**21±9**	**1.0**	**8.30±2.20**	**0.0**	**1.94**
				IN to PC (I3)					
L6_BC	L6_PC	1.9±1.0	0.44±0.25	195±190	200±320	1.0	10.40±6.20	0.0	1.94
PT	**PC**	**1.9±1.0**	**0.32±0.14**	**144±80**	**62±31**	**3.3**	**6.40±1.70**	**0.0**	**1.94**

Proximal Targeting inhibitory mtypes: N/L/SBC, CHC. N/LBC etypes: cNAC, dSTUT, cSTUT, bSTUT have I3, while the rest of etypes; and SBC (except: cACint and dNAC) and CHC mtypes have I2 short-term dynamics. Distal Targeting inhibitory mtypes: BP, DBC, BTC. L1_GABAB- comprise all non NGC mtypes in L1

Table S4: Thalamocortical synaptic pathways. Values taken from the internal connectivity (Table S2) are marked in bold. Physical dimensions are the same as in Table S2.

Pre	**Post**	$\hat{g}$	U_{SE}	D	F	N_{RRP}	τ_{decay}	$\hat{g}_{ratio}$	U_{Hill}
				VPM, POm to Sst+IN (E1)					
*	Sst+	**0.2±0.1**	**0.09±0.12**	**138±211**	**670±830**	**1.5**	**1.74±0.18**	**0.8**	**2.79**
				VPM, POm to PC (E2)					
VPM	L23_PC	1.7±0.6	0.75±0.1	**671±17**	**17±5**	**1.5**	**1.74±0.18**	**0.7**	**2.79**
VPM	L4_PC	1.1±0.4	0.75±0.1	**671±17**	**17±5**	**1.5**	**1.74±0.18**	**0.7**	**2.79**
VPM	L56_PC	2.4±0.9	0.75±0.1	**671±17**	**17±5**	**1.5**	**1.74±0.18**	**0.7**	**2.79**
POm	PC	1.7±0.6	0.75±0.1	**671±17**	**17±5**	**1.5**	**1.74±0.18**	**0.7**	**2.79**
				VPM, POm to PV+IN (E2)					
VPM	L4_PV+	1.4±0.4	**0.72±0.12**	**227±70**	**13±24**	**4.5**	**1.74±0.18**	**0.8**	**1.09**
VPM	L6_PV+	3.1±1.0	**0.72±0.12**	**227±70**	**13±24**	**4.5**	**1.74±0.18**	**0.8**	**1.09**
VPM	L235_PV+	2.2±0.4	**0.72±0.12**	**227±70**	**13±24**	**4.5**	**1.74±0.18**	**0.8**	**1.09**
POm	PV+	2.2±0.4	**0.72±0.12**	**227±70**	**13±24**	**4.5**	**1.74±0.18**	**0.8**	**1.09**
				VPM, POm to 5HT3aR+IN (E2)					
*	5HT3aR+	**0.4±0.1**	**0.50±0.02**	**671±17**	**17±5**	**1.5**	**1.74±0.18**	**0.8**	**1.94**

Sst+ inhibitory mtypes: MC and BP, DBC, BTC (cACint etype only). PV+ inhibitory mtypes: N/LBC, CHC. 5HT3aR+ mtypes: the rest of the mtypes not listed above (e.g. NGC, SBC, and everything in L1).

Table S5: Validation of PSP amplitudes (see Figure 3B1)

Pre	**Post**	*in vitro* (mV)	*in silico* (mV)	Reference
L23_PC	L23_PC	1.00±0.70	0.99±0.67	Feldmeyer et al. (2006)
L23_PC	L5_TTPC	0.30±0.30	0.30±0.24	Reyes and Sakmann (1999)
L4_EXC	L4_EXC	1.59±1.51	1.62±1.31	Feldmeyer et al. (1999)
L4_SSC	L23_PC	0.70±0.60	0.66±0.34	Feldmeyer et al. (2002)
L4_SSC	L5_STPC	0.60±0.40	0.59±0.33	Feldmeyer et al. (2005)
L4_SSC	L6_PC	0.29±0.16	0.30±0.30	Qi and Feldmeyer (2016)
L5_TTPC	L5_TTPC	1.30±1.10	1.24±0.73	Markram et al. (1997)
L5_STPC	L5_STPC	0.80±0.20	0.75±0.40	Le Bé et al. (2007)
L6_BPC	L6_TPC:A	0.21±0.00	0.22±0.15	Berger (2009)
L6_IPC	L6_BPC	0.42±0.18	0.42±0.21	Berger (2009)
L6_IPC	L6_IPC	1.05±0.31	1.09±0.81	Berger (2009)
L6_TPC:C	L6_IPC	0.18±0.00	0.19±0.13	Berger (2009)
L6_TPC:C	L6_TPC:C	0.43±0.22	0.43±0.29	Berger (2009)
L6_TPC:A	L6_BPC	0.32±0.27	0.31±0.17	Berger (2009)
L6_TPC:A	L6_TPC:C	1.19±0.15	1.10±0.63	Berger (2009)
L6_TPC:A	L6_TPC:A	1.51±0.98	1.45±1.11	Berger (2009)
L23_PC	L1_GABAB-	1.10±0.30	1.09±0.83	Wozny and Williams (2011)
L4_EXC	L4_FS	2.20±2.20	2.17±2.46	Beierlein et al. (2003)
L5_TTPC	L5_MC	0.28±0.30	0.28±0.33	Silberberg and Markram (2007)
L6_IPC	L6_BC	1.59±1.60	1.56±1.48	Berger (2009)
L6_TPC:A	L6_BC	2.20±3.28	2.02±1.44	Berger (2009)
L6_TPC:C	L6_BC	1.29±1.65	1.28±0.84	Berger (2009)
L6_PC	L6_MC	0.20±0.12	0.15±0.14	Berger (2009)
L1_NGC	L23_PC	0.58±0.10	0.54±0.41	Wozny and Williams (2011)
L1_GABAB-	L23_PC	0.27±0.04	0.26±0.13	Wozny and Williams (2011)
L4_FS	L4_EXC	1.10±0.80	1.14±0.81	Beierlein et al. (2003)
L5_MC	L5_TTPC	0.50±0.40	0.47±0.25	Silberberg and Markram (2007)
VPM	L4_EXC	2.40±2.00	2.51±2.10	Beierlein et al. (2003)
VPM	L4_FS	4.10±3.20	4.09±2.52	Beierlein et al. (2003)
VPM	L6_EXC	1.20±0.80	1.28±1.96	Beierlein and Connors (2002)
VPM	L6_FS	3.90±3.50	3.11±2.57	Beierlein and Connors (2002)
Thick-tufted mtypes: L5_TPC:A, L5_TPC:B. Slender-tufted mtypes: L5_TPC:C, L5_UPC.				

Table S6: Validation of first PSP amplitudes' CVs (see Figure 3B2)

Pre	**Post**	*in vitro* (mV)	*in silico* (mV)	Reference
L4_EXC	L4_EXC	0.37±0.16	0.25±0.06	Feldmeyer et al. (1999)
L4_EXC	L4_FS	0.27±0.13	0.38±0.25	Beierlein et al. (2003)
L4_FS	L4_EXC	0.25±0.11	0.28±0.09	Beierlein et al. (2003)
L4_SS	L5_STPC	0.33±0.20	0.43±0.06	Feldmeyer et al. (2005)
L4_SS	L6_PC	0.50±0.11	0.51±0.06	Qi and Feldmeyer (2016)
L4_SS	L23_PC	0.27±0.13	0.32±0.07	Feldmeyer et al. (2002)
L5_TTPC	L5_TTPC	0.31±0.14	0.39±0.09	Barros-Zulaica et al. (2019)
L5_STPC	L5_STPC	0.58±0.24	0.51±0.06	Le Bé et al. (2007)
L23_PC	L23_PC	0.33±0.18	0.43±0.15	Feldmeyer et al. (2006)
L234_PC	L234_NBC	0.32±0.08	0.21±0.08	Wang et al. (2002)
Thick-tufted mtypes: L5_TPC:A, L5_TPC:B. Slender-tufted mtypes: L5_TPC:C, L5_UPC.				

Table S7: Validation of mPSC frequency (see Figure 3E2)

Pre	**Post**	*in vitro* (Hz)	*in silico* (Hz)	Reference
E	L23_PC	8.20±2.90	9.36±4.38	Brasier and Feldman (2008)
E	L4_PC	11.90±2.40	15.64±7.84	Brasier and Feldman (2008)
E	L6_CC	2.80±0.80	3.87±2.14	Yang et al. (2020)
E	L6_CT	0.95±0.36	1.41±0.74	Yang et al. (2020)
I	L5_PC	21.10±4.80	16.06±6.74	Ling and Benardo (1999)
Cortico-cortical mtypes: L6_UPC, L6_IPC, L6_HPC. Cortico-thalamic mtypes: L6_TPC:A, L6_TPC:C.				

Table S8: Assumptions. Additionally, we assume that various input data generalizations between brain regions, organisms and animal ages do not affect validity. They are not listed again.

	Anatomy
Inherited	All assumptions about the model's anatomy are inherited from the companion paper (Reimann et al., 2024), where they are described in Section 5.2.
	Neuron Physiology
Structuring	We assume that me-types are sufficient to capture the diversity of neuron dynamics. In particular, this includes a single firing type for pyramidal cells and no met-types. See discussion for further details.
Generalization	Optimization of ion channel densities to match somatic electrophysiological features, creates accurate dendritic activity. Whilst we validated several dendritic properties, the battery of tests could be increased. Moreover, multimodal fitting approaches can now be used to construct single-neuron electrical models with patch clamp and high-density microelectrode arrays (Buccino et al., 2024). The model assumes that electrical models optimized for a given me-type can generalize to different m-types of the same e-type. Importantly, the quality of generalization is tested, with poor generalizations rejected. As optimization methods become more efficient and more data is available, such assumptions can be relaxed. Future work would benefit from single cell protocols applied to many different met-types.
Modeling	11 generic ion channels are sufficient to capture accurate neuronal dynamics. We discuss how larger sets of ion channel models could be used in future. The model assumes that ion channel densities are constant for each neurite type (soma, axon initial segment, apical and basal dendrites), except for HCN channels (which increase exponentially with distance from the soma in apical and basal dendrites) and Na^{2+} channels (which decrease exponentially with distance from the soma in apical dendrites). More data on the spatial distribution of ion channels for different neuron types would be very useful to constraining future optimizations.
Data	*In vitro* recordings of single cell protocols are sufficiently informative of *in vivo* dynamics.

Synaptic Physiology

Structuring The model assumes that synaptic physiology is specific to m-types, rather than me-types or even more specific classes.

Generalization The model assumes that for the fitting of synaptic parameters, PSP data can be generalized to pathways with missing data. New work in mouse presents techniques for recording PSPs at larger scale.

Modeling Modeling the NMDA Mg^{2+} block is sufficient to capture the voltage-dependent nature of NMDA currents.

Missing input compensation

Modeling Input compensation at the soma can capture the effect of missing input. This is further considered in the Discussion. Comparing to glutamate uncaging studies would test the dendritic processing characteristics of neurons under different missing input compensation schemes.

Inputs from other brain regions are independent between neurons. In the future, it is possible that temporal synchronization of different brain regions recorded in openly available brain wide electrophysiology studies could be combined with innervation patterns from other brain regions to better constrain the synchrony of inputs.

Structuring Missing input is specific for layer-wise E/I populations. Input compensation could be made more specific, e.g., for inhibitory subpopulations.

Data Spike sorting bias is constant across neuron populations. Our latest work Laquitaine et al. (2024) predicts how biases could be different between subpopulations. These predictions could be incorporated in future work.

Thalamic stimulus

Modeling We assume that thalamic neurons activated in a single whisker deflection are randomly distributed in a barreloid of the VPM corresponding to a cortical barrel, and that individual neuron spikes are drawn from a population PSTH. To our knowledge there is little data about the spatial distribution of thalamic fibers activated during a specific whisker stimulus. Combined intracellular recording of thalamacortical projection neurons stimulated during a single whisker deflection and an anatomical reconstruction of the stimulated fibers would improve the pattern of synaptic activations innervating the cortex and allow more precise modeling of single neuron and network integration. This goal is now much closer, given that the temporal population response of our model is now accurate on the millisecond timescale.

Comparison of evoked activity to spike sorted recordings

Data We additionally assume that similarity with spike sorted PSTHs is sufficient for validation of stimulus evoked activity. As discussed through-out the paper, such recordings contain bias, and also do not compare against the internal dynamics of single neurons. We believe this paper sets the stage for meaningful comparisons to a large quantity of existing analyses of intracellular recordings in the barrel cortex. Calcium imaging also offers a useful measure of sparsity in L23 in both spontaneous and evoked settings, and could simultaneously be compared alongside intracellular responses to active whisker touch stimuli (O'Connor et al., 2010). The mouse barrel cortex would offer an excellent model for reconciling a broad range of previous findings at these levels. Our model's evoked response can now also be compared directly to local field potential data as in (Rimehaug et al., 2023).

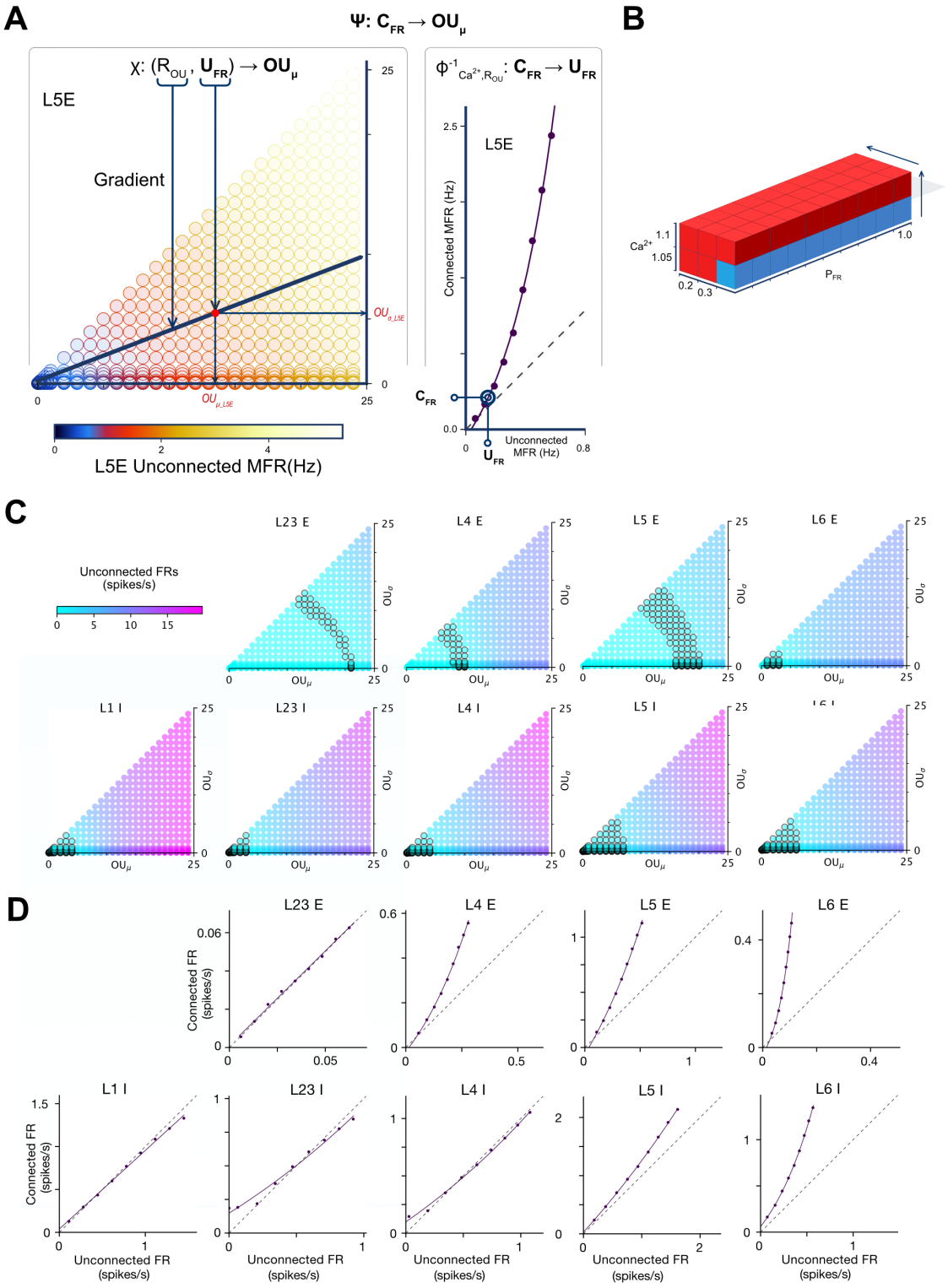

Figure S1: Spontaneous activity calibration: estimating χ and ϕ. A: Estimation of χ and ϕ for L5 E (illustration). $\Psi_{Ca^{2+},R_{OU}} : \boldsymbol{C_{FR}} \mapsto \boldsymbol{OU_{\mu}}$ is estimated by dividing it into the two functions χ and ϕ, which are determined separately. Left: $\chi : (R_{OU}, \boldsymbol{U_{FR}}) \mapsto \boldsymbol{OU_{\mu}}$. The color of each point shows the mean unconnected FR in a single column for L5E for different combinations

of OU_μ (x-axis) and OU_σ (y-axis). For a given value of R_{OU} interpolation is used over the datapoints to estimate the predicted FRs along a line of gradient R_{OU} starting at the origin. As FRs increase monotonically with increasing OU_μ and OU_σ, the interpolation can be used to estimate the OU_μ and OU_σ combination that will produce a given target unconnected FR. Right: $\phi_{Ca^{2+},R_{OU}} : \boldsymbol{U_{FR}} \mapsto \boldsymbol{C_{FR}}$. In each iteration, 10 simulations of the seven hexagon subvolume are run for a range of target P_{FR} values. For each population (i.e. L5 E) an exponential is fit to unconnected vs. connected firing rates, and used to estimate unconnected firing rates which will achieve target connected firing rates on the next iteration. **B:** Visualisation of the meta-parameter space. The algorithm is run for a single combination of Ca^{2+} and R_{OU} (blue), and is then generalised for other combinations (red). **C:** Data for estimation of χ for each population. Population FRs from unconnected simulations of a single column. Simulations vary by OU_μ and OU_σ. Colour shows FR. Black circles show region where FRs are greater than 0 and less than the population's *in vivo* reference FR. The dependence of unconnected FR on OU_μ and OU_σ is heterogeneous across populations. **D:** Final estimation of $\phi_{1.1,0.4}$ for each neuron group. Exponential fit of unconnected vs connected FRs for each population after 5th iteration. The final fits are heterogeneous across populations.

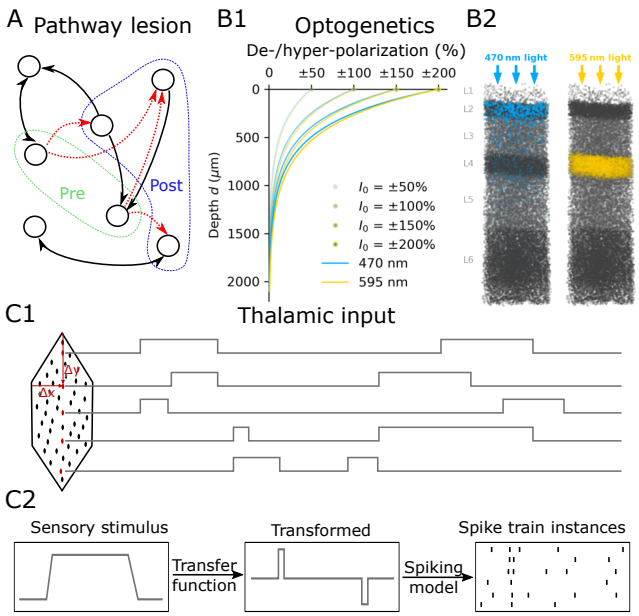

Figure S2: *In silico* experimental methods. A: Synaptic pathway lesions. After selecting a pre- (green) and post-synaptic (blue) population of neurons, connections between them in the specified direction are removed (red arrows). **B:** Optogenetic manipulations. **B1:** Decay with depth of the strength of a stimulus applied to mimic the effect of optogenetic manipulations with 470 nm (blue) and 595 nm (yellow) light. Indicated for exemplary intensities (values of I_0). **B2:** Targeted neuronal populations in two *in silico* optogenetic experiments. Density of affected cells (combination of expression level and light depth) indicated by the corresponding color of light. Unaffected populations in grey. Left: Excitation of inhibitory populations. Right: Inhibition of PCs in L4. **C:** Stimulation with thalamic inputs. **C1:** Each thalamic fiber in the model is assigned a position in a flat coordinate system. Based on the coordinates, type of fiber (VPM vs. POm), or randomly, time series of sensory stimulation are assigned to the fibers. **C2:** Sensory stimuli are transformed by a transfer function capturing pre-thalamic processing. The transfer function can simply be identity. The transformed signal is then used with a spiking model to generate stochastic spike trains that serve as inputs into a simulation.

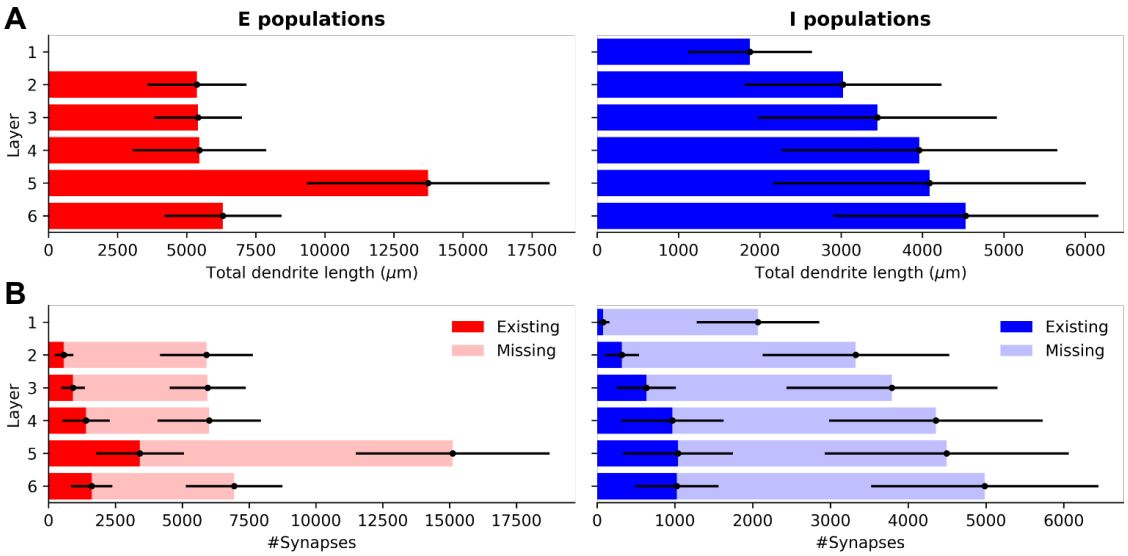

Figure S3: Mean dendritic length and missing synapses by population. A: Mean dendritic length by population. Error bars show ±SD. **B:** Mean estimated number of missing synapses by population. Existing and missing synapses are stacked. Error bars show ±SD.

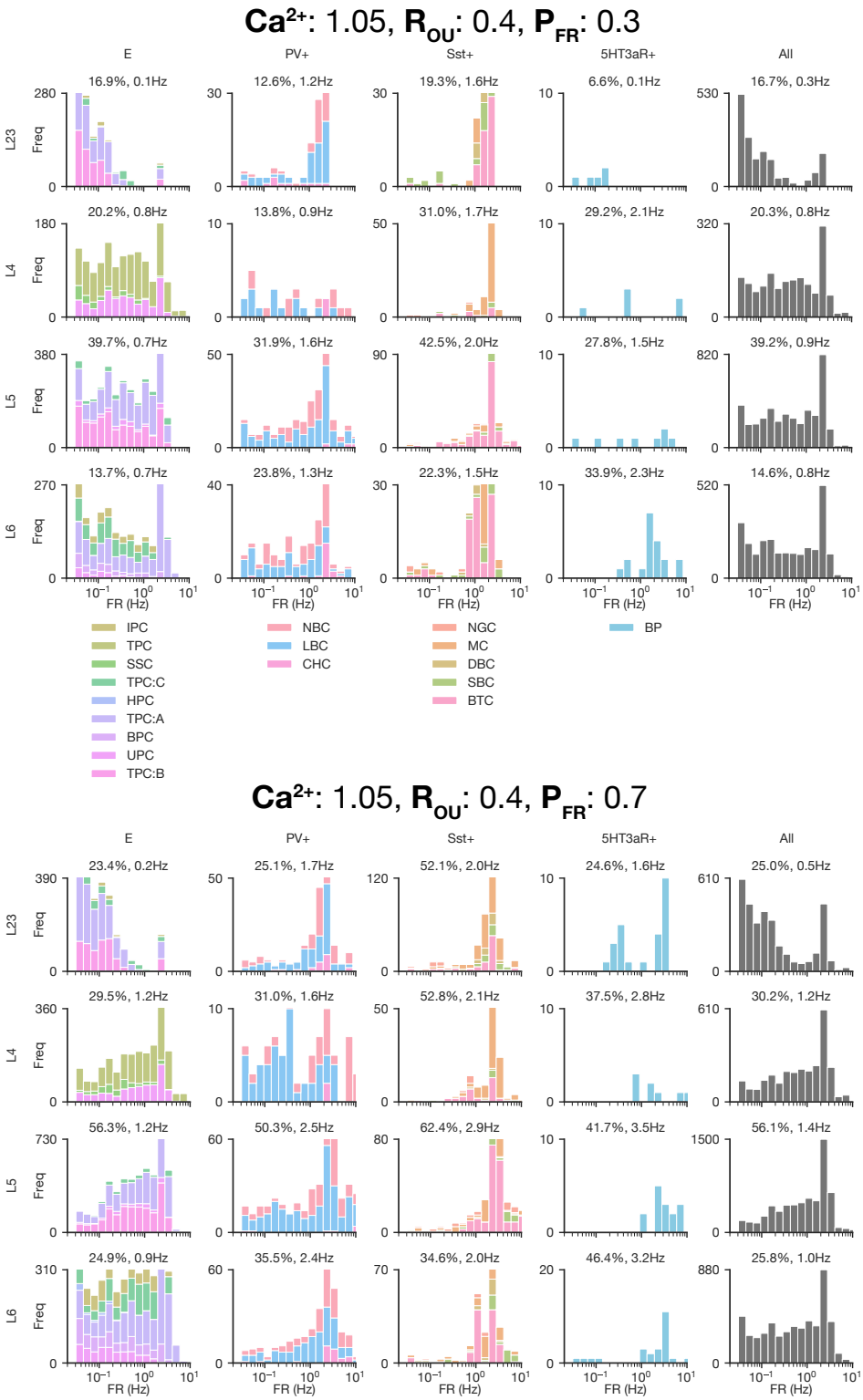

Figure S4: Spontaneous activity firing rate distributions. Firing rate distributions of different subpopulations colored by m-type for two meta-parameter combinations, each over 50 seconds of simulation. Neurons which spike zero or one times are excluded. Titles of each subplot show the percentage of neurons spiking at least once, and the mean firing rate of neurons of neurons spiking at least once.

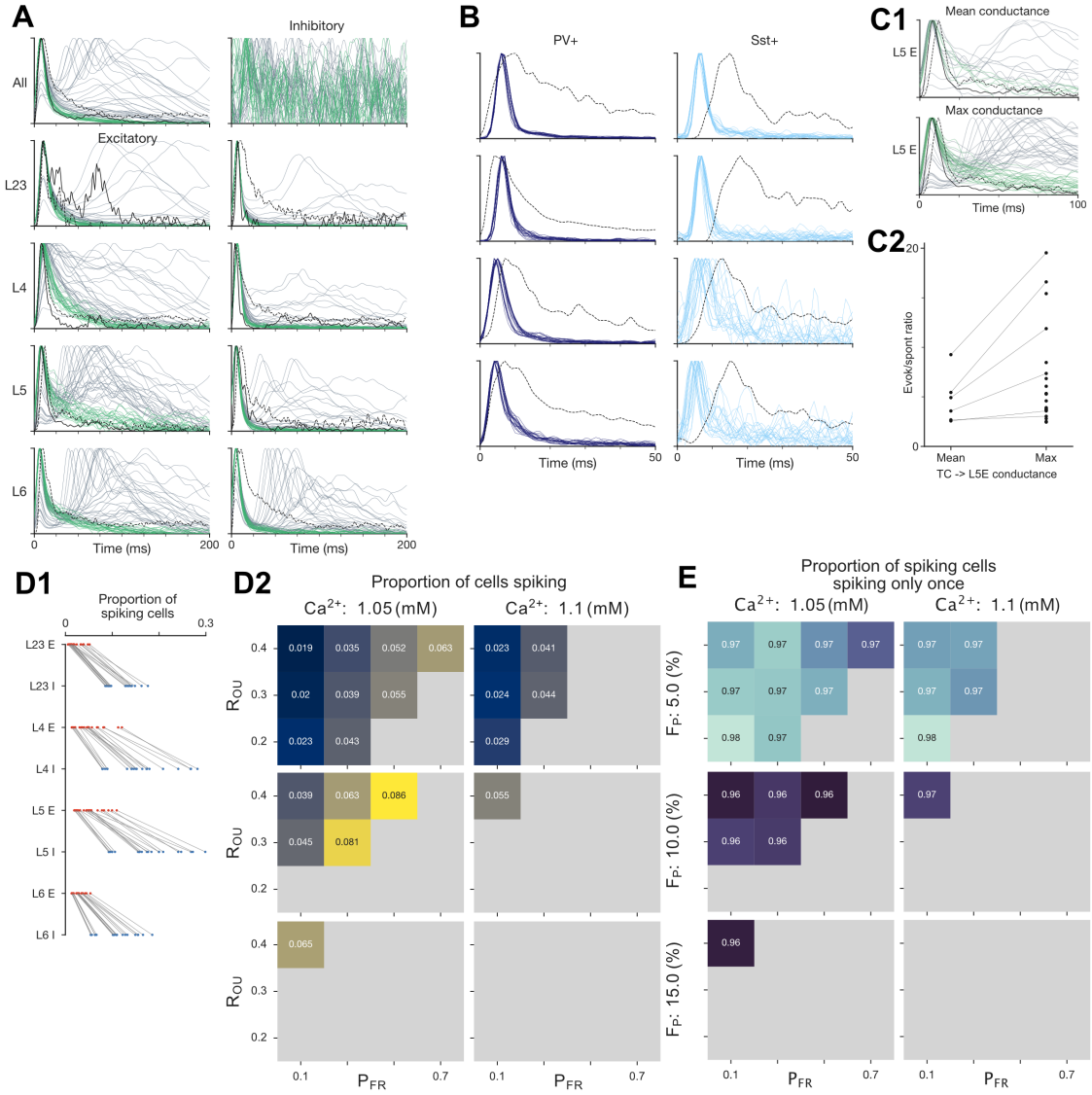

Figure S5: Whisker deflection responses - supplementary. A: PSTHs in response to the single whisker deflection stimulus for all parameter combinations. PSTHs of simulations which passed the initial criteria are coloured green, whilst those which did not are coloured grey. **B:** Layer-wise PV+ and Sst+ subpopulation PSTHs for simulations which passed the criteria. **C:** Analysis of evoked responses of L5 E under two simulation cases. The first case uses the mean of the VPM to L4 E and L6 E synaptic conductance for the VPM to L5 E conductance, whilst the second uses the maximum of the two values (VPM to L6 E). **C1:** For the two simulation cases, L5 E PSTHs for the criteria passing (green) and failing (grey) simulations. For the mean case, some of the simulations that do not burst or do not have a secondary rebound, fail the criteria because of low signal to noise ratio. **C2:** Ratios between evoked and spontaneous activity of L5 E population for criteria passing simulations. There are fewer criteria passing simulations for the mean case, and those that do are much lower than the *in vivo* reference (40.2). **D1:** Proportion of spiking cells by population in the central column over 100ms following stimulus onset. Each line represents a different criteria passing simulation. **D2:** Heatmap showing the effect of the meta-parameters on the proportion of spiking cells over the entire central column. **E:** Heatmap showing the effect of the meta-parameters on the proportion of spiking cells which spike only once over 100ms following stimulus onset.

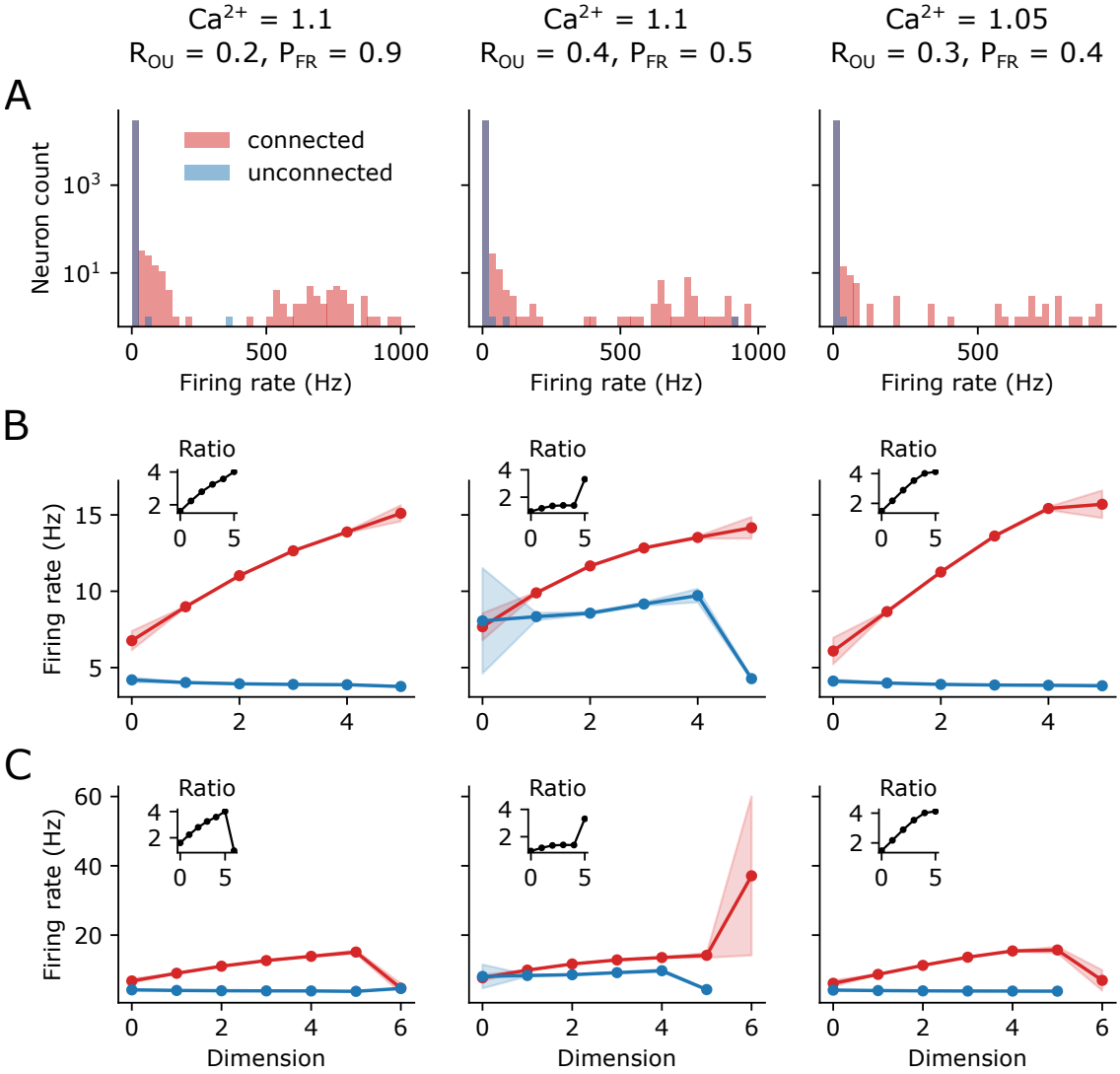

Figure S6: Firing rate statistics. A: Histograms of the inverse of inter-spike intervals (ISI) (a proxy of non-zero firing rate) for three different meta parameter combinations of $[Ca^{2+}]_o$, R_{OU} and P_{FR} for the connected (red) and unconnected (blue) circuits. **B:** For each dimension, the markers show the weighted average of the inverse ISI for all neurons, where the weights are given by node participation in the given dimension. Shaded regions show standard error of the mean. Color scheme as in A. Inset, ratio of connected vs. unconnected means i.e., ratio of the red vs. blue curves. Note that the minor dependence on the unconnected firing rate can be explained by the correlation between dimension and the layer of a neuron, combined with different firing rates in different layers. **C:** Same as B but additionally showing dimension 6.

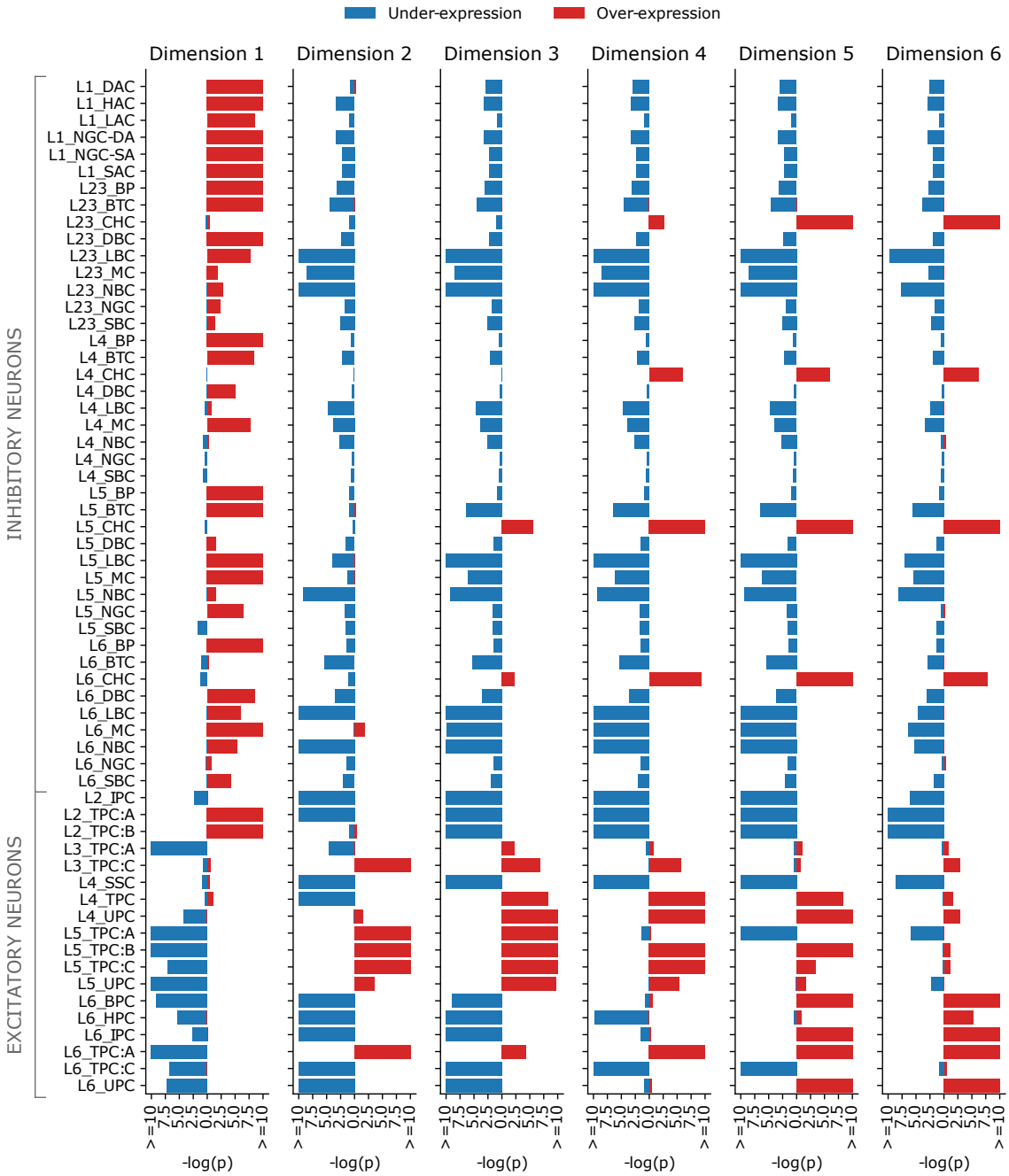

Figure S7: Over/under expression of neurons that maximize node participation. Negative logarithm of the probability of the over-/under expressions (see Methods), in red respectively blue, for all mtypes, calculated for the top 5% of neurons that maximize node participation in each dimension.

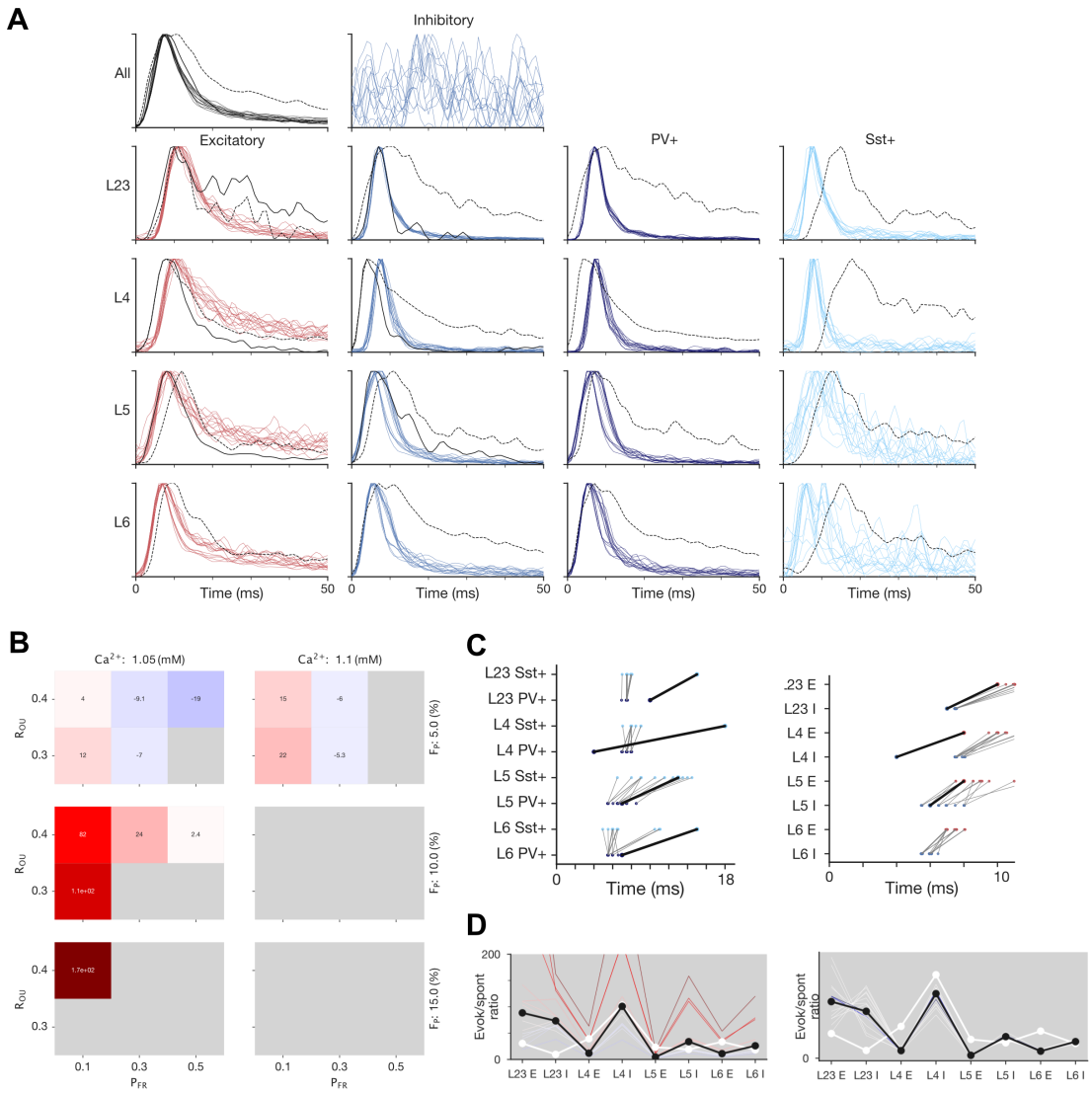

Figure S8: Active whisker touch responses - supplementary: Same as Fig. 5 but using an active whisker touch VPM stimulus and *in vivo* reference for the active whisker touch paradigm (see Methods).

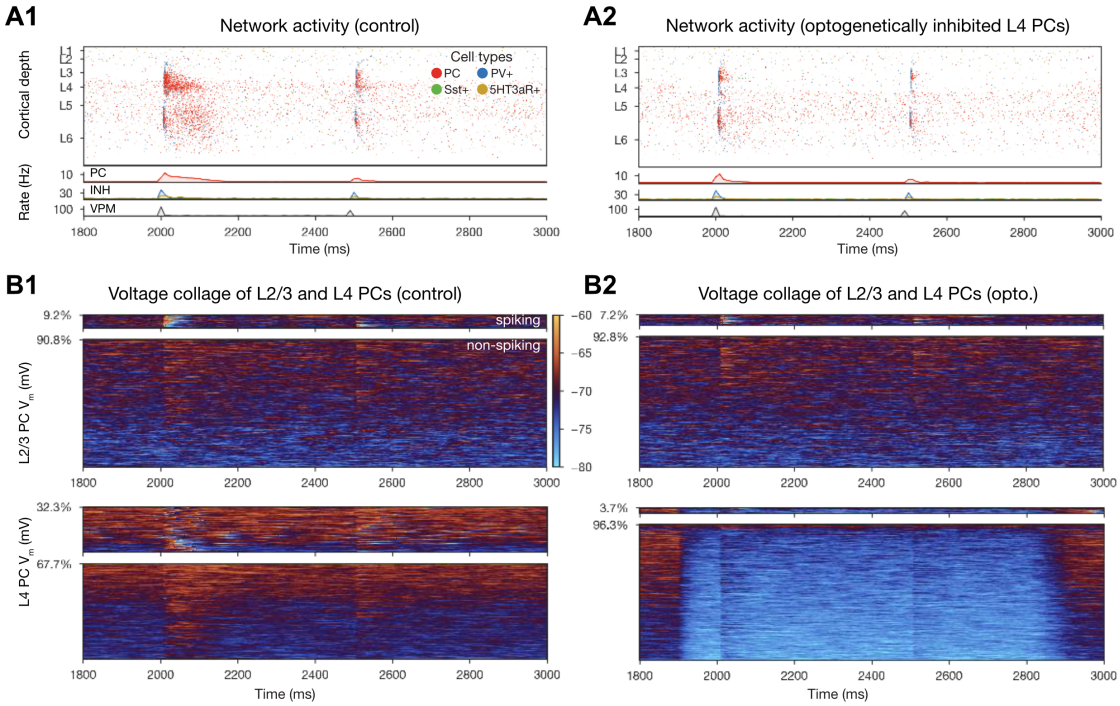

Figure S9: Additional validations: reproducing the experiments of Varani et al. (2022). A: Raster plots of the microcircuit's activity and population firing rates below. **A1**: Control conditions, **A2**: 95% of L4 PCs inhibited (by direct somatic current injection depicted in B above, see Methods). **B**: Voltage traces of all L2/3 (top) and all L4 (bottom) PCs. Panels show spiking traces (top), and subthreshold traces (bottom). **B1** and **B2** depict the same conditions as C above.

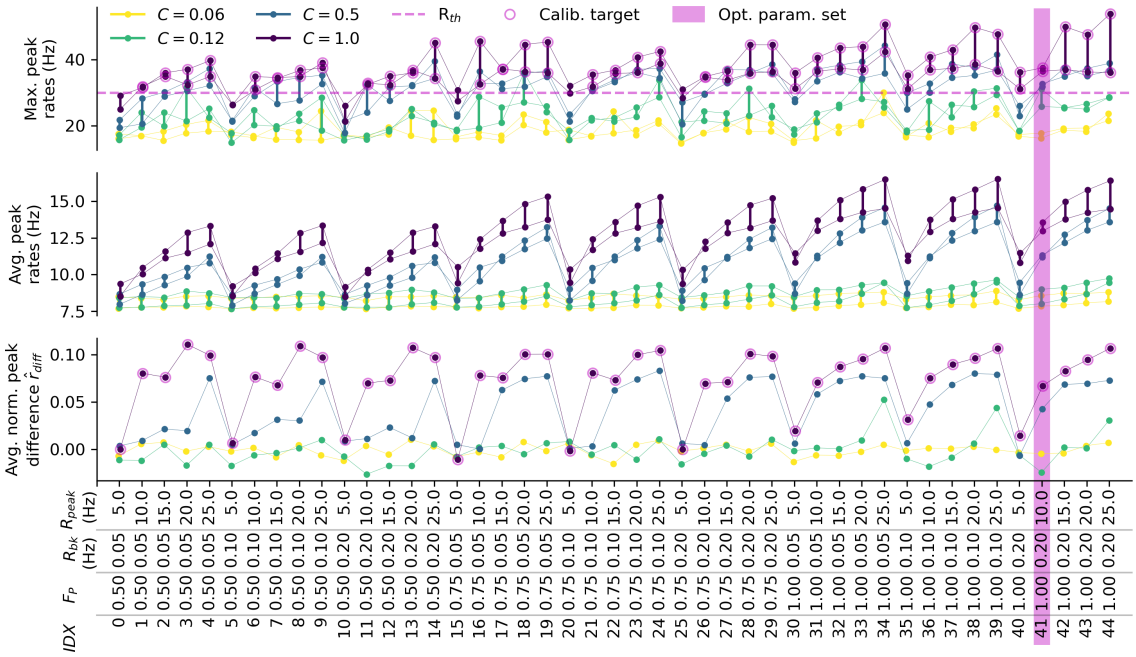

Figure S10: Calibration of the drifting grating stimulus based on peak firing rates. The drifting grating stimulus was calibrated by running a parameter scan of 45 simulations to determine optimal values for F_P, R_{bk}, and R_{peak}. The maximum (top) and average (middle) of the first and second peak firing rates r_1 and r_2 (connected points) over the whole population of PCs, together with the average of the normalized peak difference (Michelson contrast) $\hat{r}_{diff}$ (bottom) are summarized. Different colors indicate different contrast levels $C \in [0.06, 0.12, 0.5, 1.0]$. The rate threshold $r_{th} = 30\,\text{Hz}$ at maximum contrast, the calibration target values that were taken into account for selecting the optimal parameter set, as well as the optimal parameter set ($F_P = 1.0$, $R_{bk} = 0.2\,\text{Hz}$, and $R_{peak} = 10.0\,\text{Hz}$), are highlighted.

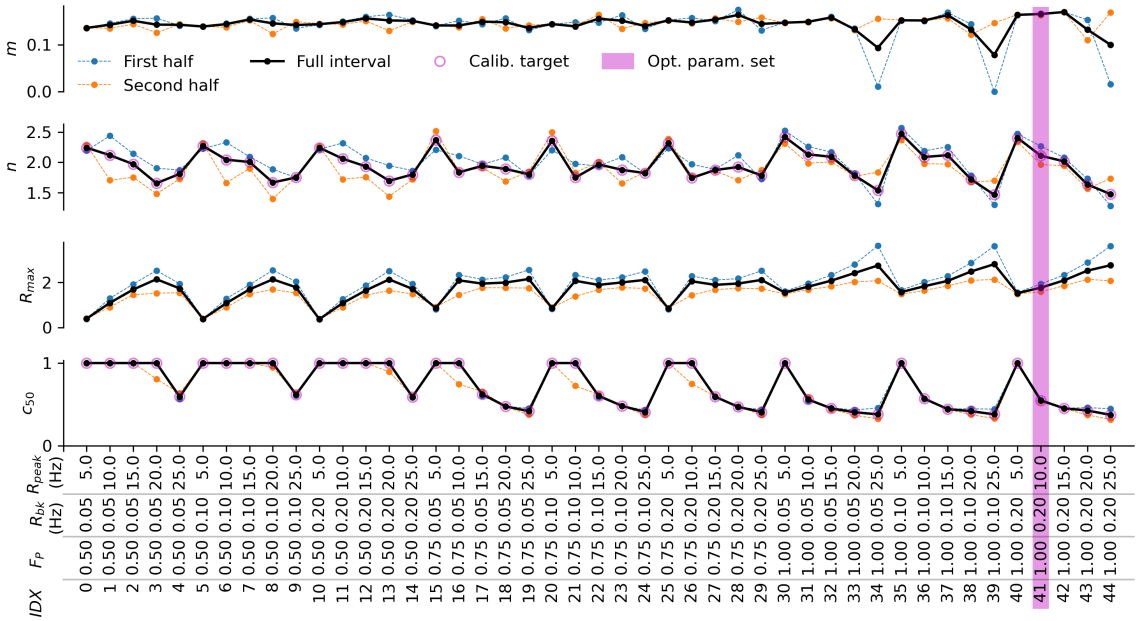

Figure S11: Calibration of the drifting grating stimulus based on sigmodal parameters. The drifting grating stimulus was calibrated by running a parameter scan of 45 simulations to determine optimal values for F_P, R_{bk}, and R_{peak}. The values of the four parameters m, n, R_{max}, and c_{50} for fitting a sigmoidal function to the average firing rates of the whole population of PCs within the full stimulation interval are summarized. Dashed lines indicate fitted parameter values when considering only the first or second half of the response interval. Calibration target values that were taken into account for selecting the optimal paramter set, as well as the optimal parameter set ($F_P = 1.0$, $R_{bk} = 0.2\,\mathrm{Hz}$, and $R_{peak} = 10.0\,\mathrm{Hz}$), are highlighted.

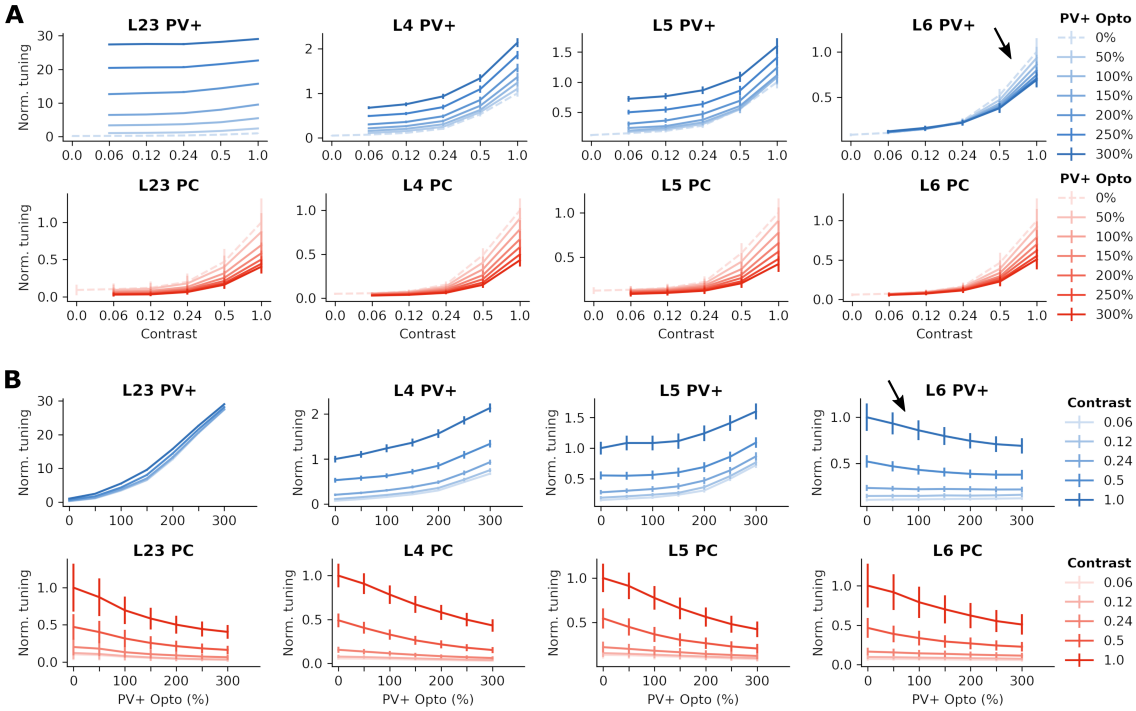

Figure S12: Contrast tuning by layer and paradoxical effect of optogenetic PV+ stimulation. A: Normalized contrast tuning functions of layer-wise PV+ (upper; blue) and PC (lower; red) subpopulations for different levels of optogenetic PV+ stimulation ranging from 0 % to 300 %, as indicated by the legend. **B:** Same data as in A, but plotted dependent on the optogenetic PV+ stimulation strength (x-axis) for the different contrasts, as indicated by the legend. At high contrasts, the optogenetic stimulation has a paradoxical effect on L6 PV+ neurons, i.e., reducing their activity (black arrows).

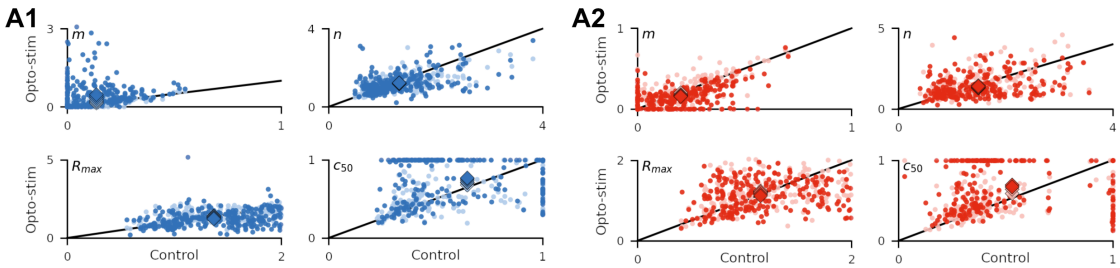

Figure S13: Sigmoidal parameter fits to contrast tuning functions. A1: Scatter plots showing the fitted sigmoidal parameter values (see Figure 6H2 inset; Methods) in control condition vs. PV+ optogenetic stimulation at lowest (50%) and highest (300%) level respectively for all 259 robustly tuned PV+ interneurons. Diamond markers indicate mean values over neurons, including all optogenetic stimulation levels from 50% to 300%. Colors as in Figure 6H legend. **A2:** Same as A1, but for all 228 robustly tuned PCs.

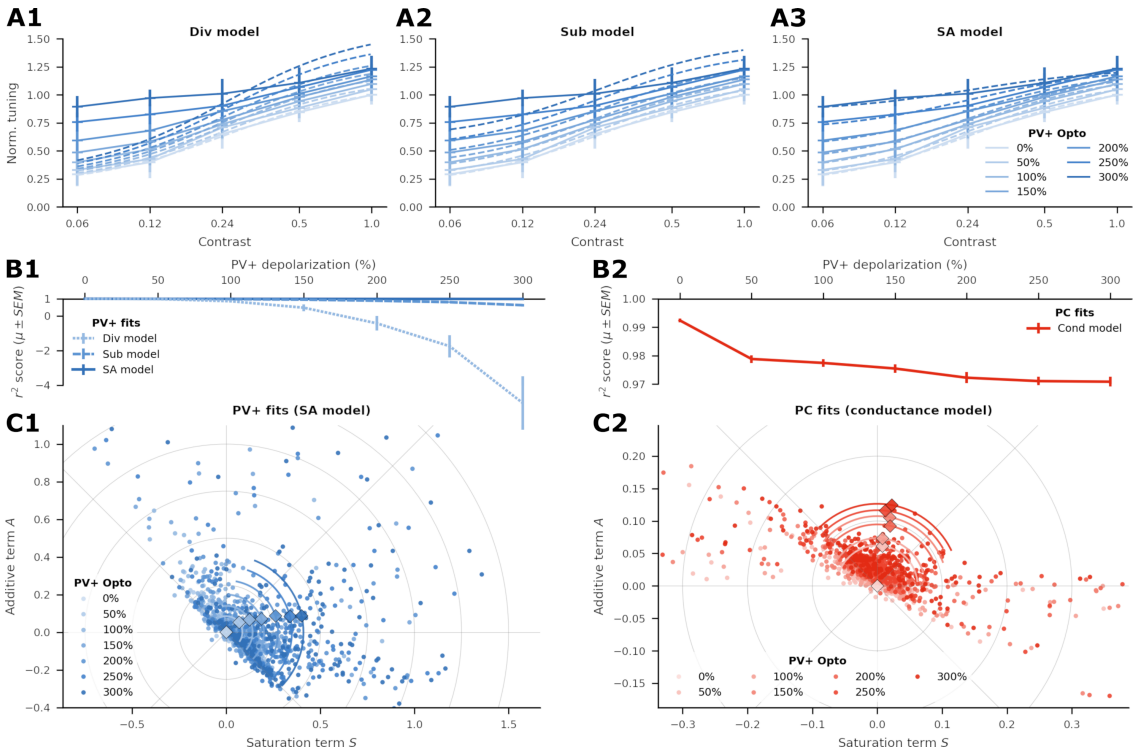

Figure S14: Modelling the effects of optogenetic stimulation of interneurons. A1-A3: Divisive scaling (Div), subtractive shifting (Sub), and saturation additive (SA) model fits (dashed lines) to responses of an exemplary PV+ interneuron (solid lines) at different levels of optogenetic PV+ stimulation, ranging from 0% (baseline) to 300%. **B1:** Goodness of Div/Sub/SA model fits ($\mu \pm SEM$ of r^2 score) for different depolarization levels over all 259 robustly tuned PV+ interneurons, showing that direct photostimulation effects on interneurons can be best described by the saturation additive model. **C1:** Polar plot of S (saturation) and A (additive) parameter values of the SA model fits to all 259 robustly tuned PV+ interneurons at different levels of optogenetic PV+ stimulation. Diamond markers indicate mean values (in polar coordinates) over neurons, colored arc lines the circular SD of the polar angles. **B2:** Same as B1, but for conductance-based model fits describing indirect photostimulation effects on all 228 robustly tuned PCs, assuming a saturating additive model description of interneurons. **C2:** Same as C1, but for the conductance-based model fits to all robustly tuned PCs.

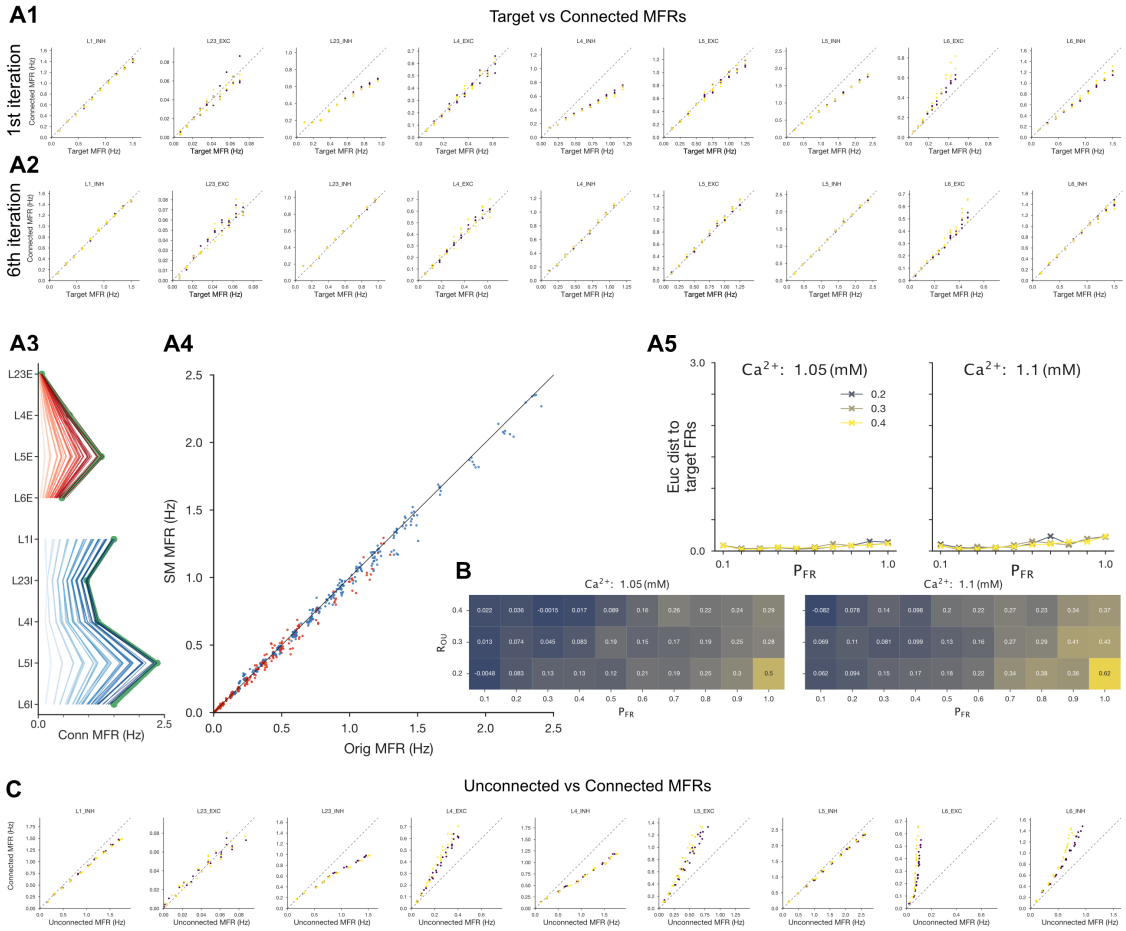

Figure S15: Re-calibration of SM-Connectome. A: The SM-connectome took 6 iterations to re-calibrate for the full 60 meta-parameter combinations. The mean conductance injections found for the original connectome for the 60 meta-parameter combinations were used for the first iteration of the re-optimisation and lead to decreases in firing rates for all inhibitory populations except L1 I (A1). In A1 and A2 blue and yellow points refer to Ca^{2+} 1.05 and 1.1 respectively. After 6 iterations the firing rates converged to the target firing rates (A2-A5) and there was minimal difference in population firing rates over the 60 meta-parameter combinations between the original and SM-connectome (A4). **B** Correlation r-values between the E and I populations, as for the original connectome in the main text. **C:** Unconnected vs connected MFRs for the different populations after the 6th iterations. Unlike for the original connetome, firing rates decrease following connection of the network.

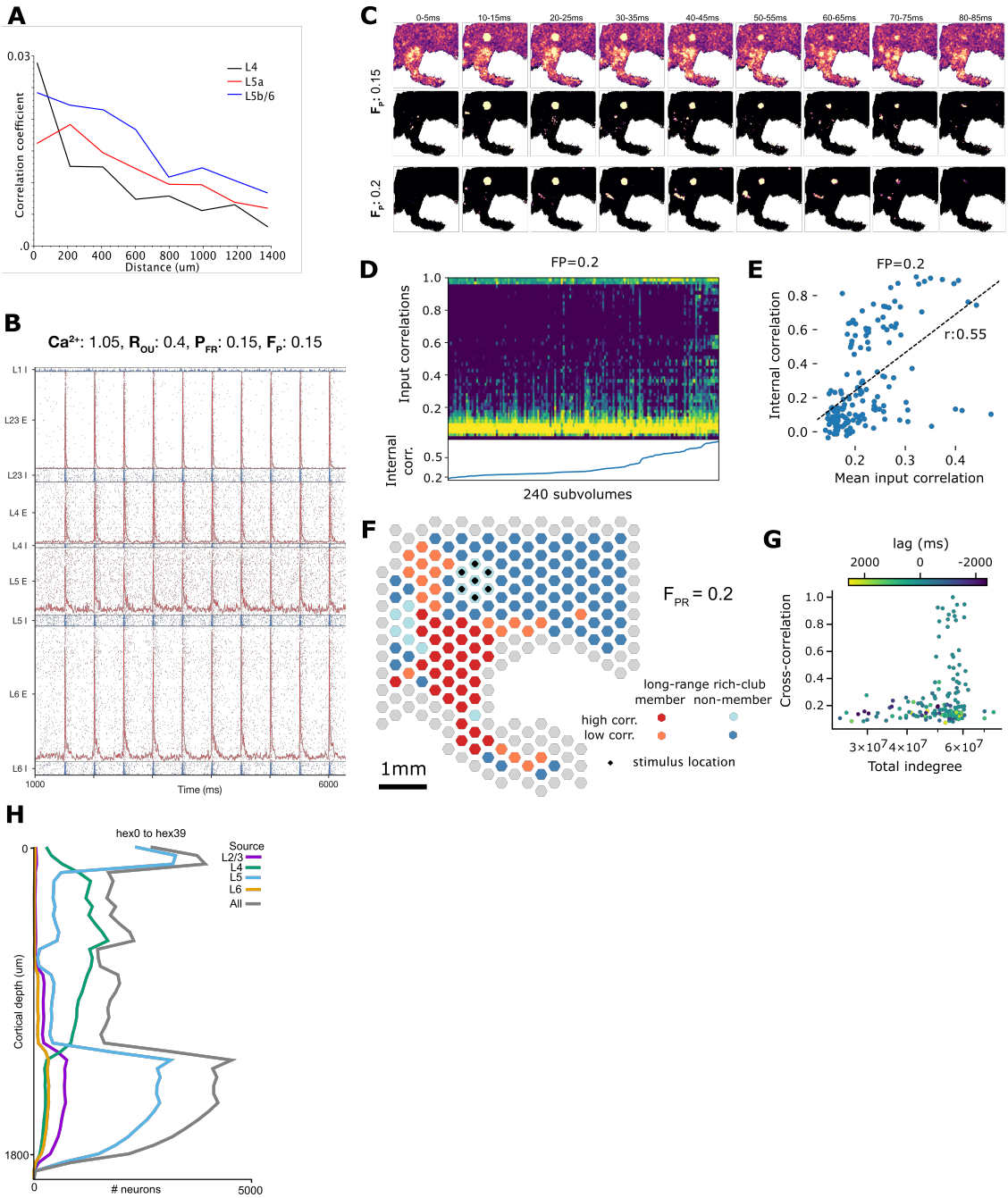

Figure S16: Full nbS1 - supplementary: **A:** Distance dependence of spiking correlations. Digitized from Reyes-Puerta et al. (2015a). **B:** Evoked responses of a single hexagonal subvolume over 10 single whisker deflections. **C:** Trial-averaged activity of the full circuit for $F_P = 15\%$ following the single whisker deflection stimulus (top). Middle and bottom: trial-averaged activity of the full circuit for $F_P = 15\%$ following the single whisker deflection stimulus for $F_P = 15\%$ and $F_P = 20\%$, showing only the top 2% of bins for each time window after the baseline activity level has been subtracted. **D:** Distribution of spiking correlations of inputs into 240 subvolumes. Calculated at reduced spatial resolution, based on connection counts and correlations between the subvolumes (see Supp. Methods). Subvolumes are sorted by the E/I correlation of neurons within them. For evoked activity with $F_P = 20\%$. **E:** Mean of the correlations of inputs into 240 subvolumes (as in D) against internal spiking correlation for all subvolumes during spontaneous activity. Black line: linear fit. Calculated based on connection counts and correlations between 50 μm hexagonal subvolumes (see Supp. Methods).

F: Classification of subvolumes based on low or high internal correlation and membership in the mid-range rich club. Data from evoked activity with $F_P = 20\%$. **G:** Indegree from the subvolume innervated by the VPM stimulus against correlation with that subvolume, indicated for all other subvolumes. Color indicates the Δt with maximum correlation. **H:** Depth dependent profile of synaptic innervation from hex0 to hex39.