Convolutional neural network models describe the encoding subspace of local circuits in auditory

cortex

Abbreviated title: Subspace encoding in auditory cortex

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Abstract

Convolutional neural networks (CNNs) provide powerful models of neural sensory encoding, but their complexity makes it difficult to discern computations that support their performance. To address this limitation, we developed a linear-nonlinear subspace model that identifies the most informative sensory dimensions captured by a CNN. A CNN was trained on single-neuron data recorded from auditory cortex of ferrets during presentation of a large natural sound set. Each neuron's linear tuning subspace was computed by applying dimensionality reduction to the gradient of CNN output relative to input. Subspace projections were combined nonlinearly to predict neural activity. The resulting model was functionally equivalent to the CNN. Analysis of trained models showed that responses of local neural populations sparsely tiled a shared stimulus subspace. Encoding properties also differed between cell types and layers, reflecting their position in the cortical circuit. More generally, these results establish a framework for interpreting deep learning-based encoding models.

Significance statement

Auditory cortex mediates the representation and discrimination of complex sound features. Many models have been proposed for cortical sound encoding, varying in their generality, interpretability, and ease of fitting. It has been difficult to determine if and what different functional properties are captured by different models. This study shows that two families of encoding models, convolutional neural networks (CNNs) and tuning subspace models, account for the same functional properties, providing an important analytical link between accurate models that are easy to fit (CNNs) and models that are straightforward to interpret (tuning subspace).

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Author contributions

J.C.W. developed neurophysiological methods, performed experiments, and analyzed data. S.P. analyzed data. S. V. N.-H. developed stimuli. S.V.D. designed experiment and analyzed data. All authors contributed to writing the manuscript.

<u>Competing interests</u>

The authors declare no competing interests.

Introduction

Auditory perception requires parsing and grouping statistical regularities in the complex and highly variable sounds encountered in everyday environments. Numerous spectrotemporal encoding models have been proposed to describe the computations performed by neurons in the auditory system, and models with increasing complexity have been shown to account for sound-evoked activity with greater accuracy [1–4]. Since the advent of deep learning methods, a number of studies have reported striking parallels between artificial networks fit to solve complex sensory problems, like face or speech recognition, and biological sensory representations, suggesting that these methods may also be used to model neural sensory processing directly [5–7]. Consistent with this prediction, convolutional neural networks (CNNs) fit directly using data from the visual and auditory cortex perform substantially better than classical linear-nonlinear spectrotemporal receptive field (LN) models and variants of the LN model [8–11].

Sensory encoding models that successfully predict time-varying neural activity can, in theory, be analyzed to determine what computations support their performance [12]. A sufficiently accurate model of cortex should reflect local circuit properties, like dendritic integration and recurrent connectivity [13,14]. However, developing encoding models that are both accurate and interpretable has proven challenging. The high prediction accuracy of CNN-based encoding models has been established, but their complexity and large number of free parameters has made it difficult to determine what nonlinear computations account for their performance. Given this problem, a concern about deep learning models is that they solve problems in ways that are not biological and thus their value to understanding biological computations may be limited [15]. Being able to understand the key computations performed by a CNN can help us generate hypotheses about neural computations, which can then be tested directly against the biological network [16,17].

Subspace, or multifilter, models are a family of encoding models, derived from the LN modeling

framework, that strike a balance between accuracy and interpretability. Subspace models define neural

responses as a nonlinear function of the output of a relatively small number of spatiotemporal or

spectrotemporal filters [2,18,19]. The set of filters constrains the stimulus subspace that modulates a neural

signal and can be easily visualized. Among other computations, subspace models can account for wide-

ranging neurophysiological phenomena, such as gain control, and logical computations, such as "AND"

gates, which cannot be captured by the LN model [19–21]. While theoretically powerful and relatively easy to

interpret, subspace models have proven difficult to fit, especially with natural stimuli, which contain high-

order statistical correlations that present challenges to model fitting algorithms. Thus, studies that fit

subspace models typically utilize simpler synthetic stimuli [2,22,23]. Studies that have applied subspace

methods to natural stimulus data have been constrained to small numbers of subspace dimensions [24,25],

and published subspace analysis methods do not transfer readily to natural stimulus datasets [10].

Here we tested the hypothesis that a large, multi-layer CNN can be flattened into a low-dimensional

encoding subspace, while maintaining high prediction accuracy. We used microelectrode arrays to record

the activity of multiple single units across cortical columns of primary and secondary auditory cortex

(AC) of awake ferrets during presentation of a large and diverse natural sound stimulus set. After fitting

CNN models to neural data, we measured the tuning subspace of each neuron by a high-dimensional local

linear approximation of the CNN followed by dimensionality reduction. A new encoding model based on

a low (3-13) dimensional tuning subspace predicted AC neural activity nearly as accurately as the full

CNN and revealed functional differences between neuronal cell types within a cortical column. Thus,

subspace models derived from the CNN provide interpretable characterizations nonlinear tuning

properties across cortical populations.

Results

A flattened convolutional neural network identifies the tuning subspace for auditory neurons

We developed a method to transform a deep and complex convolutional neural network (CNN) model into an interpretable subspace filter model of neural sound encoding. Single-unit neural activity was recorded across layers of auditory cortex of awake, passively listening ferrets using linear microelectrode arrays [26,27]. Recordings were performed in primary (A1, 53 sites) and non-primary (PEG, 14 sites) auditory cortex (2874 units, 3-123 units/site, mean 43 units/site, 4 animals). To characterize the sound encoding properties of each neuron, data was collected during presentation of natural sound stimuli. The performance of encoding models is typically limited by the diversity of stimuli used to measure tuning [12]. To maximize stimulus sampling diversity and match neural integration dynamics in the ferret [28], sequences of brief natural sound segments (duration 50-800 ms, mean 129 ms) were presented in rapid succession with occasional silent gaps (0.2-2 sec). The sound segments were drawn from a large natural sound library and sampled to maximize the diversity of spectrotemporal patterns presented. A single experiment presented approximately 6200-56000 unique sound segments (900-8100 sec) for model fitting.

Figure 1. Mapping from convolutional neural network (CNN) to subspace encoding models. **A.** Population CNN

model predicts time-varying neural activity recorded at a single site during presentation of a natural sound library. A

dynamic STRF (dSTRF) is the collection of locally linear approximations of the CNN, computed as the gradient of

the CNN response relative to the stimulus spectrogram. The neuron's tuning subspace is estimated by principal

components analysis (PCA) of the dSTRF across all timepoints. The subspace receptive field (SSRF) is then the

mean response to stimuli projecting to each point in the tuning subspace. **B.** Subspace filters (left) are convolved

with the stimulus spectrogram (second column, gray shading) to produce a projection into each dimension (3/7

highest-variance filters shown). The projection defines a point in the tuning space at each moment in time, and the

SSRF indicates the predicted response at that time (third column, green shading). In this example, the SSRFs contain

two distinct patches that produce a strong response (dark green, upper left and lower right in dimension 1 vs. 2

heatmap). Numbers indicate example timepoints (dashed vertical lines at left). Averages across x or y axes of the

SSRF show the mean response as a function of the projection onto individual tuning dimensions (fourth column). In

this example, marginal response functions are nonlinear and nonmonotonic, with strong responses for both positive

and negative projections. Dashed vertical lines indicate zero stimulus (silence), which is not necessarily aligned to

the low point of the tuning curves. **C.** Subspace model prediction (purple, aggregated across all significant filters)

overlaid with the actual peri-stimulus time histogram (PSTH) response (gray, r=0.579). **D.** LN model fit for the

same neuron (left), LN model prediction (orange) overlaid with actual PSTH (middle, r=0.310), and average LN

model prediction for stimulus projections onto the first two dimensions of the subspace model (right). LN tuning is

constrained to a one-dimensional subspace, which cannot capture the complex tuning of the SSRF in A.

A four-layer convolutional neural network (CNN) was used to model the functional relationship between

the stimulus spectrogram and the time-varying neural response (Fig. 1A, Pennington and David, 2023).

To leverage statistical power for model fitting, a population architecture was used, in which the first three

model layers were shared across neurons within a recording site, and the final dense layer weighted

activity from the final shared layer to predict the activity of individual neurons [10]. The unique stimuli used

for model fitting varied across recording sites. Model performance was evaluated using a held-out test set

(six 18-sec segments), which was fixed across all experiments and presented 10-20 times on trials

interleaved with the fit stimuli. Consistent with previous studies [9,10], the CNN model predicted time-

varying neural activity in the test set more accurately than a linear-nonlinear spectrotemporal receptive

field (LN) model (Fig. 1B-C, Fig. 2B, n=2337/2874 sound-responsive units, p<0.05 above-chance

prediction for either model, permutation test corrected for multiple comparisons).

While the CNN-based auditory encoding model can account for neural response dynamics more

accurately than a traditional LN model, the multiple layers of nonlinear processing make it difficult to

understand what computations account for the increased predictive power. We developed a method to

"flatten" the layers of a deep network into a compact set of transformations that can be visualized more

readily. Previous work has shown that a CNN-based encoding model can be visualized with the dynamic

STRF (dSTRF), the derivative of the model response relative to the input stimulus at each point in time

(Eq. 5) [9]. Analytically, this method is similar to saliency analysis sometimes used to understand deep

learning models [29]. dSTRF analysis produces a large collection of spectrotemporal filters (Figs. 1A),

which provide a piecewise linear approximation of the stimulus-response relationship, with each dSTRF

centered around the spectrotemporal input at a different point in time. dSTRFs for a single neuron often

vary substantially but show some regular patterns in their structure (Fig. S1). For a compact visualization

of dSTRF variability, we performed dimensionality reduction using principal components analysis (PCA)

on the collection of dSTRFs for each neuron. For most A1 neurons, 3-16 principal components (mean 11)

accounted for most of dSTRF variance (>95%), and 3 components accounted for a mean of 81% of

dSTRF variance (Fig. 2A). The components measured for a single neuron often shared a best frequency

but differed in spectral and/or temporal modulation tuning (examples in Figs. 1B, S2-S5).

Previous studies of sensory encoding have proposed that neural representation can be described by a

subspace, or multifilter, encoding model [2,19,30–32]. In this family of models, each neuron is characterized by

one or more linear filters, and sensory responses are predicted entirely from the projection of the stimulus

into this low-dimensional subspace. In the case of one filter, the subspace model reduces to the LN model.

The large collection of filters in the dSTRF describes the gradient of model outputs over the full set of fit

stimuli. We surmised, thus, that the principal components of the dSTRF defined a tuning subspace

analogous to that of multifilter models. To visualize how the subspace can account for sound encoding,

we computed the largest principal components of the dSTRF for each neuron. We projected the stimulus

into this subspace and computed the average neural response across stimuli at each point in this

representation (Figs. 2, S2). *Subspace receptive fields* (*SSRFs*) show the average response to the stimulus

projected jointly onto a pair of dimensions (Fig. 1B, second column from right), and subspace tuning

curves show the average response to stimuli varying along a single subspace dimension (Fig. 1B, right

column). Analogous to receptive fields defined with respect to receptors in peripheral sensory areas, the

SSRF indicates the region of the tuning subspace that evokes a spiking response. The SSRF can be

nonmonotonic and have multiple peaks. In contrast, predictions of the LN model projected into the same

subspace are constrained to lie in a one-dimensional subspace consistent with a single linear filter

instantiated in the LN model (Fig. 1C).

Figure 2. Equivalent performance of CNN and subspace encoding models. **A.** Thin lines show cumulative dSTRF

variance explained as a function of principal component count for each neuron (n=2337 AC units). Thick line

represents mean. The subspace encoding model used dimensions accounting for 95% of dSTRF variance (mean 11

dimensions). **B.** Scatter plot compares prediction correlation (noise-corrected correlation coefficient) between the

LN and CNN encoding models. Gray dots indicate prediction correlation of single units, and black dots show the

median for each recording site (median across all units 0.416 vs. 0.600, p<1.0e-10, Wilcoxon signed-rank test). **C.**

Scatter plot comparing subspace (SS) versus CNN model performance, plotted as in C (median 0.584 vs. 0.600,

p=1.0e-7). **D.** Box plots compare model performance, as a fraction of response variance explained (squared

correlation coefficient) relative to the full CNN encoding model (dashed line). Dots indicate site medians (n=67,

models from B and C highlighted in dark gray). Subspace models were tested with variable number of PCA

dimensions used to define inputs (80-99% of dSTRF variance). Polynomial models (right) constrained the mapping

from subspace to neural response to be linear (Poly-1) or a second order polynomial (Poly-2). For this dataset,

prediction accuracy was maximal for the 95% subspace model and did not increase significantly for the 99%

subspace model. Black bars highlight performance comparisons between pairs of models (Wilcoxon signed-rank

test, numbers indicate exact *p* values).

Subspace encoding model is functionally equivalent to the CNN

The spectrotemporal tuning subspace provides a flattened neural network model. A CNN may contain many layers of many units, but the subspace tuning model describes the underlying computations as convolution by a single layer of spectrotemporal filters followed by a nonlinear combination of those filter projections, reflected in the SSRF. The SSRF provides a lookup table for the neural response at each stimulus timepoint, thus providing a compact visualization of the nonlinear computations that define a neuron's encoding properties (Fig. 1).

While the subspace model provides a visualization of tuning captured by the CNN, it need not account for neural responses as accurately as the full model. To determine how well the subspace representation accounts for time-varying neural responses, we fit a new model (Fig. 2A), where neural responses were predicted using only the projection into the tuning subspace. A small neural network with three fully connected layers was used to fit the receptive field within the subspace (SSRF, Eq. 7). The subspace model was able predict neural responses with nearly the same accuracy as the full CNN (median r=0.585 vs. 0.600, p=1.0e-7, Wilcoxon signed-rank test, Fig. 2C). Overall, the subspace model accounted for an average of 0.954 of the response variance explained by the CNN (Fig. 2D). A direct comparison of time-varying neural activity predicted by the two models showed strong correlation, indicating that the two models are functionally nearly equivalent, while equivalence was substantially lower between the CNN and LN models (Fig. S3A). Moreover, the shape of SSRFs fit for the subspace model were strongly correlated with the mean actual response to stimuli projected into the tuning subspace, indicating that tuning in the SSRF did in fact account for sound features that modulated the neural response (Fig. S4).

The dimensionality of the tuning subspace is not fixed *a priori*, and some criterion must be specified for how many PCA dimensions to include in the subspace (Fig. S5). We compared performance for models using variable numbers of subspace dimensions, determined by the fraction of dSTRF variance explained.

Median cross-validation performance improved for models including filters accounting for up to 95% of

dSTRF variance. There was no additional improvement for higher dimensionality, indicating that the

additional dimensions were dominated by noise in the CNN fit (Fig. 2D). When results were broken down

by cortical subregion, similar performance was observed for the subspace model in both areas (A1: 0.955,

PEG: 0.946 median fraction of CNN variance explained). Thus, the relatively small number of subspace

dimensions captures the majority of the functional response characteristics of the full CNN.

The tuning subspace describes the set of spectrotemporal patterns that influence a neuron's activity, but it

does not constrain the nonlinear computations performed within that space. If a neuron's response is

simply a linear weighted sum of the stimulus subspace projection, it should behave like a single linear

filter, as in the LN model (Fig. 2B). Indeed, a model constrained to use a linear combination of subspace

projections (Poly-1) performs similarly to the LN model (0.491 vs. 0.564 median fraction CNN variance

explained, Fig 2D). The slightly worse performance likely reflects the absence of a sigmoid nonlinearity

in the Poly-1 model. Previous studies implementing spike-triggered covariance have modeled subspace

tuning with a second-order polynomial [19,21]. A second-order model in the tuning subspace performs better

than the LN model, but worse than the full CNN or full subspace model (Poly-2, 0.829 relative variance,

Fig. 2D). Thus, while second-order interactions account for some of the subspace tuning, higher-order

nonlinearities are required to fully describe the SSRF.

Previous attempts to fit subspace models directly to neural data, without an intervening CNN-based

model, have had mixed results and generally required carefully tuned hyperparameters [2,10,25,30,32]. For the

current data, subspace models trained directly on the neural data performed similarly to but not as

accurately as those estimated using the CNN-based analysis (Fig. S3B-D). The CNN-based method also

produced less noisy subspace filters, and measures of subspace tuning from the CNN were also stable,

even when only a relatively small number of dSTRFs were included in the PCA (Fig. S6A-D). The use of

natural sounds produced more compact measures of the tuning subspace. When a new subspace model

was constructed using an equivalent number of random noise stimuli to define subspace filters, the

resultant model showed slightly lower prediction accuracy and required more dimensions (i.e., subspace

filters, Fig. S6E-F). Thus, the natural sound-based model provides a compact and efficient

characterization of natural sound encoding. This model may not generalize to arbitrary noise stimuli as

accurately as a model fit with a larger synthetic stimulus set, but it is adequate for the natural stimuli used

here.

Neurons within a cortical column sparsely tile the local tuning subspace

The linear microelectrode arrays recorded the activity of multiple neurons across layers at the same

location in cortex. Thus, the tuning of simultaneously recorded neurons within versus across recording

sites provided insight into sound features represented topographically in AC. The most prominent feature

in AC is tonotopy, smooth changes in neuronal best frequency that define AC subfields [33,34]. In addition,

topographic organization has been reported for tuning to multiple other features, including spectral

bandwidth, temporal modulation rate, and binaural contrast [35–37]. Within a single recording site, subspace

filters showed broad similarity in tuning to stimulus frequency and bandwidth (examples in Fig. 3A, Fig.

S5). However, more fine-grained tuning to spectral and temporal modulations differed across neurons.

Nonlinear tuning within the subspace also varied. The SSRF was sometimes confined to a small region,

producing sparse responses to sounds, but other times showed broad tuning and responses to a wide range

of stimuli (compare units 6 and 7, Fig. 3B-C). Thus, despite sharing a similar tuning subspace, PSTH

responses differed substantially within the same recording site (Fig. 3D).

Figure 3. Diversity of subspace models within a single recording site. **A.** Three largest-variance subspace filters for

eight example units, one per row. Labels for each unit indicate spike width (N: narrow, R: regular) and cortical

depth (L13: layers 1-3, L4: layer 4, L56: layers 5-6). Bottom row shows site-wide subspace filters, computed from

dSTRFs aggregated across all units. **B.** Two-dimensional subspace receptive fields (SSRFs) for dimensions 1 vs. 2

(left) and 1 vs. 3 (right), computed as the average predicted response to stimuli projecting to each point in the tuning

subspace. Darker green indicates higher spike rate. Black lines show trajectory of stimuli in the subspace during 0.4-

1.2 sec in panel D. Thin green lines outline the valid SSRF region, i.e., the area sampled by at least five occurrences

of the stimulus used for model fitting. **C.** Tuning curves show marginal projections of the SSRF along individual

subspace dimensions. Numbers indicate tuning symmetry index (TSI, Eq. 10), and color indicates TSI category

(orange: asymmetric, blue: symmetric downward-facing, green: symmetric upward-facing). Dashed vertical lines

indicate zero stimulus (silence), which is not necessarily aligned with the minima/maxima of symmetric curves. **D.**

Top row shows 4-sec segment of spectrogram from the natural sound sequence used to test prediction accuracy.

Each row below shows the predicted PSTH response (black) overlaid with the actual response (gray). Numbers

indicate prediction correlation (r), microns below cortical layer 3/4 boundary (dp) and spike width in ms (sw).

To quantify tuning similarity within a recording site, we compared the tuning subspace for each neuron to

the shared subspace, computed for the entire recording site (Fig. 3A). The shared tuning subspace was

computed by concatenating dSTRFs across all units in the same site. We performed the same PCA

procedure as for single units, above, and the dimensions explaining the most dSTRF variance defined the

stimulus subspace for the entire site (Fig. 3A, bottom row). We quantified similarity between the single

neuron- and site-wide filters using a subspace similarity index (SSI, Eq. 9), the mean cosine similarity

between all combinations of the four largest subspace filters, which accounted for an average of 85% of

dSTRF variance across all recording sites (Fig. 1B). An SSI of 1 indicates a complete alignment of

subspaces, and SSI of 0 indicates no alignment (i.e., orthogonality). Within-site SSI was contrasted

against SSI computed between the neuron and the shared subspace for a different recording site. Because

population CNN models were fit simultaneously for all neurons within a site, the shared model layers

could bias subspace filters to be similar and, thus, bias SSI toward higher values. To control for this

potential bias, the SSI comparison was restricted to experiments in which the same natural sounds were

presented during recordings from 2-3 different sites (40 sites total). A single model was fit using data

pooled across sites, and SSI was compared only between neurons in the same model fit. Thus, any bias

toward similarity was balanced for within-site and between-site comparisons. The comparison revealed

that SSI was greater within than between sites (median 0.55 vs. 0.35, p=2.5e-11, sign test, Fig. 4B). This

difference was the same when fewer or more than four subspace dimensions were used to compute SSI

(Fig. S7). Thus, neurons recorded from the same site tended to share a similar tuning subspace.

Despite the similarity in tuning subspaces within a recording site (e.g., Fig. 3A), PSTH responses to the

same stimuli varied substantially across neighboring neurons (Fig. 3D). To gain a clearer understanding

of shared encoding properties within a recording site, we measured the signal correlation (correlation

coefficient) between the PSTH predicted by the subspace model for pairs of neurons within and across

sites (Fig. 4C, data matched to the SSI comparison). Despite the high SSI within site, average signal

correlation was relatively low, although it was still higher within-site than between sites (median 0.17

versus 0.14, p=3.6e-10, sign test). Thus, despite spanning similar tuning spaces, pairs of neurons tended

to produce very different time-varying activity.

The similarity of tuning subspaces within a recording site suggested that response properties of individual

neurons could be projected into and compared within the shared, site-wide tuning space. For each neuron,

we computed the SSRF in the site-wide tuning space. We defined the high-activity region of the SSRF as

the area with >80% of its maximum value, initially focusing on the SSRF for the two largest subspace

dimensions. High-activity SSRFs for individual neurons often spanned a relatively small area and were

distributed across the tuning subspace. The substantial scatter of SSRFs within the subspace is consistent

with the observation that PSTH responses differ substantially between units (Fig. 3D). Marginal tuning

curves were often symmetric around non-zero stimulus values (Fig. 3C), explaining why many high-

activity SSRFs were centered at locations away from the origin (intersection of dashed lines in 3B) in the

subspace. This distribution suggests that tuning of a local population sparsely tiles the shared tuning

subspace. An implication of sparse tiling is that high-activity regions of SSRFs for different neurons

should not often overlap. To test this prediction, we measured the maximum overlap (i.e., intersection) of

high-activity SSRF regions across an entire site. In an example site with 40 units, the maximum overlap

was 7 (20% of units, * in Fig. 4D). If neurons all shared the same tuning, maximum overlap should be

equal to the number of units. If tuning is random, the amount of overlap will depend on the size of the

SSRFs. To test how closely the SSRFs resembled a random distribution, we shuffled the position of each

SSRF and computed a maximum average overlap of 6 (Fig. S8). Thus, the number of neurons with

simultaneous high activation for any stimulus was nearly the same as for a collection of randomly

organized SSRFs. We observed the same result across subspace dimensions and recording sites (Fig. 4E,

S8). Maximum overlap varied with the number of neurons per site, but on average it was only 4% greater

than expected by chance and 71% less than full overlap, i.e., if all neurons shared the same SSRF. Thus,

while neurons in a recording site tend to share a spectrotemporal tuning subspace, their responses are

relatively uncorrelated, and their SSRFs tile the shared subspace.

Figure 4. Sparse tiling of a shared tuning space within recording sites. **A.** Subspace similarity index (SSI) compares

two tuning subspaces by computing the mean cosine similarity between all pairs of dimensions in the two subspaces.

SSI was computed between each neuron and the site-wide average of the same site (within-site) and a different site

presented with the same stimuli and fit simultaneously with the same population CNN (between-site). **B.** Scatter plot

compares SSI for single units and site-wide averages between-site and within-site. Gray dots show individual units;

black dots show mean for each recording site. SSI within-site is significantly greater than between-site (0.55 vs.

0.35, p=2.6e-11, sign test, n=39 recording sites). **C.** Scatter plot of correlation between predicted PSTH response

(signal correlation) for pairs of units, using the validation dataset and plotted as in B. Correlation between predicted

PSTHs was relatively low in all cases, but median correlation within-site was significantly greater than between-site

(|0.17 vs. 0.14, p=3.6e-8, Wilcoxon signed-rank test). **D.** SSRF of each neuron (n=40, same site as Fig. 3) computed

for dimensions 1 and 2 of the shared, site-wide tuning subspace. Filled contours show the high-activity SSRF where

each unit reaches >80% of maximum firing rate. The full set of SSRFs tiles most of the subspace, and maximum

overlap across the subspace is 7/40 (*). **E.** Scatter plot of fraction maximum overlapping SSRFs in the shared

dimension 1 and 2 subspace for shuffled- versus actual high-activity SSRFs (n=39 sites). Fraction of maximum

overlap was not significantly different from overlap in the shuffled SSRFs (p=0.09, Wilcoxon signed-rank test). **F.**

High-activity SSRFs of regular-spiking units (n=32, left, gray) and narrow-spiking units (n=8, right, red), replotted

for site in D. **G.** Scatter plot compares mean fraction of subspace area covered by SSRFs across each recording site,

for regular- versus narrow-spiking neurons (n=39 sites, mean regular: 0.076, narrow: 0.115, p=4.4e-5, Wilcoxon

signed-rank test).

SSRFs typically spanned a small region of the tuning subspace, but their size did vary (compare units 6

and 7 in Fig. 3). Previous studies have found that some inhibitory interneurons have broad sensory tuning

[38], which would be consistent with larger SSRFs. To determine if we could explain variability in SSRF

size by cell type, we used action potential spike width to classify units as putative excitatory (regular

spiking) or inhibitory (narrow spiking) neurons [39]. We measured peak-to-trough width of each spike and

observed a bimodal distribution, delineating a boundary of 0.35 ms between regular- and narrow spiking

groups (Fig. S9B [40]). We then compared the area of high-activity SSRFs between these groups. While

narrow-spiking neurons were less common, each group of neurons tiled the tuning subspace (Fig. 4F).

Narrow spiking neurons also had consistently larger SSRFs than regular spiking neurons (Fig. 4G). Thus,

in the same way that inhibitory neurons can have broader tuning to sound features like tone frequency [41],

their SSRFs also span a larger area of the site-wide tuning subspace.

Local subspace overlap depends on neuronal cell type and cortical depth

While neurons in the same recording site shared broadly similar tuning subspaces (Fig. 4B), there was

still variability between neurons (Fig. 3A). We next asked what factors explain this within-site variability

of tuning subspaces. The insertion of electrode arrays normal to the brain surface sampled activity across

depths in the same cortical column. We used current source density and local field potential power

profiles to determine depth, using standard methods (Fig. S9A, [42,43]). We also classified units as regular

spiking (putative excitatory) and narrow spiking (inhibitory), as described above (Fig. S9B). Model

prediction accuracy was slightly higher in superficial cortical layers and for narrow spiking neurons (Fig.

S9C). Average spike rate was also higher for narrow spiking neurons, consistent with previous reports of

higher tonic firing rate in inhibitory neurons (Fig. S9E, [14]).

A comparison of SSI between all pairs of neurons in an example recording site showed that subspace

similarity varied with both cortical depth and spike width (Fig. 5A). SSI tended to be higher for narrow

spiking neurons in superficial layers and lower for regular spiking neurons in deeper layers. This pattern

is consistent with observations for individual neurons (e.g., compare similarity of Fig. 3A units 1-2 versus

units 7-8).

We averaged effects of cell type on SSI across recording sites for pairs of neurons grouped by their

cortical depth (200-μm bins) and spike width (narrow vs. regular). Consistent with the example site,

average SSI was higher between pairs of narrow spiking neurons in superficial layers (Fig 5B-C). This

tendency toward higher SSI in superficial layers was driven primarily by the average depth of the units

being compared. SSI decreased slightly for neurons separated by a large difference in depth, but this

effect was weaker than the dependence on average depth (Fig. 5D). We quantified the dependence of SSI

on cell type with a linear mixed-effects model (Eq. 11). For neurons with less reliable auditory responses,

we expected the population model architecture to impose tuning properties that resembled the site average

and thus inflate SSI between pairs of noisy neurons. To control for this potential bias, prediction

correlation and mean spike rate (both correlated with response reliability, [44]) were included as regressors

in the model. Animal identity ($n=4$) was also included as a random effect to account for between-subject

variability.

The full mixed-effects model revealed that both mean depth (averaged between neurons) and spike width

(narrow-narrow, narrow-regular, regular-regular categories) significantly predicted SSI in A1, confirming

the greater SSI between pairs of superficial and narrow spiking neurons (depth, χ^2=566.6, p<2e-16; spike

width, χ^2=495.8, p<2e-16; width x depth, χ^2=52.8, p=3.5e-12, n=42140 pairs, see Table S1 for detailed

results). Model prediction correlation and neurons' mean spike rate also had significant effects

(prediction, χ^2=1052.5, p<2e-16; rate, χ^2=290.9, p<2e-16). These prediction accuracy and spike rate

effects are likely to be independent of cell type effects, since depth and spike width showed relationships

to these variables distinct from their relationship to SSI (compare Fig. 5C and Figs. S9C-D). As a

particular example of this dissociation, narrow spiking neurons had both higher SSI and higher prediction

accuracy, but prediction accuracy is negatively correlated with SSI on average. Data from PEG also

showed the effects of cortical depth and spike width, although effect size was slightly weaker, possibly

reflecting the smaller sample size of this dataset (Table S1).

Figure 5. Subspace similarity within a local A1 population depends on neuronal cell type and cortical depth. **A.** Heatmap shows subspace similarity index (SSI) between each pair of single units from a single recording site, grouped by spike width (narrow, red; regular, gray) and then sorted by cortical depth. **B.** Mean SSI between pairs of neurons within recording site, grouped by spike width and 200 um bins, and averaged across all sites (narrow: n=205 units, regular: n=1459 units, 42140 pairs total, Fig. S9). **C.** Mean SSI by cortical depth (x axis) and spike width (color), for each unit paired (i.e., average across each depth in upper and lower triangles in B). Both cortical depth and spike width significantly predicted SSI (Table S1). Error bars indicate 2 SEM and are larger for narrow spiking neurons because of their smaller sample size. Vertical lines indicate boundaries between cortical layers 3-4 and 4-5. **D.** Mean SSI as a function of distance (difference in depth) between the neuron pair (x axis) and spike width (color), plotted as in C.

Diversity of nonlinear responses within the tuning subspace

Inspection of the subspace models shows a diversity of SSRFs across neurons, varying in size and shape

(Fig. 3). These differences could reflect distinct elements of the underlying cortical circuit. As

demonstrated above, larger SSRFs are associated with narrow-spiking, putative inhibitory neurons (Fig.

4F-G). To further quantify SSRF properties, a marginal tuning curve was calculated for each subspace

dimension by projecting the stimulus into that single dimension and measuring the mean response for

each value of that projection (Fig. 3C). Marginal tuning curves varied in their degree of symmetry [45],

ranging from completely asymmetric (as would be expected for the linear-nonlinear model) to completely

symmetric (consistent with a second-order polynomial model, examples in Fig. 3C). Among symmetric

tuning curves, the majority were downward facing, producing high firing range over a relatively small,

bounded range of inputs and a decrease in firing rate at large positive and negative values. In addition, a

minority of tuning curves were upward facing, producing high firing rate for large positive and negative

inputs. Inspection of example neurons showed that the downward versus upward orientation of the

symmetric tuning curves had distinct impact on the time-varying neural response. Neurons with

downward-facing tuning curves tended to respond sparsely to a small number of stimuli (e.g., Fig 3, unit

7), while neurons with upward facing tuning curves tended to respond to many stimuli (e.g., Fig. 3, unit

4). Thus, the properties of the nonlinear tuning surface qualitatively impacted a neuron's behavior.

Figure 6. Diversity of subspace tuning nonlinearities across cell types. **A.** Distribution of TSI values measured from

the marginal tuning nonlinearity of all subspace dimensions (n=1632 regular, 374 narrow AC units, 11181

unit/subspace dimension combinations, accounting for 95% of dSTRF variance for each unit). Shading indicates

classifications as symmetric downward (TSI<-0.3, left), asymmetric (-0.3 < TSI < 0.3, middle), and symmetric

upward (TSI>0.3). **B.** Fraction of tuning nonlinearities in each TSI category, grouped by cortical depth (x-axis) and

spike width (color), for the same set as in A. Examples of nonlinearities from each category are inset above the

plots. Upward symmetric nonlinearities are less common overall but more common for narrow-spiking units in

cortical layer 4 (between dashed lines, generalized linear mixed effects model: spike width, χ^2=62.0, p=3.4e-15;

depth, χ^2=3.9, p=0.14, spike width x layer, χ^2=13.6, p=0.0011, full details in Table S2). **C.** Fraction of positive (>0.3,

blue) and negative (<-0.3, green) TSI, for subspace dimensions grouped by spike width and cortical layer (see Fig.

S10 for analysis including dimensions with asymmetric TSI near 0). Fraction of positive TSI is significantly greater

for narrow than regular spiking neurons in layer 4 (L4, **p=7.2e-6, Z test, generalized regression model) and layers

5-6 (L56, *p=0.024). Error bars indicate 1 SEM, computed by jackknifing. **D.** Heatmaps show two-dimensional

histograms of AC units binned according to their number of symmetric upward (TSI > 0.3, x-axis) and symmetric

downward (TSI < -0.3, y-axis) subspace dimensions. Data for regular-spiking units at left (gray); narrow-spiking at

right (red). Numbers indicate the percent of units falling in dashed boxes, with exclusively upward- or downward

symmetric nonlinearities (*significantly different from chance, p<0.0001, permutation test). Data are shown only for

the first five subspace dimensions (n=739 regular, 144 narrow-spiking, subset of units with at least 5 significant

dimensions).

To quantify both the symmetry and the vertical orientation of the marginal tuning curves, we defined a

tuning symmetry index (TSI), computed from the average slope and curvature of each tuning curve (Eq.

10). A TSI of 1 or -1 indicates a completely symmetric upward- or downward-facing tuning curve,

respectively, and a value of 0 indicates a completely asymmetric tuning curve with a uniformly positive

or negative slope. Tuning curves were grouped into terciles by their symmetry index, corresponding to

peaks that occurred naturally at -1, 0, and 1 in the distribution of values (Fig. 6A, S10A-B, TSI<-0.3, -

0.3<TSI<0.3, and TSI>0.3). We then measured how the proportion of each TSI group varied with spike

width and cortical depth (Fig. 6B). For regular spiking neurons, TSI was most often negative, and it did

not vary substantially with depth. For narrow spiking neurons, on the other hand, TSI was more likely to

be positive, especially at depths just below the layer 3-4 boundary.

We used a generalized linear-mixed effect model to quantify the relationship between cell type (spike

width and cortical depth) and the sign of TSI for each subspace dimension of each neuron (Eq. 12,

detailed in Table S2). To account for the apparent nonmonotonic relationship between depth and TSI,

depth was cast as a categorical variable, corresponding to layers 1-3 (depth < 0), layer 4 (0 < depth < 200)

and layers 5-6 (depth > 200). The occurrence of asymmetric TSI (-0.3<TSI<0.3) was relatively constant

across cortical depths. Thus, we excluded data in this category to permit training of a binary classifier for

positive versus negative TSI (Fig. 6B-C, n=5644/8179 A1 unit/filter pairs with TSI < -0.3 or >0.3). As

suggested by the data, spike width had a large regression weight (χ^2=62.0, p=3.4e-15). There was no

effect of cortical depth alone (χ^2=3.89, p=0.14), but there was an interaction between depth and spike

width, reflected primarily in layer 4 (depth 0-200, χ^2=13.6, p=0.0011). Similar effects were observed in

PEG (Table S2).

In several example units, tuning nonlinearities for the highest variance subspace dimension were more

likely to be asymmetric than other dimensions (Dim. 1, Fig. 3C). TSI in this asymmetric range is

consistent with the monotonic nonlinearity implemented in LN models [45]. The tendency for the first

dimension to be asymmetric was similar across all cell types (Fig. S10C-D). While the fraction of

dimensions with TSI near 0 differed between first versus later subspace dimensions, the relatively greater

likelihood of positive TSI for narrow spiking neurons was consistent when only dimensions with TSI < -

0.3 or > 0.3 were considered (Fig. S10E-F).

We also observed that, within a single unit, symmetric tuning nonlinearities tended to all be upward or

downward facing across subspace dimensions (compare columns 2 and 3, Fig. 3C). To quantify this

effect, we counted the number of subspace dimensions for each A1 unit with TSI < -0.3 or TSI > 0.3. The

histogram of counts showed that units were much more likely than chance to have nonlinearities only in

one of these categories (Fig. 6D, dashed boxes, permutation test, shuffling TSI values across neurons).

Consistent with their tendency toward positive TSI (Fig. 6C), all the subspace dimensions for many

narrow spiking neurons had only TSI > 0.3. Thus, when the subspace model revealed symmetric

nonlinear tuning, the direction of the tuning curve within a single unit (upward or downward) was

consistent across subspace dimensions.

Discussion

We find that a low-dimensional sensory tuning subspace can be readily extracted from a CNN-based encoding model for neurons in auditory cortex (AC). A new encoding model, based only on the projection of stimuli into the subspace, performs nearly as well as the original CNN. Thus, this simpler and more interpretable model accounts for the key computations performed by the CNN. Analytically, the subspace model is closely related to multifilter models estimated using spike-triggered covariance (STC) and maximally informative dimensions (MID), establishing a conceptual link between CNNs and these previously proposed architectures [2,19]. While CNNs have been shown to account for sensory coding qualitatively better than other encoding models, understanding their key computations has been challenging [5,8]. We find that subspace models clearly describe nonlinear response properties and elucidate functional differences between neuronal cell types, distinguishing functional properties between narrow- and regular-spiking neurons and between neurons at different cortical depths (Fig. 7). The current study focuses on neurons in the auditory system, but subspace analysis is a general method that can be applied to a wide range of sensory and other neural systems.

Figure 7. A. Conceptual framework for sparsely tiled subspace receptive fields (SSRFs) in local cortical circuits. The site-wide tuning subspace determines the range of sensory inputs reaching the local population in a cortical column. Shaded volumes indicate the maximum response areas of single units to stimuli projected into three

dimensions (Dim 1-Dim 3) of the tuning subspace. While most neurons receive these inputs, strong recurrent

inhibition drives each neuron to respond to distinct stimuli, reducing SSRF overlap within the shared space (Fig. 4).

The larger SSRFs for inhibitory neurons (red) may reflect broadly tuned inhibition that pushes tuning of excitatory

neurons (gray) to a narrower range of stimuli. **B.** Representative schematic SSRFs reflecting the observed

distribution of temporal symmetry index (TSI, Fig. 6). For visualization, tuning surfaces show responses (z axis) to

stimuli projected onto the first two subspace dimensions (Dim 1/Dim 2, x-/y axes). For most regular spiking neurons

(top row, gray), tuning nonlinearities are mostly downward symmetric (TSI < -0.3), producing responses to a narrow

range of stimuli. For some narrow-spiking neurons, nonlinearities are upward symmetric (TSI > 0.3), producing

"bowl-like" tuning, with responses to many high-contrast stimuli in the tuning subspace. Neurons in both groups

often have monotonic tuning along the first subspace dimension (TSI ≈ 0). The exemplar SSRFs can tile the

subspace if they are shifted along Dim 1 and rotated around the z-axis.

Selectivity within a tuning subspace forms a sparse code in local cortical

populations

While it is generally agreed that neurons in the same cortical column encode similar sensory features,

they can still differ substantially in their specific response properties [46,47]. Our analysis of local neural

populations in AC revealed that nearby neurons share a similar sensory tuning subspace, but their

individual subspace receptive fields (SSRFs) sparsely tile that subspace (Fig. 7A). Inputs from thalamus

to cortex are relatively low-dimensional and may determine the small number of dimensions in the site-

wide tuning subspace. Recurrent inhibition within a much larger cortical population can drive individual

neurons to respond to distinct stimuli within this subspace [38,48]. Thus, for any single stimulus, only a small

fraction of neurons will produce strong responses, while their neighbors will be suppressed. This

computation is often associated with gain control mechanisms and has been proposed to produce a sparse

population code [49,50]. A sparse representation can facilitate selection of sensory features for binding

features into objects and selecting information to guide behavior [51]. This sparse tiling also accounts for the

relatively low signal correlations we observe in activity evoked by natural sounds, even though nearby

neurons all share basic tuning properties, like best frequency and tuning bandwidth [47].

Flattened CNNs reveal sensory tuning subspaces

Understanding computations by which the brain extracts and encodes information from dynamic natural

sounds is a long-standing problem in sensory neuroscience [12]. The classic linear-nonlinear

spectrotemporal receptive field (LN STRF) describes encoding as convolution of the sound spectrogram

with a single linear spectrotemporal filter, followed by a static rectifying nonlinearity [52,53]. Subspace

encoding models have been proposed as a generalization of the LN STRF, in which the stimulus is

convolved with two or more filters, and the response is then a nonlinear combination of the projection

into this tuning subspace [2,18,19]. The subspace extracted from a CNN describes multiple sensory features

that influence neural activity and the nonlinear interactions that shape responses. Peak activations in the

SSRF provide a means of determining optimal stimuli, an approach that is used to study neural DNNs [8,54].

In addition, equal-amplitude contours on the tuning surface predict stimuli that produce an invariant

response, an approach that can be tested with closed-loop experiments.

While informative, subspace models can be difficult to fit directly to neural data, especially for natural

stimuli [10], and their implementation has been limited to 2 or 3 subspace filters [2,25,55]. In contrast, large

CNN models can be fit readily to large natural stimulus datasets [8,11,56]. The flattening process developed in

this study effectively uses large amounts of activity simulated by the CNN model to fit a subspace model.

The resulting subspace model can account for time-varying neural activity nearly as accurately as the full

CNN. In addition to facilitating subspace analysis, this relationship establishes a direct conceptual link

between deep learning-based encoding models and multifilter encoding models.

Tuning within sensory subspaces accounts for gain control and sensory invariance

The shape of tuning nonlinearities imposes qualitative differences in how a subspace dimension

influences neural response properties [2]. Asymmetric nonlinearities produce a response characteristic of

the LN model, where spike rate changes monotonically with stimulus contrast. If the nonlinearity is

symmetric, a stimulus will have the same effect on spiking, whether it projects to a large positive or

negative value in the tuning subspace (Fig. 7B). In most neurons, symmetric nonlinearities were

downward facing (inverted-U), meaning that large positive or negative stimulus projections produced a

decrease in firing. Downward-facing nonlinearities may explain contrast gain control effects often

observed in sensory cortex [57,58]. Models implementing multiplicative context fields, have shown that gain

control is spectrotemporally tuned for individual neurons [59]. Here, the subspace model identifies a set of

subspace dimensions with an inverted-U nonlinearity, suggesting that suppressive effects may be tuned to

a low-dimensional subspace instead of just a single dimension. Moreover, the nonlinearities are not

necessarily symmetric around 0, and thus are not simply a function of contrast. Instead, the suppressive

dimensions reduce responses to stimuli that deviate from one that optimally activates the neuron, enabling

local populations to tile the tuning subspace (Fig. 7).

Tuning nonlinearities in other AC neurons are symmetric and upward facing (upward-U, Fig. 7B,

bottom). For these subspace dimensions, a stimulus feature projecting to a large positive or negative value

produce an increase in firing. Individual dimensions are, by definition, orthogonal, but examples show

that pairs of filters can lie in quadrature (Fig. 3). This organization produces responses that are tuned to a

spectrotemporal feature but invariant to its phase. Complex cells in the visual cortex are described as

having tuning invariant to spatial phase, but reports of analogous computations in AC have been less

consistent [60]. We observe phase invariance for both spectral and temporal modulations. In the case of

modulations on the temporal axis, this computation can produce rate coding of temporally modulated

sound [61]. Phase invariance on the spectral axis (Fig. 1) produces a response to narrowband tones invariant

to their precise frequency but suppressed by broadband stimuli. This form of invariance has not

previously been reported for AC neurons, suggesting a new, nonlinear computation by the auditory

system.

Cell type dependence of subspace properties

In the current study, all neurons from the same AC recording site had similar subspace tuning, consistent

with previous observations of topographic maps for sound features [47,62]. However, the degree of similarity

within a site depended on neuronal cell type. It is hypothesized that functional differences between cell

types provide insight into computations performed by local cortical circuits [13]. Previous work has shown

cell-type dependence of frequency tuning and adaptation properties [41,63–65]. However, the relationship

between local circuit position and other spectrotemporal encoding properties is less regular, suggesting

that variability is nearly as large within- as between local populations [46,66].

We found that the similarity of tuning subspaces was especially high between pairs of narrow spiking

(putative inhibitory) neurons in superficial layers, and it was weakest for regular spiking (putative

excitatory) neurons in deeper layers. Superficial inhibitory neurons receive intracortical inputs and are

hypothesized to mediate top-down control of sensory processing [67,68]. In a specific topographic location, a

top-down signal may thus specifically amplify or suppress representation of stimuli in the shared tuning

subspace of these superficial neurons. More diverse tuning in deeper layers may describe the range of

features for which responses are also modulated by the selective top-down signal. Such a mechanism

might mediate selective attention to auditory features. For example, attention to the pitch of a particular

voice may amplify responses to other sound features that occur coherently with that pitch [69].

Nonlinear properties of the SSRF also vary with neuronal cell type (Fig. 7B). Most tuning nonlinearities

were downward facing, indicating a suppression of responses consistent with contrast gain control.

However, neurons with narrow spike width and positioned below the layer 3/4 boundary were much more

likely to have upward facing nonlinearities. The most prominent inhibitory cell type in AC layer 4 is the

parvalbumin positive (PV) interneuron [14]. PV neurons provide feedforward inhibition of thalamic inputs

that can shape the frequency tuning of nearby pyramidal cells [13,41]. Invariance to the phase of

spectrotemporal modulation may produce a broadly tuned response, leading to inhibitory gain control in

their post-synaptic targets. Thus, the comprehensive characterization provided by the subspace encoding

model enables linking distinct computations to specific elements of local cortical circuits. Experiments

that characterize subspace tuning of neuron populations with defined connectivity, like superficial

inhibitory neurons that receive top-down cortical feedback [70] or subcortical-projecting pyramidal neurons

[65], will provide greater insight into the role of local circuits in shaping cortical representations. Moreover,

studying if and how top-down feedback affects the size and overlap of SSRFs will provide insight into

how cortical circuits shape sound representations to guide sensory behavior.

Material and Methods

Surgical procedures

All procedures were performed in accordance with the Oregon Health & Science University Institutional

Animal Care and Use Committee (IACUC) and conform to the standards of the Association for

Assessment and Accreditation of Laboratory Animal Care (AAALAC) and the United States Department

of Agriculture (USDA). Four neutered young adult ferrets (3 male, 1 female) were obtained from a

supplier (Marshall Farms). In each animal, sterile head-post implantation surgeries were performed under

anesthesia to expose the skull over the auditory cortex (AC) and permit head-fixation during

neurophysiology recordings. Surgeries were performed as previously described [71]. After removing tissue

and cleaning the skull, two stainless steel head posts were anchored along the midline using light-cured

bone cement (Charisma, Kulzer). To improve implant stability, 8-10 stainless self-tapping set screws were

mounted in the skull. Layers of bone cement were used to build the implant to a final shape amenable to

neurophysiology and wound margin care, which included frequent cleaning and sterile bandaging.

Following a two-week recovery period, animals were habituated to head-fixation and auditory

stimulation.

Acoustic stimuli

Stimuli for model fitting consisted of large sequences of natural sound segments. Segments were drawn

from one of two large corpora: Audioset or Pro Sound Effects (PSE) (Core 3 Complete). The Audioset

corpus is comprised of recordings from over 2 million YouTube videos [72]. The PSE corpus is comprised

of 371,089 high-quality recordings and sound effects (over 3,000 hours of audio). We selected 484,375

segments from each corpus (250k 50-ms segments, 125k 110-ms segments, 62.6k 190-ms segments, etc.).

Five segment durations were used (50, 110, 190, 420, and 780 ms). The pseudo-logarithmic distribution

of durations avoided exact integer multiples to minimize the likelihood of harmonic ringing in the neural

675 responses. Each sequence was 17.79 seconds in duration and included 124 segments (64 50-ms segments,

676 32 110-ms segments, 16 190-ms segments, etc.) plus 5 segments of silence, one per duration. The

677 ordering of segments was random and the sound level of segments was sampled from a uniform

678 distribution with a 20 dB range. Segments were combined using crossfading at the boundary to avoid

679 click artifacts (10 ms Hanning window).

681 Segments were selected by randomly sampling audio files without replacement from the Audioset and

682 PSE corpus. To avoid selecting highly similar segments, an auditory excitation pattern was computed for

683 each segment, and segments were selected to have distinct excitation patterns. The excitation pattern was

684 computed by multiplying the power spectrum ($|FFT(x)|^2$) of the segment with cosine filters designed to

685 coarsely mimic cochlear filtering in the ferret, followed by compression (raising the outputs to the 0.3

686 power). The structure of the cosine filters has been described previously for humans [73]. The only

687 difference is that we used an alternate formula for calculating ERB_N derived based on [74]:

$$\frac{1}{0.31 * (1 - 0.533)} f^{(1-0.533)} \tag{1}$$

688 We excluded segments whose excitation pattern was similar to a previously selected segment from the

689 same recording (r > 0.8) or whose excitation pattern was similar (r > 0.8) to more than 5% of previously

690 selected segments (computed by randomly sampling up 10,000 previously selected segments). Audioset

691 contains a large amount of speech and music. To prevent these stimuli from dominating the stimulus set,

692 we prevented any one of the category labels from the Audioset ontology from comprising more than 20%

693 of the selected Audioset segments.

695 For computational speed, we only excerpted segments from the first 10 seconds of each sound file (some

696 PSE files are much longer than this duration). Stereo sounds were converted to mono by selecting the left

697 channel, and all stimuli were resampled to 44100 Hz. For each file, we divided the recording into frames

698 of the desired segment duration (hop equal to half the segment duration). Segment durations were 20 ms

longer than those noted above to allow for crossfading. We computed the power of each frame and

discarded any frames whose power was 25 dB below the maximum power across all frames in that

recording (to discard silent periods). We also discarded frames that violated the excitation pattern

similarity criteria described above. We then selected the segment with the greatest power from those

remaining.

Stimuli for model testing consisted in part of 4 sequences created using the same approach described

above. In addition, the test set contained 2, 18-second sequences composed of 1-second segments of

natural and synthetic sounds tested in prior experiments from our lab [10]. These included 6 synthetic

segments comprised of tones and noises and 18 natural sound segments that included ferret vocalizations,

marmoset calls, speech, music, and environmental sounds. Each sequence was composed of 12 segments

with a 500-ms buffer period between each segment. Thus, in total, the test set consisted of 6 sequences

with a total duration of ~100 seconds (4*17.79+2*18=107.16). These sequences were presented between

10 and 20 times depending on the amount of recording time available.

Digital acoustic signals were transformed to analog (National Instruments), amplified (Crown), and

delivered through a free-field speaker (Manger) placed 80 cm from the animal's head, 0° elevation, and

30° contralateral to the recording hemisphere. Stimulation was controlled using custom MATLAB

software (https://bitbucket.org/lbhb/baphy) and all experiments took place inside a custom double-walled

sound-isolating chamber (Professional Model, Gretch-Ken). Each stimulus sequence was presented at 65

dB SPL (RMS power).

Neurophysiology

Neurophysiological recordings were performed in awake, passively listening animals while head-fixed.

To prepare for neurophysiological recordings, a small craniotomy (0.5-1mm) was opened over AC.

Recording sites were targeted based on tonotopic maps and skull landmarks [75,76] identified during

implantation surgery. Initially, tungsten microelectrodes (FHC, 1-5MΩ) were inserted into the craniotomy

to characterize tuning and response latency. Short latency responses and tonotopically organized

frequency selectivity across multiple penetrations defined the location of primary auditory cortex (A1) [75],

whereas secondary auditory cortex (posterior ectosylvian gyrus, PEG) was identified as the field

ventrolateral to A1. The border between A1 and PEG was identified from the low-frequency reversal of

the tonotopic gradient.

Once a cortical map was established, subsequent single-unit recordings were performed using two

different electrode configurations. Experiments in animal 1 recorded neural activity using acute insertion

of 64-channel silicon electrode arrays, which spanned 1.05 mm of cortical depth [26]. Experiments in

animals 2-4 recorded activity using Neuropixels short NHP probes (IMEC, 384/960 selectable channels,

[77]). Probe tips were sharpened in lab or purchased pre-sharpened to permit penetration of dura.

Neuropixels probes were implanted semi-chronically using a manual microdrive (modified from [78])

secured on the animal's implant with dental cement. The array was implanted and allowed to settle for at

least 18 hours to permit stable recordings. After recordings were complete at one site, the probe was

explanted, sterilized, and reimplanted in a new craniotomy. Typically, about 150 of the 384 active

channels spanned the depth of AC, as determined by current source density analysis (see below).

Electrophysiological signals were amplified (RHD 128-channel headstage, Intan Technologies, or

Neuropixels headstage, IMEC), digitized at 30 kHz (Open Ephys) [79], and saved to disk for further

analysis.

Spikes were sorted offline using Kilosort2 (https://github.com/MouseLand/Kilosort2) [80], and sorting

results were manually curated in phy (https://github.com/cortex-lab/phy). A contamination percentage

was computed by measuring the cluster isolation for each sorted and curated spike cluster, which was

classified as a single unit if contamination percentage was less than or equal to 5%. Clusters with

contamination above 5% were classified as multi-unit and excluded from analysis.

Laminar depth analysis

We used current source density analysis to classify units by cortical layer (1/3, supragranular; 4, granular;

5/6 infragranular). The local field potential (LFP) signal was generated by lowpass filtering either the raw

signal from the 64-channel silicon probe or the LFP signal from the Neuropixel probe below 250Hz using

a zero-phase shift (filter-filter method) 4th order Butterworth filter, followed by down-sampling to 500Hz.

A custom graphical interface was used to mark boundaries between layers, based on features of average

sound-evoked LFP traces sorted by electrode depth (https://github.com/LBHB/laminar_tools). Layer-

specific features included the pattern of current source density (CSD) sinks and sources evoked by best

frequency-centered broadband noise bursts. Patterns were selected to match auditory evoked CSD

patterns seen in AC of multiple species [81,82,43]. Each unit was assigned a layer based on the boundaries

above and below the channel where its spike had the largest amplitude.

Spike width classification

We classified neurons as narrow- and broad-spiking based on the average width of the waveform. Width

was calculated as the time between the depolarization trough and the hyperpolization peak [39]. The

distribution of spike width across neurons was bimodal, and the categorization threshold was defined as

the minimum between the bimodal peaks. Filtering properties differed between 64-channel probes and

Neuropixels, thus categorization threshold was defined as 0.35 ms and 0.375 ms, respectively. Consistent

with studies in other systems, recordings from optogenetically labeled GABAergic neurons in ferret

auditory cortex have demonstrated that these inhibitory neurons fall entirely in the narrow-spiking group

[40].

Convolutional neural network (CNN) encoding model

Encoding model analysis was used to describe the transformation from stimulus spectrogram to neural

response. The sound-evoked response was defined as the peristimulus time histogram (PSTH), $r(t)$, a

neuron's time-varying spike rate, sampled at 100 Hz (10 ms bins). Model input was the spectrogram,

$s(f,t)$, of the sound waveform, computed using a second-order gammatone filter bank [83]. The spectrogram

was fixed for each model rather than fitting the spectrogram's parameters, since we have observed little

benefit on model performance from this additional complexity. The filter bank consisted of $F = 32$ filters

with f_j spaced logarithmically from $f_{low} = 200$ to $f_{high} = 20,000$ Hz (approximately 1/6 octave per bin).

Filter bank output was smoothed, downsampled to 100 Hz to match the sampling of the neural PSTH, and

log-compressed to account for the action of the cochlea. For the stimulus spectrogram, defined as a

function of sound frequency and time, $s(f, t)$, a causal encoding model prediction at time, t, for neuron, i,

is then a function of the stimulus up until that time, $r_i(t) = H_i[S(t)]$, where $S(t) = [s(f, 1) \dots s(f, t)]$.

<u>Linear-nonlinear model.</u> The linear-nonlinear spectrotemporal receptive field (LN) model is widely used

in studies of neural auditory coding [1,84,85] and was used as a baseline reference for this study (Fig. 1). To

leverage statistical power in the neural population data and permit direct comparison with the population

CNN model, below, the LN model was implemented using a shared filter space across neurons in each

recording site. The population LN model is analytically identical to the traditional single-neuron LN

model but performs with slightly greater accuracy for neurons with low response reliability [10]. The first

stage of the population LN model convolves a bank of M finite impulse response (FIR) filters, h, with the

stimulus spectrogram:

$$r_m(t) = \sum_f^F \sum_u^U h_m(f, u)\, s(f, t - u) \tag{2}$$

795 Here, we used $M{=}100$ filters, each containing $F = 32$ spectral channels and $U = 25$ temporal bins. Filters

796 are implemented with rank-1 factorization. Higher rank filters could be used, but we have found that in a

797   trade-off between larger filter bank (greater M) and higher-rank filters, the additional filters provide better

798   model performance [44]. Activity in this filtered space is then linearly weighted to generate a linear

799   prediction for each neuron i:

$$r_{lin,i}(t) = \sum_{m}^{M} w_i(\mathrm{m}) \, r_m(t) \tag{3}$$

800   Finally, this linear prediction is passed through a double exponential nonlinearity to account for spiking

801   threshold and firing rate saturation to produce the final prediction of the PSTH response. The double

802   exponential nonlinearity is:

$$\mathrm{r}_i(\mathrm{t}) = \mathrm{b}_i + \mathrm{a}_i \, \exp\left[-\exp\left(k_i(r_{\mathrm{lin,i}}(t) - s_i)\right)\right] \tag{4}$$

where the baseline spike rate, saturated firing rate, firing threshold, and gain are represented by b, a, s and

k, respectively [44].

<u>Population CNN model.</u> The CNN model employed an architecture developed in a previous study of

natural sound encoding in AC [10]. Like the LN model, this architecture fit a shared subspace across

neurons recorded simultaneously from the same local population. The time-varying activity of individual

neurons was computed in the final layer, as the weighted sum of outputs from the penultimate (shared)

model layer [8,10]. The full model consisted of two convolutional blocks, followed by two dense layers.

Each convolutional block was composed of a dense layer and a set of finite-impulse-response (FIR) filters

with ReLU activation. The FIR filters operated on each output of the dense layer separately. Thus, each

convolutional block effectively performed the computation of a spectrotemporal receptive field (STRF) in

the standard LN model [10]. The first block contained 80 filters that each integrated across the 32

spectrogram channels and then performed convolution over the 15 preceding 10-ms time bins (80 32x15

filters, Eq. 2). The second block contained 100 80x10 linear filters. These convolutional blocks were

followed by two densely connected layers: 1) 100x100 with ReLU activation, and 2) 100xN with a double

exponential nonlinearity, identical to that used in the LN model (Eq. 4) and fit individually for each

neuron (N: number of neurons being fit).

Model optimization

All fitting was performed exclusively with the estimation dataset, and the validation set was used only for

measuring prediction accuracy. Prior to fitting, all input (stimulus) and output (time-varying spike rate)

channels were normalized to a range of 0 to 1. Model parameters were then fit using TensorFlow's

implementation of the Adam algorithm for stochastic gradient descent [86], using a mean squared error

(MSE) loss function, with L2 regularization (alpha=10^{-4}). Loss was computed for all neurons in the

dataset simultaneously. We evaluated the use of a Poisson loss function for model optimization [30] and

observed similar but slightly lower prediction accuracy than for models trained with MSE loss. To obtain

an initial coarse fit and prevent falling into local minima, the final double exponential nonlinearity was

replaced with a simple level shift, and the fit was performed with a relatively high learning rate (0.01) and

stop tolerance for fit loss (0.001). The double exponential was then restored and fitting continued with

smaller learning rate (0.001) and tolerance for fit loss (10^{-4}). To mitigate overfitting, an 8-fold jackknifing

procedure was used, in which a distinct 12.5% of the fit set was excluded from the fit data set for each

model fit. For each jackknife sample, the model was fit starting at 5 random initial conditions, making 40

model fits in total. The highest performing model for each jackknife was saved for subsequent analysis.

Tuning subspace analysis

<u>Dynamic spectrotemporal receptive field (dSTRF) measurement.</u> While the population CNN model

describes a complex nonlinear function, the stimulus-response relationship at each time point during

stimulation can be approximated as a linear spectrotemporal receptive field, termed the dSTRF. This

locally linear approximation can be measured as the derivative of the response predicted by the CNN

model for the i-th neuron at each timepoint, t, $r_i(t) = H_i[S(f, 0 \ldots t)]$, relative to the input stimulus

spectrogram, $S(f, t)$,

$$d_{i,t}(f,u) = \frac{d\, r_i(t)}{d\, S(f,t-u)} \tag{5}$$

Intuitively, the dSTRF is a locally linear approximation of a nonlinear function, analogous to fitting an

LN model using only small perturbations in the stimulus at each frequency, f, and time lag, u. The dSTRF

was measured with a maximum time lag, U=250 ms, which corresponds to the maximum integration time

of the population CNN. We measured the dSTRF by computing the Jacobian of the population CNN

output at each fit stimulus timepoint, which is equivalent to Eq. 5. To reduce noise, the dSTRF was

measured using each of the 8 jackknife model estimates. A shrinkage function (soft threshold for

mean/standard error<1) was used to attenuate noise in the dSTRF average across jackknifes [87]. Thus, for a

single neuron and stimulus of length (in samples) T, the final dSTRF consisted of T linear

spectrotemporal filters, $d_{i,t}(f,u)$.

<u>Subspace encoding model.</u> This model was derived from the CNN to determine if the CNN captured the

same functional properties as previously proposed subspace models [2,30,32]. The large collection of dSTRFs

measured for each neuron was projected into a low dimensional space by principal component analysis

(PCA). The frequency, f, and time lag, u, dimensions of the dSTRF were reshaped into a single axis, and

PCA was performed along the complementary time axis, t. A low-dimensional subspace was then defined

by the N components explaining the most variance in the dSTRF, $g_{i,j}(f,u)$, $j = 1 \dots N$. For most

analysis, we chose N to account for 95% of variance, but different threshold values were assessed in some

analyses. For subsequent analysis, the stimulus was projected into this low dimensional subspace,

$$x_j(t) = \sum_f^F \sum_u^U g_{i,j}(f,u)\, s(f,\, t-u), \tag{6}$$

Nonlinear tuning in the subspace was visualized as a subspace receptive field (SSRF), the mean actual or

predicted firing rate at each point in that space. To determine how well the tuning subspace accounted for

sensory responses, the stimulus was projected into the subspace, and a densely connected three-layer

neural network was used to model the relationship between the time-varying stimulus projection and

neural activity in the fit data. Each layer contained 15 linear units, followed by a nonlinearity (layers 1-2:

rectified linear unit; layer 3: difference of exponentials sigmoid). Thus the network could fit an arbitrary

SSRF,

$$r(t) = F\big(x_1(t), x_2(t), \ldots, x_N(t)\big) \tag{7}$$

This model could account for many nonlinear interactions within the subspace but could not account for

any spectrotemporal tuning outside of the N subspace dimensions. We tested several variants of the

model, including additional dense layers and more units per layer, but no improvement in prediction

accuracy was observed for larger architectures.

<u>Second-order subspace model.</u> Multifilter models using spike-triggered covariance use a second order

model to define the relationship between a subspace representation and the neural response. To

implement this architecture, we used a second order model to fit the mapping between stimulus subspace

and time-varying response. For the N-dimensional subspace stimulus, $x_1(t) \ldots x_N(t)$, the second order

model response is:

$$r(t) = \sum_{i,j}^{N} w_{ij} x_i(t) x_j(t) + \sum_{i}^{N} v_i x_i(t) + r_0 \tag{8}$$

Second-order coefficients, w_{ij}, are weights applied to products of values in the subspace channels i and j.

When $i=j$, a positive value indicates an increase in response when the projection on that dimension has

either a large positive or negative value, and a negative value indicates a decreased response.

<u>Subspace similarity index (SSI).</u> To measure the similarity of tuning between two sets of N subspace

filters, i and j, we computed the sum of the cosine similarity (CS) between each pair of filters and

normalized by the number of filters.

$$SSI_{i,j} = \sum_{m,n}^{N,N} CS\big[g_{i,m}(f,u), g_{j,n}(f,u)\big] \Big/ N \tag{9}$$

The summed cosine similarity across dimensions is an implementation of Grassman distances used for

measuring the similarity of subspace projections [88]. For the current study, we measured SSI between the

$N=4$ largest filters from each neuron.

Tuning symmetry index (TSI). To characterize the shape of the marginal tuning curve for a single

subspace dimension, TSI distinguished between symmetric downward facing (values near -1), symmetric

upward facing (values near 1) and asymmetric (values near 0). For tuning curve, $y(x)$, with derivative,

$y'(x)$, and second derivative, $y''(x)$, we define the TSI,

$$
\text{TSI} = \begin{cases} 1 - \left|\sum_x y'(x)\right| / \sum_x |y'(x)|, & \text{if } \sum_x y''(x) > 0 \\ -(1 - \left|\sum_x y'(x)\right|/\sum_x |y'(x)|), & \text{otherwise} \end{cases} \tag{10}
$$

In cases where y' is always positive or negative (asymmetric), the ratio of sums reduces to 1 and thus

gives a TSI value of 0. If y' has equal amounts positive and negative (symmetric), the ratio will be zero,

and the average curvature, captured by $y''(x)$, will determine if TSI is -1 or +1. The derivative was

approximated by discretizing the tuning curve with 20 bins spanning 99% of the values in x spanned by

the stimulus projection onto that dimension.

Statistical analysis

For all pairwise statistical tests we performed a Wilcoxon signed-rank test (sign test), and for unpaired

comparisons we used a Mann-Whitney U test. Significance was determined at the alpha = 0.05 level.

Units were considered sound-responsive if either the LN or CNN model predicted test responses above

chance ($p<0.05$, permutation test, corrected for multiple comparisons, n=2337/2874 units).

Linear mixed-effects models (lme4 package in R version 4.4.3) were used to assess relationships between

neuronal cell type and SSI and TSI metrics. For the SSI model (fit using the lme4::*lmer function*), the

outcome was SSI for a pair of neurons, i and j (Table S1). Inputs were mean cortical depth, D (-750-750

μm relative to the layer 3-4 boundary), depth difference between neurons, Δ, and spike width category W

(narrow-narrow, narrow-regular, regular-regular), and interactions between depth and width variables

(β_{DW}, $\beta_{\Delta W}$):

$$\text{SSI}_{i,j} = \beta_0 + \beta_D D + \beta_\Delta \Delta + \beta_W W + \beta_{DW} DW + \beta_{\Delta W} \Delta W +$$
$$\beta_r (r_i + r_j)/2 + \beta_m (m_i + m_j)/2 + \beta_a a_i$$

(11)

CNN prediction accuracy (r) and mean rate (m) were also included as predictors, and animal identity was

included as a random effect (a). Significance of individual parameters was determined by a *t test*, and

goodness of fit was measured by a χ^2 test (Type II Wald using the car::Anova package). Prior to statistical

modeling, continuous predictors (D, Δ, m, r) were normalized (using the *scale* function in R).

For TSI, we used generalized mixed-effect models (lme4::glmer function) with a logistic regression link

function (Table S2). The outcome was whether TSI was positive (TSI > 0.3) or negative (TSI < -0.3), and

data with intermediate TSI values were excluded. Predictors were neuron depth (L, corresponding to

cortical layers 1-3 ($d_i < 0$ μm), layer 4 ($0 < d_i < 200$), and layers 5-6 ($d_i > 200$) layer), spike width (w),

mean rate, (m) and CNN prediction accuracy (r).

$$p(\text{TSI}_i > 0.3) = \beta_0 + \beta_L L_i + \beta_w w_i + \beta_r r_x + \beta_{Lw} L_x w_i + \beta_r r_i + \beta_m m_i + \beta_a a_i \qquad (12)$$

Animal identity was included as a random effect (a). Significance of individual parameters was

determined by a *z test*, and goodness of fit was measured by a χ2 test (Type II Wald using the car::Anova

package). Prior to statistical modeling, continuous predictors (mean rate and CNN prediction accuracy)

were normalized (using the *scale* function in R).

Data and code availability

All data used in this study is available open-access in Zenodo (https://zenodo.org/records/17211353).

Analysis was performed using the Neural Encoding Model System library

(https://github.com/LBHB/NEMS/). Scripts to generate the study figures will be included in the data

repository.

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