Inference of drug off-target effects on cellular signaling using Interactome-Based Deep Learning

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Abstract

Many diseases emerge from dysregulated cellular signaling, and drugs are often designed to target specific nodes in cellular networks e.g. signaling proteins, or transcription factors. However, off-target effects are common and may ultimately result in failed clinical trials. Computational modeling of the cell's transcriptional response to drugs could improve our understanding of their mechanisms of action. Here we develop such an approach based on ensembles of artificial neural networks, that simultaneously infer drug-target interactions and their downstream effects on intracellular signaling. Applied to gene expression data from different cell lines, it outperforms basic machine learning approaches in predicting transcription factors' activity, while recovering most known drug-target interactions and inferring many new, which we validate in an independent dataset. As a case study, we explore the inferred interactions of the drug Lestaurtinib and its effects on downstream signaling. Beyond its intended target FLT3 the model predicts an inhibition of CDK2 that enhances downregulation of the cell cycle-critical transcription factor FOXM1, corroborating literature findings. Our approach can therefore enhance our understanding of drug signaling for therapeutic design.

Introduction

In many diseases, such as cancer, alterations in gene expression or protein function lead to dysregulated intracellular signaling, with pathological effects[1–4]. This may be counteracted by perturbing cellular signaling using drugs, in particular small molecules have been used for decades to revert cells to a healthy state or kill cancerous cells[1], e.g. inhibition of Ras-mediated signaling in anticancer therapy[5]. This approach aims to affect signaling through specific drug-target interactions, but the drugs do not necessarily function through their proposed mechanism of action (MoA)[6] and off-target effects are common[7]. Understanding the contributions of on- and off-target effects of drugs is important for the development of safe therapeutics and their success in the clinic.

Systems pharmacology approaches have been developed to decipher the MoA of drugs. Several of these utilize data from chemical perturbation experiments[8–10]. For example, these approaches may utilize the transcriptomic profiles of perturbed cells to identify key genes associated with specific therapeutic or adverse effects[11] or elucidate their signaling mechanism based on their gene expression profile and large datasets of known drug-target interactions[12,13]. With the advent of Machine Learning (ML) and large-scale high throughput screening (HTS) datasets, such as the L1000 dataset[14], consisting of thousands of drug perturbations tested on cancer cell lines, these approaches have become more efficient, e.g. leading to the identification of novel potential therapeutic targets[15] and to direct characterization of the transcriptomic profile of perturbations[16]. However, these approaches do not explicitly model the signal propagation that underlies these effects and their predictions can therefore not be directly interpreted in terms of molecular mechanisms.

Signaling networks provide a scaffold to comprehensively describe a drug's MoA. Molecular networks have been used to agglomerate signature MoA predictions[17], as the basis for large-scale computer models to facilitate genome-scale simulations of perturbations[18,19]. This has become feasible due to the extensive

46 characterization of the intracellular signaling network[20,21] and improvements in parameter fitting
47 methods. For example, in early work, Saez-Rodriguez and Alexopoulos et al.[22], used Boolean modeling on
48 a small small-scale signaling network to predict inflammatory signaling in HEPG2 cell lines while inferring
49 interactions that were missing from the initial network. In more recent work, Fröhlich et al.[23] developed
50 a large-scale mechanistic model using ordinary differential equations (ODEs) to predict the response to
51 drug perturbations in 120 different cell lines. Alongside the signal network, this model relied on a sparse
52 network of drug-signaling protein interactions that was manually curated from the literature. However,
53 despite major advances, the parameter fitting of ODE-based models could require problematically long
54 computational times when applied to genome-scale networks.

55 Artificial neural networks (ANNs) allow for rapid parametrization of large-scale models. While the
56 interpretability of such models could be a concern, this can be circumvented by constraining them to only
57 allow mechanistically plausible predictions. For example by only allowing connections in the ANN that
58 correspond to interactions of the intracellular signaling network, which has been used to predict receptor
59 stimulation from gene expression data[24]. We recently expanded on this concept and developed a
60 framework to simulate signal propagation using a recurrent neural network (RNN), thereby allowing
61 feedback loops to be incorporated in the formalism[25]. Using this framework, termed, Large-scale
62 knowledge EMBedded Artificial Signaling network (LEMBAS), we successfully trained a model to predict
63 the transcription factor activity of macrophages in response to different ligand stimulations. For this, we
64 took advantage of both a prior knowledge network of signal transduction, and a transcriptional regulatory
65 network[26]. The latter was used to infer transcription factor activity from gene expression using the VIPER
66 algorithm[27], which tests for regulon enrichment on gene expression signatures. We also adapted the
67 LEMBAS framework to replicate the prediction of drug responses from the Fröhlich study with
68 indistinguishable accuracy and much faster parametrization time. However, both of these approaches
69 depend on prior knowledge of drug-target interactions and were not designed to infer new drug targets.

70 Because it is improbable that all drug-target interactions have already been discovered, in particular for
71 newly developed drugs, inference of new interactions could be of importance to completely explain the
72 effects of drugs. Many different ML approaches have been developed to infer new potential interactions
73 using bioactivity data, dose responses, and large databases of prior knowledge containing known drug-
74 target interactions[15,28–30]. However, current ML approaches focus on inferring single drug-target
75 interactions or binding affinities, either based on chemical structures[31,32] or gene expression profiles[15],
76 without fully utilizing the signaling network. They thus lack direct interpretability and the ability to
77 comprehensively describe the signaling cascades arising from off-target MoA.

78 Here we have developed an approach to predict network-wide signaling responses to drugs that considers
79 both on- and off-target effects. We expand the ANN-based signaling framework[25] to combine a prior
80 knowledge network of signaling[20], a network of known drug-target interactions, and the drugs' chemical
81 structure similarity with other drugs, to simultaneously infer drug-target interactions and simulate the
82 regulatory effect of known and inferred interactions in drug perturbation experiments. We use publicly
83 available data on the transcriptomic response to drug perturbations, that we process further to infer
84 transcription factor activities. We use the data to train cell-line-specific signaling models that we use to
85 identify potential off-target effects of drugs alongside MoAs that can explain them. We validate the
86 inferred interactions using an independent dataset and explore some of the predicted MoAs using in silico
87 simulations and public gene knock-out data.

88 Results

89 A model for predicting network-wide signaling of drugs via modeling of on- and off-target effects

90 We developed an approach (denoted as DT-LEMBAS) for predicting the regulatory effect of drug
91 perturbations, while simultaneously inferring unknown drug-target interactions (Figure 1A). The model
92 consists of two interconnected sub-modules: the first module takes drugs' concentration as input and

93 gives their signaling effect on drug targets as output, while the second module is LEMBAS, a published
94 model of intracellular signaling that takes a drug's signaling effects as input and returns the transcription
95 factor (TF) activity as output[25]. LEMBAS is a recurrent ANN model of intracellular signaling, where the
96 connections are based on prior knowledge of the intracellular signaling network, thereby constraining the
97 model to mechanistically plausible predictions.

98 In the case of drug perturbations, such as treatment with small molecules, the prior knowledge of the
99 drugs' molecular interactions may be incomplete, thus creating the need to infer potential off-target
100 signals. To achieve this we utilize both known drug-target interaction information, taken from the Broad's
101 Institute Repurposing Hub[33], and pre-calculated chemical similarity between drugs, using their ECFP4
102 molecular fingerprints[34]. We encode the drug-target interactions as a trainable spare weight matrix and
103 the chemical similarity as a drug-drug similarity matrix, forming a pre-defined drug/target space (Figure
104 1A). The concentration of a drug of interest is taken as input and, based on the similarity with other drugs
105 and its known targets, the module is allowed to infer potential drug-target interactions that are
106 propagated as input signal to the LEMBAS module. We train the combined model to fit TF activity data
107 while minimizing a few regularization terms, aimed at controlling the number of new inferred drug-target
108 interactions from the drug module, alongside regularizations and other priors previously developed for
109 LEMBAS[25] (see methods).

110 Performance in predicting activities of individual transcription factors

111 To train our model, and evaluate its performance in predicting activities of individual transcription factors,
112 we used gene expression data from the L1000 dataset[14]. As the purpose of this study is to examine the
113 short-term signaling of drugs, to avoid self-regulatory effects we excluded long-period experiments and
114 used only perturbations where cell lines were treated with a drug for less than 12 hours.

115 As ANNs are known to overfit the data, before performing any subsequent downstream analysis of the
116 predicted MoA of drug perturbations it is useful to determine which TFs the model is able to predict
117 correctly. Similarly, it is necessary to ensure that the predictions of the drug module generalize sufficiently
118 well for the inferred drug-target interactions to be trusted. Cross-validation is a common validation
119 strategy, where some of the data is withheld from the training set, however, in this dataset, drugs only
120 appear once per cell line, meaning that there would be no training data available for the drug using this
121 approach. An additional challenge for ML methods using chemical representations is misleading high
122 performance due to memorization of similar structures[35].

123 To circumvent these issues, we devised a validation strategy (Supplementary Figure 1) that makes use of
124 data from different cell lines to construct the drug module, while applying a cross-validation schema to
125 the signaling module. Specifically, we select cell lines with data from at least 200 drugs in common,
126 resulting in 9 cell lines. We then use the cell line with the most samples available (VCAP) to train a model.
127 For the remaining 8 cell lines we keep the drug module unchanged and train only the signaling part of the
128 model using 80% of the drugs available while validating using the remaining 20%, i.e. fivefold cross-
129 validation. We confirm that validation drugs are highly dissimilar in their chemical structure from training
130 drugs, thereby avoiding information leakage from similar drugs (Supplementary Figure 3). We find that
131 the model predicts the activities of many TFs with high accuracy, and a similar behavior is observed across
132 all cell lines (Figure 1B). Notably, there is a big variation in the performance between individual TFs, and
133 since we are aiming to utilize some of them for downstream analysis it would be useful to find a principled
134 way to identify high-performing TFs. We hypothesize that some TFs will be poorly fitted by the model
135 during training due to various reasons, e.g. because their data may be noisy, that they may not be
136 contributing to the transcriptomic profile of the cell, or that their activity cannot be explained by the prior
137 knowledge signaling network. Indeed, TFs that are well-fitted during training (rank≤25% in training based
138 on Pearson correlation) are overrepresented among the high-performing TFs in validation, while most TFs

139 that are poorly fitted (rank≥75% in training) also perform poorly in validation (Figure 1C, Supplementary
140 Figure 6). Similar results can be observed if the drug module is initially trained in other cell lines such as
141 A375 and A549 (Supplementary Figure 5).

142 To determine if these validation results are in line with what could be expected given the data, we
143 benchmark them against four basic machine learning techniques. Specifically, we compare the models'
144 ability to predict TF activities with: 1) an ensemble of 50 simple feed-forward artificial neural networks
145 (ANN) that take as input the ECFP4 molecular fingerprints of drugs 2) an ensemble of 50 Graph
146 Convolutional Neural Networks (GCNN)[36] representing drugs' chemical structures as graphs, 3) an
147 ensemble of 50 Support Vector Machines (SVMs), and 4) an ensemble of 50 KNN models. Additionally, as
148 two types of null models, we train two models where we 1) shuffle the input matrix of drug concentrations
149 (X) during the training of the drug module, thereby generating a randomized drug module, or 2) we shuffle
150 the outputs (Y) during re-training of the signaling part for each cell line, generating a randomly weighted
151 signaling network. Our model outperforms these approaches, as well as the null models, based on a non-
152 parametric two-sample Wilcoxon test (Figure 1C). The validation performance for the top 10% fitted TFs
153 during training is generally high (Figure 1D), achieving an average Pearson correlation of ~0.5
154 (Supplementary Figure 2B), with the performance of some TFs higher than ~0.8 and p-values ≤ 10^{-6} (see
155 Supplementary Figure 4 for the adjusted p-values for all of the correlations). This suggests that we can
156 rely on the predictions for some of the TFs in our subsequent analysis.

157 ## Constraining the number of inferred interactions via weight regularization

158 We make use of the assumption that drugs will not interact with most targets to make more specific
159 predictions. To control the number of inferred interactions, we utilized an L2-based regularization scheme
160 for the weights of the drug module such that infinite regularization constrains the module to only make
161 use of known drug-target interactions and zero regularization allows every possible interaction without

162 penalty (see methods). Since we cannot know in advance which targets a drug does not affect (true
163 negatives) we instead aim to find a good trade-off between sensitivity and specificity in inferring
164 interactions, as well as prediction performance. We utilized an integrated gradient score approach[37] (see
165 methods) to quantify the confidence in a drug affecting a target node in the signaling network and we
166 inferred interactions by identifying a cut-off for the absolute value of that score (see methods). With
167 increasing regularization, the trade-off between sensitivity and specificity saturates (Figure 1E) when
168 inspecting their geometric mean (optimal G-mean) at the cut-off that maximizes it. To quantify the
169 amount of interactions at different regularization levels we define a metric, New Discovery Rate (NDR), as
170 the number of new interactions inferred divided by the number of total interactions inferred by the
171 model. We find that for increasing regularization levels, this metric decreases and slowly goes to zero, as
172 intended (Figure 1E). Meanwhile, for increasing regularization levels the True Positive Rate (TPR)
173 increases and saturates, indicating that with increasing regularization the model depends more on prior
174 knowledge, and as intended it does not exclude a lot of prior knowledge interactions to reduce the total
175 inferred interactions (Figure 1E). Similarly, for every regularization level at different gradient score
176 thresholds the G-mean and TPR increase and start saturating after λ= 1E-04 while the NDR decreases until
177 it becomes almost zero (Supplementary Figure 7A). This result appears to be robust to using a different
178 error-based method to infer interactions (see methods, and Supplementary Figure 7B). Finally, for the
179 average performance of individual models (not the ensemble) trained using different regularization levels,
180 we observe that zero regularization outperforms infinite regularization (Figure 1F). This indicates that the
181 addition of inferred interactions contributes to the model's predictive power. However, there is not a clear
182 trend for intermediate levels of regularization, nevertheless, it seems that for the regularization level λ=
183 5E-03, the performance is slightly higher than its neighboring levels (Figure 1F). This could perhaps be due
184 to the locally higher NDR at that regularization level (Figure 1E and Supplementary Figures 7). Because of

185 this, alongside the higher performance, we selected this regularization level for the models trained in this
186 study (including the models in Figure 1C).

187 Inferring drug-target interactions with integrated gradient scores

188 The model is constructed to allow inference interactions that are not part of the prior knowledge to better
189 explain transcriptional data. To extract which drug-target interactions have been inferred, we use
190 integrated gradients to assign an importance score to each interaction (see methods). In the case of a
191 linear drug module, used in this study, the score is proportional to the module's weights (Supplementary
192 Figure 8). A negative score corresponds to a potential inhibition of a target node from a drug of interest,
193 while a positive score corresponds to activation.

194 To identify a cut-off level for the score we investigate how the model's performance decreases as more
195 interactions are removed (see methods). Briefly, for each drug, we successively remove more interactions,
196 based on the absolute value of the score, and determine how this affects the error of the model in
197 predicting the activity of all TFs (Figure 2A). As can be expected, removing interactions with low scores
198 does not affect the error of the model, while at some critical level, the error sharply increases and
199 plateaus. This means that the model's low-scoring interactions are not needed to explain the TF activity,
200 while for high-scoring interactions, the error of the trained model increases dramatically. For each drug
201 in each trained model, we define the cut-off at a 25% percentage increase in error. This approach was
202 chosen because of its high NDR (Supplementary Figure 7) and because it allows us to infer many new
203 interactions which at the same time are necessary for the model to correctly predict the TF activity.
204 Subsequently, we utilize the ensemble of models to also score the confidence in inferring an interaction
205 by using the frequency of appearance in multiple models.

206 The first step to evaluating the validity of this approach to infer drug-target interactions is whether it can
207 retrieve most of the prior knowledge interactions (on-target effects), as these are expected to be able to

208 explain at a large level the observed transcriptional profile. Indeed, when training a model for the A375
209 cell line, we can retrieve most of the interactions in the prior knowledge used in training the model while
210 also inferring approximately 13000 more interactions (Figure 2B-2C), which can potentially be
211 undiscovered direct drug-target interactions, indirect effects or false interactions (false positives). It
212 seems that prior knowledge interactions are inferred by most of the models in the ensembles, while
213 undiscovered interactions appear mostly with low frequency, with some of them appearing in many
214 models (Figure 2C). We observe similar results when training models and inferring drug-target interactions
215 using the A549 and VCAP cell lines (Supplementary Figure 9). Based on this, we hypothesized that it could
216 be possible to predict if an inferred interaction is a true direct interaction, based on the number of times
217 it was inferred by different models.

218 Evaluating the inference of direct interactions by an ensemble of models

219 We make use of an independent drug-target interaction database to evaluate the predictive power of the
220 model. While we know the existing true drug-target interactions (true positives), the true negatives are
221 unknown, and it is not clear to which extent predicted interactions can be trusted. To partially overcome
222 this limitation, we make use of a more comprehensive database, DrugBank[13], for the drugs present in our
223 trained framework, to establish a set of true interactions that were not present in the prior knowledge
224 used to construct the model. We then attempt to predict these interactions depending on how frequently
225 they are inferred in our models. From a frequency of 0.75 (interaction inferred for 37 out of 50 models),
226 there is a statistically significant difference between the model's accuracy in predicting drug-target
227 interactions and the null accuracy obtained by assigning everything to the predominant class (No
228 Information Rate: NIR) (Figure 2D). In addition to accuracy, we also consider the following evaluation
229 metrics: precision, recall, and the F1 score, which is the trade-off of precision and recall for imbalanced
230 data (Figure 2E).

231 We find that including interactions that appear in any model is much too lenient, resulting in poor
232 precision (1.97%) and accuracy (14.35%), and the predictions of individual models do not perform better
233 than chance with an accuracy of ~75%. However, for increasingly frequent interactions both precision and
234 accuracy increase markedly, with perfect precision (100%) for the most frequent predictions (Figure 2E).
235 At high inference frequencies recall decreases drastically, meaning that the inference threshold may be
236 too strict, The F1 score (which is a trade-off between precision and recall) generally increases until it
237 reaches a maximum of 71.84 % for an interaction appearing with a frequency score of 0.88 (44 out of 50
238 models). This is the same number of models which corresponds to the higher accuracy (99.22%) and the
239 lowest p-value signifying statistical significance in the difference between accuracy (99.22%) and NIR. We
240 observe similar results for models trained on A549 and VCAP cell lines (Supplementary Figure 10). This
241 evaluation showed a higher accuracy than we could expect from naively guessing that an interaction does
242 not exist, which supports the hypothesis that interactions appearing in multiple models are more likely to
243 correspond to direct interactions which enables the potential for inferring novel drug-target interactions.
244 We provide all inferred drug-target interactions alongside frequency scores in Supplementary Data File 1,
245 e.g. Dacinostat, a known histone deacetylase inhibitor, is found in both A375, A549 and VCAP cell lines,
246 by more than 40 models, to interact with KDR which is a type III receptor tyrosine kinase.

247 We tested if the inferred off-target effects could help explain the lethality of drugs. Off-target effects are
248 primarily thought to cause side effects, but instead, they may contribute to the drug's efficacy in some
249 cases[8,38]. We tested if the inferred targets could help predict the lethality of drugs tested on different the
250 9 cell lines in our study that were also present in the NCI60 drug screen[39]. Inspired by Vijay & Gujral who
251 developed an ANN model to predict changes in cell migration of cancer cells using drugs' target profile[40],
252 we trained random forest (RF) models to predict lethality using the drug targets and cell line identity as
253 input and keeping data from experiments on the A549 cell line as an independent test set. However, the
254 performance of an RF model trained on the prior knowledge data and the one trained on inferred

255 interactions (with a 0.88 frequency score) performed equally well (Supplementary Figure 13). Both RF
256 models achieve a correlation of 0.94 in the test set (p-values $1.5x10^{-6}$ and $2x10^{-6}$ respectively). It seems
257 for the data used here the on-target effects can already fully explain the lethality observed, and that the
258 inferred interactions do not contribute further to the performance. This performance is also dependent
259 on the number of models used to infer interactions (Supplementary Figure 12).

260 Identification of transcription factors regulated by off-target effects

261 After establishing frequency thresholds for trusting predicted drug-target interactions, we make use of
262 the signaling module to investigate their predicted mechanism of action (MoA), in terms of inducing TF
263 activity. We first identify whether the model predicts that there are marked off-target effects in response
264 to a perturbation, by removing all of the input signal outputted by the drug module except the signal
265 corresponding to the known targets and use it as input to predict the induced TF activities (Figure 3A). We
266 consider the difference between the models' original predicted TF activities and the ones where off-
267 targets are masked out (ΔTF) as a proxy for the magnitude of the off-target effects on specific TFs.
268 Samples where a TF has been activated (here considering activity≥0.75) or inhibited (activity≤0.25), and
269 with a high off-target effect are of interest for investigation (Figure 3B). When this contributes to the
270 observed direction of TF regulation, it may be considered a perturbation with off-target effects. We
271 further restrict our analysis to TFs whose activity is predicted well by the model (of the A375 cell line), by
272 making sure that the average of the performance in validation and training of the model for that TF is
273 higher than 0.6. An example of this is the case of the drug Lestaurtinib, where the model predicts an
274 inhibitory off-target effect on FOXM1 (Figure 3B). FOXM1 is a TF critically associated with the cell cycle,
275 considered a master regulator overexpressed in most human cancers[41]. For this reason, we select FOXM1
276 and Lestaurtinib for further analysis, but more drugs that have an off-target effect on some TFs, in A375,

277 A549 and VCAP cell lines, are provided in Supplementary Data File 2, together with their activity, off-target
278 and performance score.

279 A subnetwork explaining off-target effects of Lestaurtinib

280 We infer all off-target interactions for the drug Lestaurtinib. As previously described (Figure 2A), we infer
281 drug-target interactions by progressively masking potential interactions based on their integrated
282 gradient score and calculating the error of the models for predicting the activity of TFs, until a sharp
283 increase in the error appears. We repeat this process just for Lestaurtinib inspecting the effects on each
284 TF independently. Strikingly the error of FOXM1 follows a trend similar to the average error across all TFs
285 (Figure 3C). Using this approach, we identify a cut-off for the gradient score and infer on average 82
286 potential interactions out of the 259 available in our training space per model (Figure 3C). Two targets of
287 Lestaurtinib exist in the prior knowledge used to train the model: NTRK1 and FLT3, and both of them are
288 retrieved for all of the models (50 of 50). Additionally, while not in the prior knowledge used for training,
289 DrugBank has another two targets for Lestaurtinib in our target space: EGFR and ADRB1, these are inferred
290 in 16 and 27 of the 50 models respectively. This means that the model retrieves the prior knowledge most
291 of the time, and additionally infers many other interactions not in the training set that act to explain off-
292 target effects.

293 We extract a sub-network explaining the MoA effects of Lestaurtinib. After inferring new targets and
294 identifying a TF with prominent off-target effects, we use the model to construct a smaller signaling
295 network explaining the mechanism of action for the off-target effects. For this we remove nodes and
296 edges in the trained signaling network models that are not important for regulating the activity of the TF
297 (Figure 3D). This is based on an importance score (see methods) where nodes are iteratively removed
298 until the removal of a node breaks the connection to the inferred targets. We use an ensemble approach

299 where the final subnetwork is constructed by margining networks derived from each trained model,
300 keeping only nodes and edges appearing in multiple models (see methods).

301 We apply this process for the case of the effects of Lestaurtinib on FOXM1, resulting in a subnetwork of
302 the intracellular signaling network that explains this off-target effect (Figure 3E). Although strongly
303 reduced, this network is still relatively large and difficult to interpret. This may be due to multiple plausible
304 mechanisms being explored simultaneously as a response to limited data together with L2 regularization
305 limitations. Alternatively, this may indicate that it is necessary to include many interactions to fully explain
306 the off-target effect that Lestaurtinib has on FOXM1 activity, and further reduction of the network would
307 be an oversimplification. Applying the simplest path algorithm to the network from each inferred target
308 (in red) towards FOXM1 (in orange) we find that inhibition of CDK1 and CDK2 could lead to the direct
309 inhibition of FOXM1 (Figure 3F). According to the model (Figure 3E), Lestaurtinib can potentially inhibit
310 FOXM1 by inhibiting CDK1 or/and CDK2 and interacting in some uncertain manner with CDK6), meaning
311 that the smaller subnetwork contains feasible intracellular interactions that can indeed explain the off-
312 target effect. Indeed it has been observed that that FOXM1 can be activated by both CDK1[42] and CDK2[42,43],
313 meaning their inhibition could lead to inhibition of FOXM1, as proposed by the model. Additionally, while
314 the interaction between Lestaurtinib and CDK2 is neither present in the prior knowledge used for training
315 nor DrugBank, it has been seen in a comprehensive kinase inhibition study that Lestaurtinib indeed inhibits
316 CDK2 with a K_d = 20 nM[44], which is markedly lower than the dose used in the L1000 study (10 um). We
317 note that CDK2 was identified as an interaction in 36 out of 50 models, bordering the previously identified
318 threshold (of 37) for identifying true direct interactions with high performance (Figure 2E-2D). CDK1 is
319 found in 35 out of 50 models while CDK6 was found in half of the models. Taken together, this indicates
320 that the model can be used to propose a MoA to explain the off-target effect that is biologically feasible
321 and potentially true, which is also cell line specific, which may serve as a basis for designing therapeutic
322 interventions or drug combinations to cancel or enhance this off-target effect.

323 ## A case study of FOXM1 regulation by CDK2

324 Since the activation of FOXM1 by CDK2 and CDK1 has been experimentally demonstrated, it may serve as
325 a useful case study for determining how well the different components in our approach recapitulate this
326 effect. First, we inspect the inference of TF activity from gene expression data, using the DoRothEA
327 regulon[26] together with the VIPER algorithm[27]. For this purpose, we retrieved Affymetrix microarray data,
328 from the Gene Expression Omnibus (GEO)[45], generated from A375 cells treated with siRNAs against
329 various transcription factors and signaling molecules[46]. We then inferred the activity of FOXM1 for the
330 measured gene expression data for CDK2 and FOXM1 knockdown as well as untreated cells and control
331 (inactive fluorescently labeled siRNAs) samples. We find that the inferred activity (z-scored) of FOXM1
332 when knocking down CDK2 is similar to a FOXM1 knockdown, while FOXM1 is way more inactive than in
333 untreated cells (centered to zero as expected) in both cases (Figure 4A). Even though this published study
334 has limited statistical power, it does indicate that our inferred activities in the L1000 recapitulate the
335 relationship between CDK2 and FOXM1, thus corroborating the proposed off-target effect.

336 Secondly, we investigate whether the inhibition of the activity of FOXM1 by Lestaurtinib is indeed
337 primarily achieved through inhibition of CDK2 and/or CDK1. For this purpose, we utilized data from ligand
338 perturbations contained in the L1000 dataset but not used for training the model. From this, we inferred
339 FOXM1 activity for ligand stimulation of the known targets of Lestaurtinib: EGFR, FLT3, and additionally
340 for stimulation with other drugs that inhibit these targets as well as the two additional targets in DrugBank
341 (ADRB1, NTRK1), and known inhibitors of CDK1, CDK2, and CDK6 (such as Alvocidib, AT-7519, and
342 Kenpaullone). We made sure to select inhibitors with at most 10 targets to minimize the risk of regulation
343 of FOXM1 through other targets. As expected, we find that the activity of FOXM1 in A375 when using
344 Lestaurtinib is much more inhibited compared to DMSO or untreated A375 cells. We also find that it is on
345 a similar level as for known CDK1 and/or CDK2 inhibitors (four inhibit both CDK1 and CDK2 (Figure 4B)).

346 Meanwhile, only a few of the ADRB1 inhibitors (another Lestaurtinib target) show a similar trend, and the
347 rest of the known targets do not inhibit FOXM1 activity at a comparable level (or not at all). This further
348 supports the proposed MoA of Lestaurtinib inhibiting FOXM1 through the off-target effect on CDK2.

349 ## In-Silico knockdowns using the model

350 Finally, we investigate if *in*-silico knockdown experiments by the model, using the proposed MoA network,
351 recapitulate the similar effects on FOXM1 activity by Lestaurtinib, and CDK2 and CDK1 knockdowns. We
352 induce a level of knockdown for a signaling node by assigning a large negative value as input. This way we
353 knock down the known targets of Lestaurtinib (EGFR, NTRK1, ADRB1, FLT3) and CDK2 and CDK1, for all of
354 the 50 trained signaling networks. Additionally, we model the signal generated by Lestaurtinib, signals
355 masked to include either its on-target effects or off-target effects, as well as the signal from DMSO as
356 control. We find that the activity of FOXM1 under Lestaurtinib is indeed much lower than DMSO and that
357 seems to be mostly due to the off-target effects (Figure 4C). We note that the on-target signal induced
358 similar activity levels as knockdowns of any of the known targets of Lestaurtinib, indicating that the model
359 can successfully recapitulate the on-target effects of Lestaurtinib on FOXM1, which, while lower than for
360 DMSO, do not seem to strongly inhibit FOXM1 activity (Figure 4C). Furthermore, increasing the
361 knockdown level for these nodes does not seem to induce much stronger inhibition of FOXM1
362 (Supplementary Figure 11C-11D), while knocking down CDK1 and CDK2 induces strong inhibition of
363 FOXM1, and depending on the knockdown strength (Supplementary Figure 11C-11D) induces similar
364 inhibition as Lestaurtinib (Figure 4C) or almost completely deactivates FOXM1 (Supplementary Figure 11A-
365 11B). Notably, if we restrict the model to only the reduced subnetwork when conducting this *in-silico*
366 experiment, we observe a similar trend for the CDK1 and CDK2 knockdowns, suggesting that indeed the
367 subnetwork is sufficient to explain the MoA of this off-target effect (Figure 4D). Taken together this case

368 study serves as a proof of concept for the utilization of the models to generate *in-silico* experiments to
369 potentially identify therapeutic interventions to cancel the off-target effect.

370 Discussion

371 Drugs do not always function entirely through their proposed MoA[6], which may cause adverse effects
372 from off-targets but may also sometimes be beneficial[8,38]. Here we developed an approach for predicting
373 the transcriptional response under drug-induced signaling, taking potential off-target effects into account.
374 The model augments the LEMBAS framework[25], which simulates intracellular signaling, with a trainable
375 module for inferring drug-induced signaling, to simultaneously predict the activity of transcription factors
376 under drug stimulation, and infer drug-target interactions that are not known. The model outperforms
377 basic machine learning methods in predicting the transcription factor activity. It retains most of the prior
378 knowledge of drug-target interactions but also predicts many more putative interactions, with a good
379 balance between sensitivity and specificity. Perhaps even more importantly, we make use of integrated
380 gradients[37], to extract subnetworks of intracellular signaling that explain the predicted MoA of off-target
381 effects on TF. In a case study of the drug Lestaurtinib's off-target effects on FOXM1 activity, we
382 demonstrated that the constructed network is biologically sensible, as we find literature support for the
383 proposed MoA.

384 Understanding how the signaling effects of drugs propagate in the cell is essential for understanding how
385 adverse effects may arise in the clinic and for designing therapy regimes that may counteract them. This
386 is particularly important for drugs that do not function through their proposed MoA. The advent of
387 machine learning and big data in biology holds promise for a more data-driven life science. However,
388 machine learning models have been criticized for their lack of interpretability[47,48] and thus many times fail
389 to explain the underlying MoA in a biological phenomenon or were never designed to do so. Embedding
390 prior knowledge into the structure of machine learning models can improve their interpretability [25,49,50].

391 Specifically, in the case of our LEMBAS models, the whole architecture corresponds to feasible interactions
392 in the intracellular signaling network. Combining this inherent structure with the inference of previously
393 unknown drug-target interactions alongside a sensitivity approach to prune nodes and edges that do not
394 contribute to its explanatory power, we were able to construct subnetworks that fully recapitulate the
395 MoA of an off-target effect.

396 Despite the drastic size reduction, the subnetworks explaining the MoA of off-target effects are still far
397 too comprehensive for immediate interpretation, and additionally, there is variation arising from the
398 dissension between different models in the ensemble, in line with observations in the literature[51]. While
399 it is possible that the network indeed needs to be this large to fully recapitulate the off-target effect, this
400 may also be the result of data limitations along with the L2 regularization used to constrain the number
401 of inferred interactions and prevent overfitting the weights of the signaling network. Multiple drug-target
402 interactions and paths in the network might be able to explain the observed transcriptional profile. When
403 lacking sufficient data to train a model that can fully distinguish between all feasible solutions, this can
404 result in the model considering multiple explanations as equally important. The former would suggest that
405 redundancy and robustness are intrinsic to cellular circuits, which implies that a reductionistic approach
406 in biology may lead to misleading or incomplete results. The latter would indicate that while the biological
407 process may be simple, we are currently too data-limited to confidently simplify the network further. This
408 problem could potentially be tackled in the future either by increasing the data used for training a model,
409 by using large transcriptomic databases such as ARCHS4[52], or by using algorithms in the drug module that
410 can indirectly infer interactions without the usage of L2 regularization.

411 In this study, the drug module, which infers drug-target interactions, is linear and relies on a pre-defined
412 space of drugs and potential targets. It only uses knowledge about the chemical similarity of drugs,
413 thereby ignoring potential structural similarities. However, the modular nature of our model allows for
414 the future development of a drug module that can incorporate knowledge about targets' structural

415 similarity and is also non-linear. A previously proposed method, called DeepCE[16], utilizes a graph neural
416 network[36] to encode the chemical structure of a drug, and an attention-based ANN[53] to combine gene-
417 level representations, which contain gene-gene interaction information, and drug representations in a
418 drug-gene interaction network to ultimately predict the gene expression profile of a sample. Similarly,
419 another approach called ChemCPA[54] also encodes the chemical structure of the drug and non-linearly
420 scales its dose and combines it with the drug representation. On this front, our drug module could also
421 incorporate a non-linear encoder to represent the chemical structure of drugs and combine it with targets'
422 representations, by building upon ideas presented in OmegaFold[55] and AlphaFold2[56], in order to infer
423 potential drug-target interactions, similar to what has been recently proposed in the ConPLex model[57],
424 after training models to ultimately predict the transcriptional profile of a cell.

425 A limitation of the present models is that they are cell line-specific and thereby do not allow an already
426 trained model to be directly used to make predictions for other cell lines. Moreover, when inferring drug-
427 target interactions solely based on one cell line-specific model, we might miss potential general drug-
428 target interactions, as a target molecule may not be expressed in this particular cellular model, thus
429 resulting in more false negatives. Finding a basal representation for each cell line, like the sequencing
430 profile of cell lines from the CCLE database[58], and using that as input to the model, could be used to train
431 a unified model that also incorporates cell lines as input in a non-predefined cell line space. Generally,
432 contextualizing a unified model or transferring predictions and MoA representation from one cellular
433 model to another would be important for the utility of the model.

434 Our framework introduces a way to conduct *in-silico* experiments of drug perturbations while
435 simultaneously being able to explain the MoA of a drug. As such, future use may be for designing drug
436 combination therapies while exploring and studying their synergistic or competitive effects, identifying
437 ways to counter drugs' off-target effects, and designing better therapeutic regimes with higher clinical
438 efficacy.

439 # Materials and Methods

440 ## Retrieving prior knowledge networks of drug-target interactions

441 Drug-target interactions for training our models were retrieved from Broad's Institute Repurposing Hub[33].
442 The network was subset to drugs with corresponding perturbations in the L1000 dataset[14]. Drugs were
443 mapped with their respective targets by multiple identifiers for the drugs, namely: 1) the drugs' SMILEs,
444 2) the International Chemical Identifier (InChIKey), 3) the PubChem Compound Identifier (pubchem_cid),
445 4) the Broad's Institute internal identifier (pert_id), and 5) the drugs' common names. The targets for
446 DMSO were manually curated from DrugBank[13]. For the evaluation of the model's ability to retrieve drug-
447 target interactions, we retrieved additional interactions from DrugBank[13], using drugs' common names.

448 ## Pre-processing of *in-vitro* transcriptomics in the L1000 dataset

449 Transcriptomic signatures of drug perturbations were retrieved from the L1000 dataset[14] (accessed via
450 GEO with accession number: GSE92742). For inferring TF activity, we utilized gene expression data of 978
451 landmark genes, measured with the L1000 assay, and additionally, 9,196 imputed genes that were labeled
452 as well-inferred by the L1000 study[14]. The data were retrieved at Level 3, one of the processing steps in
453 the pipeline of the L1000 dataset, containing normalized gene expression data. We considered only
454 *exemplar* signatures, which, according to the L1000 definition, are the signatures with highest the
455 transcriptional activity score (TAS) in the case of multi-signature perturbagens, i.e. technical duplicates.
456 Briefly, the TAS metric inherent to the L1000 dataset quantifies signal strength and reproducibility, and
457 definitions and further information is available in the CLUE platform[59] glossary. Additionally, we keep only
458 drugs with at least one known target in the prior knowledge signaling network (see methods section for
459 constructing the prior knowledge signaling network). After inferring TF activity and further filtering data
460 to keep only high-quality TF activity data, we keep perturbations with at least 400 unique drugs per cell
461 line (the number of conditions previously found to achieve high performance when training a LEMBAS

462 signaling model[25]). This filtering results in 9 cancer cell lines and for evaluation purposes (see evaluation
463 method section), resulting in a drug space of 233 unique drugs. The log-scaled dose is used as input to
464 train models ($dose_{scaled} = \log_{10}(dose + 1)$). For the *in-silico* validation case study of Lestaurtinib, we
465 utilized the level 5 z-score transformed data were replicates are already aggregated, and specifically for
466 shRNA, ligand, and control (DMSO-treated and untreated cells) data we kept aggregated signatures
467 derived from at least 3 technical replicates.

468 ## Pre-processing of *in-vitro* Affymetrix microarray data

469 For the publicly available siRNA experiments[46], we retrieved Affymetrix microarray data from the Gene
470 Expression Omnibus (GEO)[45], under the GSE31534 ascension number. The raw microarray gene expression
471 data were normalized using the Robust Multichip Averaging (RMA) algorithm[60] included in the *affy* R
472 package[61]. The normalized expression values were used to infer TF activity (see below).

473 ## Inference and pre-processing of transcription factor activity data

474 The activity of transcription factors (TFs) was inferred from transcriptomics data using the VIPER
475 algorithm[27] coupled with the Dorothea regulon[26]. The VIPER algorithm calculates the enrichment of
476 known regulons (TFs), which act as proxies of TF activity. The activity of a TF is calculated based on the
477 expression of downstream genes known to be regulated by this specific TF, utilizing a known transcription
478 regulatory network. The Dorothea regulon contains known regulatory interactions and thus can be used
479 to build a regulatory network. Here we kept only high-confidence interactions (confidence levels A and
480 B).

481 After inferring the TF activity of the pre-processed transcriptomic data in the L1000 dataset, we filtered
482 TFs with high variance across technical replicates, to ensure we kept only high-quality estimations of TF
483 activity, and then we filtered technical replicates that were not correlated enough with the other replicate

484 signatures. To filter TFs, we first build a null distribution of TF activity variance by permuting 100 times
485 the rows (samples) of the activity matrix, labeling this way random profiles as technical replicates, and
486 then calculating the variance of the activity of each TF across each group of replicates. This way a null
487 distribution of TF activity variances is built for each TF. The actual distribution of TF activity variances
488 across replicates is compared with the null distribution, using a one-tailed Kolmogorov–Smirnov statistical
489 test, to test whether the actual variance across replicates is less than the random variance. If the p-value
490 is greater than 0.05 the tested TF is removed and will not be utilized in downstream analysis. To filter
491 replicates, we build a null distribution of random correlations between TF activity profiles, by randomly
492 sampling 1000 times an equal number of signatures as the number of replicates, calculating the Pearson's
493 correlation between each pair and taking the mean correlation as a proxy of how similar the replicates
494 are within a sample. We repeat this for every possible number of replicates within a sample. Then we
495 calculate the correlation between each actual technical replicate with all others in a sample and count
496 how many random correlations are equal to or higher than the mean correlation of the technical
497 replicates, to calculate the probability of observing a given correlation due to change. If the p-value is
498 more than 0.05 we remove the sample and all of its replicates. Finally, we merge replicate signatures by
499 using the median of their TF activity profiles. In case there is only one replicate, we keep the sample as it
500 is.

501 Reconstructing a prior knowledge of signaling network

502 We reconstructed a prior knowledge intracellular signaling network (PKN), to constrain our ANN signaling
503 model, from protein-protein interactions retrieved from the OmniPath database[20]. Only human
504 interactions from the OmniPath core set were included and further restricted to interactions originating
505 either from the KEGG[62], InnateDB[63], or SIGNOR[21] resources. First of all, we remove TFs and drug targets
506 not included in the core prior knowledge network. Then we trim the PKN by removing nodes and edges

507 from the network if for some nodes there was no path from any drug to any TF. Additionally, nodes were
508 removed if they had only a single source and target that both were the same node. Finally, we removed
509 TFs and drug-target interactions if a target or TF is not in the final trimmed PKN. Drugs that remained with
510 no target in the constructed prior knowledge are removed from our data used to train and validate the
511 model.

512 Model architecture

513 The model consists of two interconnected modules. First, a drug module that takes as input the
514 concertation of a drug, in a pre-defined drug-target space, infers drug signaling. This utilizes the known
515 drug-target interactions (W_{DT}) and the pre-calculated chemical similarity (denoted as W_{sim} with [d x d]
516 dimensions, where d is the number of drugs available), using the tanimoto similarity of drugs ECFP4
517 fingerprints[34], between drugs in the drug space. Ultimately the drug signaling (S with [n x t] dimensions,
518 where n is the number of conditions and t is the number of available targets) which is the output of the
519 drug module is given by: $S = bn\left(X * \left(W_{sim} \odot W_{drug}\right)\right) * W_{DT}$. Specifically, the input concentration
520 matrix (X) of available drugs is first multiplied by the element-wise product between the pre-calculated
521 chemical similarity and a trainable weight matrix (W_{drug}), acting as a trainable scaler of chemical
522 similarity, and thus controlling to which extent chemical similarity should contribute to the models'
523 predictions. The result of this operation is passed through a batch normalization layer[64] with a momentum
524 of 0.6, and, during training only, a dropout layer[65], with a drop-out rate of 0.1. Finally, it is multiplied with
525 a sparse trainable weight matrix (W_{DT}) containing known drug-target interactions (dimensions [d x t]).
526 The drug signaling (S) generated by the drug module, which represents the signal created by the drugs in
527 a pre-defined drug-target space, is used as the input to the second module.

528 The second module is the LEMBAS framework[25] which contains a recurrent ANN model of intracellular
529 signaling, where the connections are based on prior knowledge of the intracellular signaling network. In

530 LEMBAS the signaling state of each node is calculated using the signaling state of the interacting node in
531 the previous time step, by multiplying it with a trainable connectivity matrix and adding a trainable bias,
532 all passed through a non-linear Michaelis–Menten-like (MML) activation function, as proposed in the
533 LEMBAS manuscript[25]. Drug signaling (S) is first projected on the signaling nodes' space and it is used as
534 input in the LEMBAS network. The state vector, describing the signaling state of each node, is initialized
535 as all 1e-3, except for TF nodes which are initialized as 0.5, and iterated for a maximum of 120 steps, after
536 which it is assumed that a steady state has been reached. Finally, the TF activity is predicted by projecting
537 from the signaling state of the network at the steady state.

538 ## Training of the model

539 A cell line-specific model is trained for 5000 epochs to ultimately predict the activity of 101 TFs, given the
540 concentration of a drug, in a pre-defined drug-target space of 233 drugs and 259 potential targets. The
541 term describing the main task of the model during training ($fitLoss$) is given by the Mean Squared Error
542 (MSE) across TFs, averaged across a batch (batch size=25) of data points used to update the weights of
543 the model during a learning cycle. There are auxiliary terms in the training loss of the model, to constrain
544 different parts of it, and we incorporated them from the GitHub repository
545 (https://github.com/Lauffenburger-Lab/LEMBAS) of the LEMBAS framework[25]. More details are included
546 in Supplementary Note 1, but we briefly list the regularization terms in this method section. The
547 $signConstraint$ constrains the sign of the weights in the intracellular network to be the same as the sign
548 of known protein-protein interactions. The weights and biases of the intracellular signaling network are
549 L2-regularized with the $NetWeightLoss$ and $biasLoss$ terms respectively. The trainable weights used to
550 project from the signaling state to TF activity were also L2-regularized in the $projectionLoss$ term.
551 Moreover, specific statistical properties for the activities of the signaling nodes are enforced with the
552 $stateLoss$ term. Finally, following the implementation proposed in the LEMBAS framework[25], to ensure

553 that the model achieves convergence by reaching a steady state we aim to constrain the absolute value
554 of the largest eigenvalue of the transition matrix, i.e., the spectral radius (ρ), to be less than 1 in the
555 $spectralRadiusLoss$ term (more details in Supplementary Note 1).

556 For the drug module, we implement two additional terms. First, we treat the drug-target interaction
557 matrix as a small network and we regularize the weights similar to what we have done in the signaling
558 network: $DTLoss = 10^{-6} * \sum\left(w_{DT,i}^2 + \frac{1}{w_{DT,i}^2+0.5}\right)$. Secondly, we implement a regularization term
559 ($DTregularization$) using the trainable W_{drug} matrix (described in the previous section), to control how
560 many new interactions should be inferred and, thus how much should the model be allowed to deviate
561 from prior knowledge by considering chemical similarity (more details in the following corresponding
562 section). The final formula describing the total training loss, which is minimized by updating the model's
563 parameters using the Adam optimizer[66] with a learning rate ranging from 10^{-8} to $2*10^{-3}$ is:

564 $$loss = fitLoss + signConstraint + biasLoss + NetWeightLoss + DTLoss + DTregularization$$
565 $$+ 10^{-3} * spectralRadiusLoss + stateLoss + projectionLoss$$

566 ## Evaluation of the model

567 To evaluate the generalization of the drug module and the LEMBAS part of the framework to unseen
568 conditions, we implement a validation procedure where we train a whole model in the cell line with the
569 most conditions available (VCAP), we freeze the weights of the drug module, and re-train only the
570 signaling network part, in every one of the other 8 remaining cell lines, by using only 80% of the available
571 drugs, while we make sure that the 20% hidden are drugs dissimilar from the ones used in training
572 (regarding their chemical structure). If the drug module is not general enough the signaling network may
573 change a lot and fail to generalize in dissimilar cases.

Regularization of the inference of drug-target interactions

To constrain the number of inferred drug-target interactions we regularize the weights of the previously described W_{drug} matrix, containing trainable weights to scale the similarity between the available drugs in our data, such as that W_{drug} is closer to the identity matrix (I). Thus, the regularization term used in the loss function is formed as:

$$\boldsymbol{DTregularization = \lambda_{DT} * \sum_{i=1}^{\#\,drugs} \sum_{j=1}^{\#\,drugs} \left(W_{drug} - I\right)_{ij}^{2}}$$

Where λ_{DT} is a free user-defined parameter, quantifying the strength of regularization. In this study, we performed an analysis, to study the effect of regularizing the drug-target interactions inference, with testing values from zero to infinity, where infinity, means we train a model using only the sparse trainable weight matrix (W_{DT}) containing known drug-target interactions. Since, the operation between W_{drug} and W_{sim}, containing pre-calculated chemical similarity, is that of element-wise multiplication, if $W_{drug} = I$, then $W_{sim} \odot W_{drug} = I$, meaning that the output of the drug module degenerates to: $S = X * W_{DT}$, meaning using only prior knowledge of drug-target interactions, which theoretically would be achieved with infinite regularization ($\lambda_{DT} \rightarrow \infty$).

The drug-target interaction inference algorithm

To infer drug-target interactions using the drug module, how much a drug affects a potential target is quantified by using integrated gradients[37] from the Captum library[67]: $InterGrad_i(x) = (x_i - x_i') \int_{a=0}^{1} \frac{dF\left(x' + a(x - x')\right)}{dx_i} da\,, x' = baseline = 0$. To identify a cut-off for identifying significantly large scores we utilize an error-based approach where we calculate the Mean Absolute Error (MAE) of the model across all TFs, after removing drug-target interactions, and thus drug input signal in LEMBAS, for increasingly higher absolute gradient score. We select as a cut-off the score that induces a 25% (or larger) increase in the model's MAE. Drug-target interactions with a smaller score than the cut-off are considered

596 insignificant, and thus are disregarded. Finally, we utilize the ensemble of models to derive a frequency
597 score for each interaction appearing in multiple models and further filter the inferred drug-target
598 interactions.

599 ## Node and edge importance in affecting a specific TF

600 To quantify the importance of a node or an edge in regulating the activity of a TF of interest we utilize a
601 customized integrated gradient approach. First, we generate for each model the input signal from the
602 drug module, and then we pass through the signaling module fractions of this signal's strength, ranging
603 from 0 to 1. We denote this input matrix X_{in}. The sum of the TF activity across all these artificial conditions
604 is used as an objective function (L_{obj}) for which the gradients for the weights (dw) and biases (db) of the
605 signaling module, are calculated using back-propagation. The node importance was calculated as:
606 $score_b = |db| * |range|$, where $range$ is the range of the node activity, for different signals' strength.
607 The edge importance was calculated as: $score_w = |dw| * |weight|$, where $weight$ is the weight of an
608 edge in the model. More details about the implementation and calculation of each term can be found in
609 Supplementary Note 2.

610 ## Identifying samples with high off-target effect

611 We remove the off-target signal and only the signal on the known targets is used to predict TF activities.
612 The difference between the original predictions of the model and the ones where off-targets are masked
613 out (Δactivity) quantifies the magnitude of the off-target effects on the TF of interest. The calculated
614 Δactivity is derived from the mean TF activity prediction from an ensemble of 50 trained models. Samples
615 where a TF has an activity≥0.75 or activity≤0.25, $|\Delta activity| \geq 0.2$, average Pearson's r (between training
616 and validation) of at least 0.5, and average validation Pearson's greater than 0.4, are considered
617 trustworthy predictions with a large off-target effect on a specific TF. For the second step, we infer drug-
618 target interactions for each model as previously discussed.

619 ## Algorithm for subsetting the network to the mechanism of action

620 To subset the signaling network for explaining the MoA of off-target effects edges are removed from the
621 whole signaling network based on their importance in regulating the activity of a TF of interest. Nodes
622 and edges are removed iteratively based on their importance (see previous section) until further removal
623 results in the removal of all target nodes or until there is no path from the drug's target to the TF of
624 interest. First, we remove nodes and get rid of disconnected parts of the network, nodes that the drug
625 cannot access through any path, and paths whose end is not the drug's target or the TF. Then we remove
626 edges and repeat the aforementioned network cleaning. The drug's targets with no path to the TF are
627 removed. Finally, we keep inferred targets that appear in at least 50% of the models, if possible, otherwise,
628 we use a cut-off that results in at least one inferred target in that subnetwork. We do the same for edges,
629 but if there is not a single edge that can be removed based on some frequency threshold, without
630 maintaining the connection between some target and the TF, we use a threshold of 50% and then we start
631 including gradually more edges to connect some target with the TF, and we keep the edges of the path
632 with the highest sum of frequency scores (regarding the frequency in appearing in multiple models). In
633 every part of this final trimming process, we also perform basic cleaning of the network by removing
634 undruggable nodes, nodes that cannot affect the TF via some path, and disconnected parts of the network.

635 ## In-silico knockouts

636 To induce *in-silico* knockouts of signaling nodes, and to validate different MoAs and off-target effects, we
637 assign a largely negative value in the input signal, that is used as input in the trained LEMBAS part of the
638 model, to the node we wish to induce a knockout. Then this signal is propagated in the network and the
639 model iterates for at least 120 steps, or until convergence.

640 ## Lethality predictions using drug-target interactions

641 Random Forest models (RF) are trained to predict the lethality of drug perturbations on cancer cell lines,
642 by using as input drug-target interactions and the cancer cell line on which the drug was tested, as a one-
643 hot encoded vector. Lethality data of drugs tested on different 9 cell lines in our study from the NCI60
644 drug screen[39] were accessed via the PharmacoDB database[68,69]. Separate RF models were trained and
645 tested using only the prior knowledge of drug-target interactions used in the drug module of our
646 framework and then using the inferred interaction. Data from the A549 cancer cell were used for
647 validation and the rest were used to train the RF models.

648 ## Statistics and reproducibility

649 For the evaluation of performance in retrieving drug-target interactions (in Figure 2), metrics and the p-
650 values were calculated, inside the *caret* R package[70], with a binomial one-tailed test comparing the
651 proportions of accuracy and NIR[71]. Statistical comparisons of models' performance in terms of Pearson's
652 correlation are conducted using a two-sided unpaired Wilcoxon test. Non-parametric Kolmogorov–
653 Smirnov tests are used to compare whole distributions (see the corresponding sections when they are
654 used for more details).

655 ## Hardware and software specifications

656 All models were expressed in and trained using the PyTorch framework[72] (versions 1.10.2 & 1.12) in
657 Python (version 3.6.13 & 3.8.8). Generally, simple simulations using one model were performed on a Dell
658 XPS 17 laptop with an Intel i9-11900h @4.9 GHz with 8 cores (16 logic processors) and 32 GB RAM. For
659 convenience, ensemble training of multiple models, random models training, and cross-validation was
660 carried out on a single-threaded computer cluster (Intel Xeon CPU @ 2.60 GHz) that allowed job
661 scheduling (using Slurm) with 16 parallel jobs. Pre-processing and statistical analysis of the results were

662 done in the R programming language (version 4.1.2). Visualization of results was done mainly using
663 ggplot2[73]. More information about the versions of each library used can be found in the GitHub provided
664 in the Data and Code Availability section.

665 Data and Code availability

666 The study did not produce new experimental data. All analyzed data that were used to train our models
667 and produce all tables and figures, as well as all the code to generate those data, figures, and tables are
668 available at the following GitHub repository: https://github.com/Lauffenburger-Lab/DrugsANNSignaling

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676 Conflict of interest

677 The authors declare that they have no conflict of interest.

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Figures

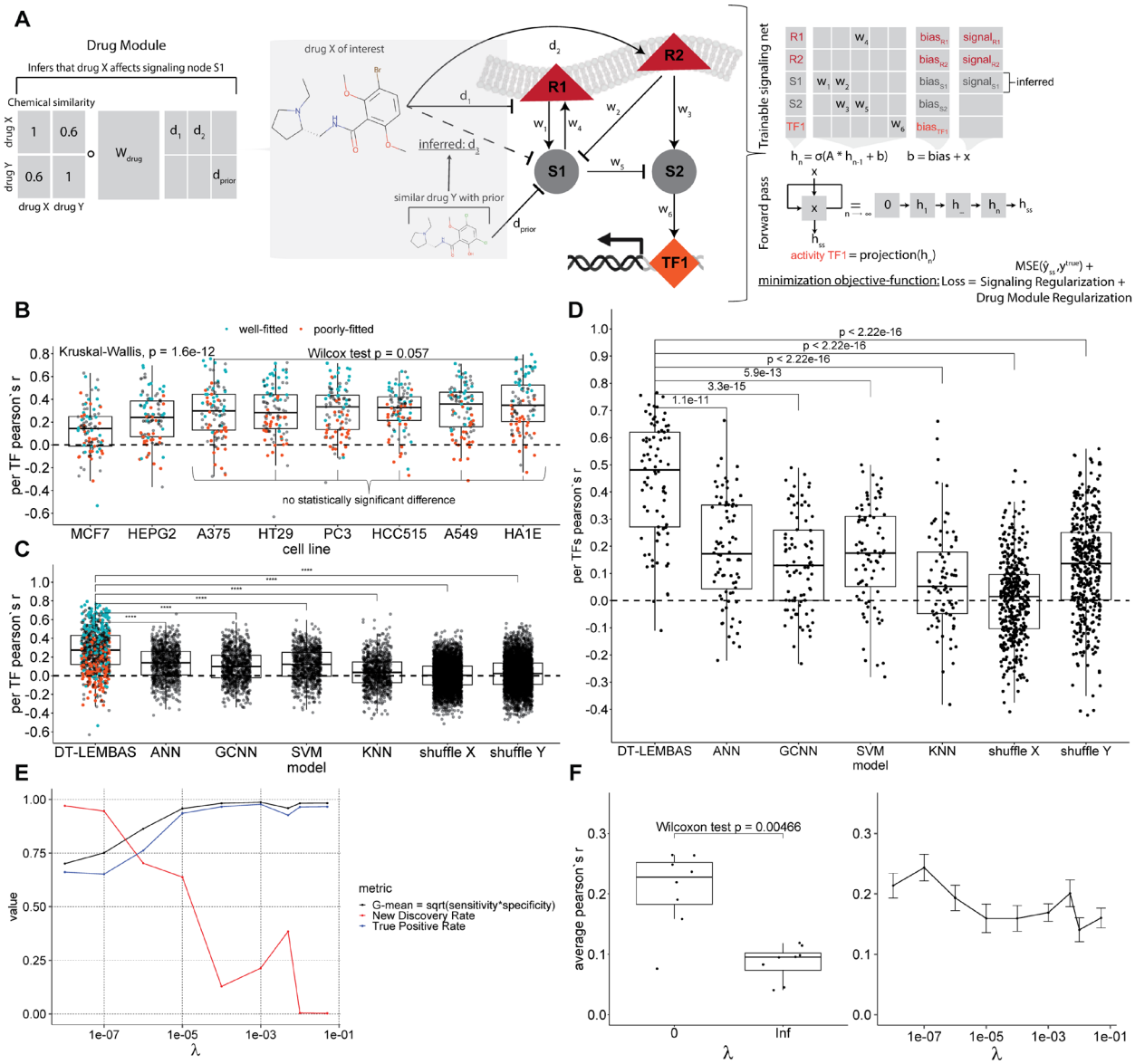
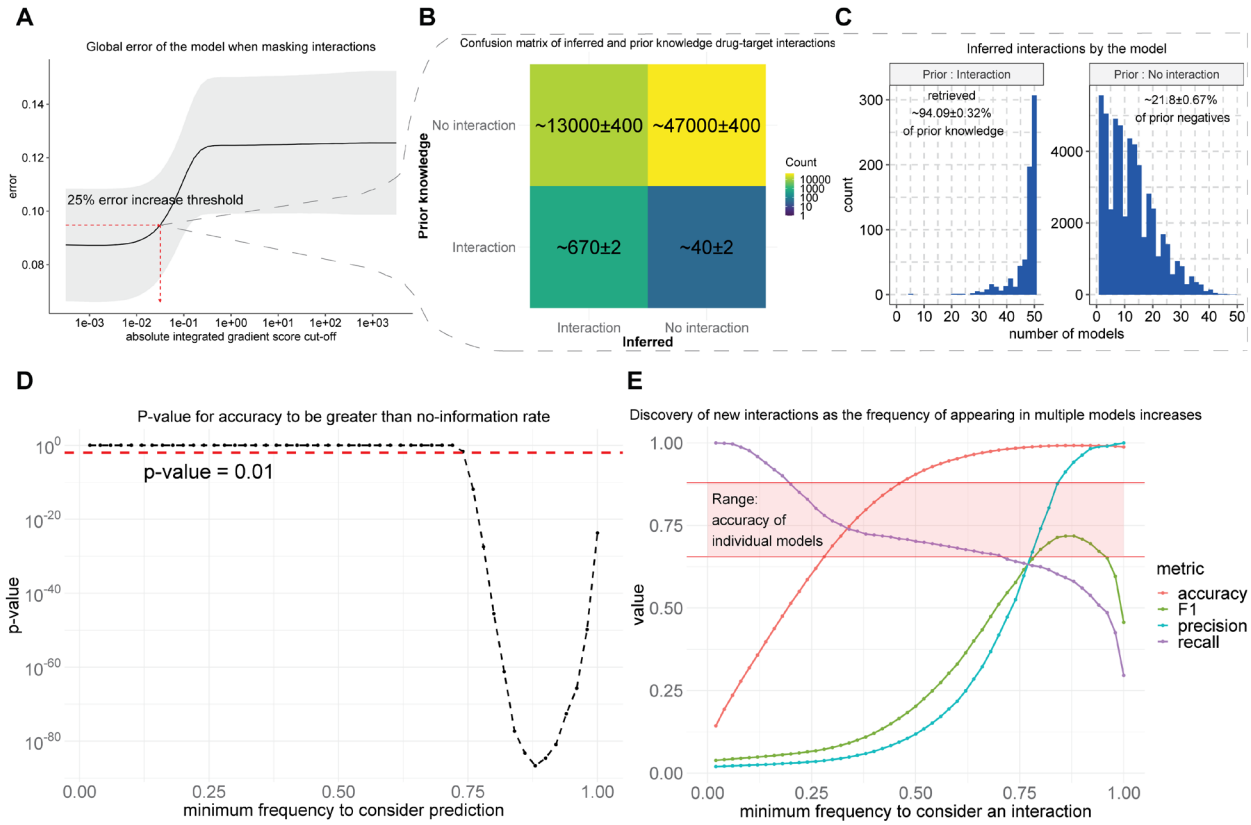


Figure 1: Model architecture and basic performance metrics. A) DT-LEMBAS' model architecture, consisting of two interconnected sub-modules: 1) a drug module that calculates drug signaling via drug-target interaction inference, based on known drug-target interactions and chemical similarity with other drugs and 2) a LEMBAS-based recurrent ANN, modeling intracellular signaling. **B)** Performance of our approach in different cell lines. **C)** Performance comparison in validation sets with standard machine learning approaches, for every TF in every cell line, using Pearson's r between predicted and actual TF activity. The model is also compared to two randomized models, derived by shuffling the inputs (X) and outputs (Y) on training. **D)** Performance comparison in validation sets, by looking only at the TFs well-fitted (here top 10%) during training. **E)** The optimal geometric mean of sensitivity and specificity for inferring drug-target interactions, and the NDR and TPR for the same gradient cut-off, at different levels of regularization **F)** Average performance across all TFs in every cell line for different levels of regularization. A two-sided unpaired Wilcoxon test was used to compare "*infinite*" and "*0*" regularizations.



<u>Figure 2: Inferring drug-target interactions in the A375 cell line from the drug module.</u> A) Error of the model as more important drug-target interactions, according to their integrated gradient score, are removed. **B)** Average confusion matrix from 50 trained models for the inferred drug-target interactions. **C)** Percentage of prior knowledge drug-target interactions and previously unknown interactions retrieved, and their corresponding frequency of appearance in multiple models. **D)** Classification performance of our approach by considering as ground truth the interactions contained both in the Broad's Institute Repurposing Hub[33] and in DrugBank[13]. Performance is calculated for an increasing frequency of an interaction appearing in multiple models. **E)** P-values from comparing accuracy with the accuracy obtained by assigning everything to the predominant class (No Information Rate: NIR), for multiple frequency scores, in this imbalanced dataset where most drugs do not interact with most targets.

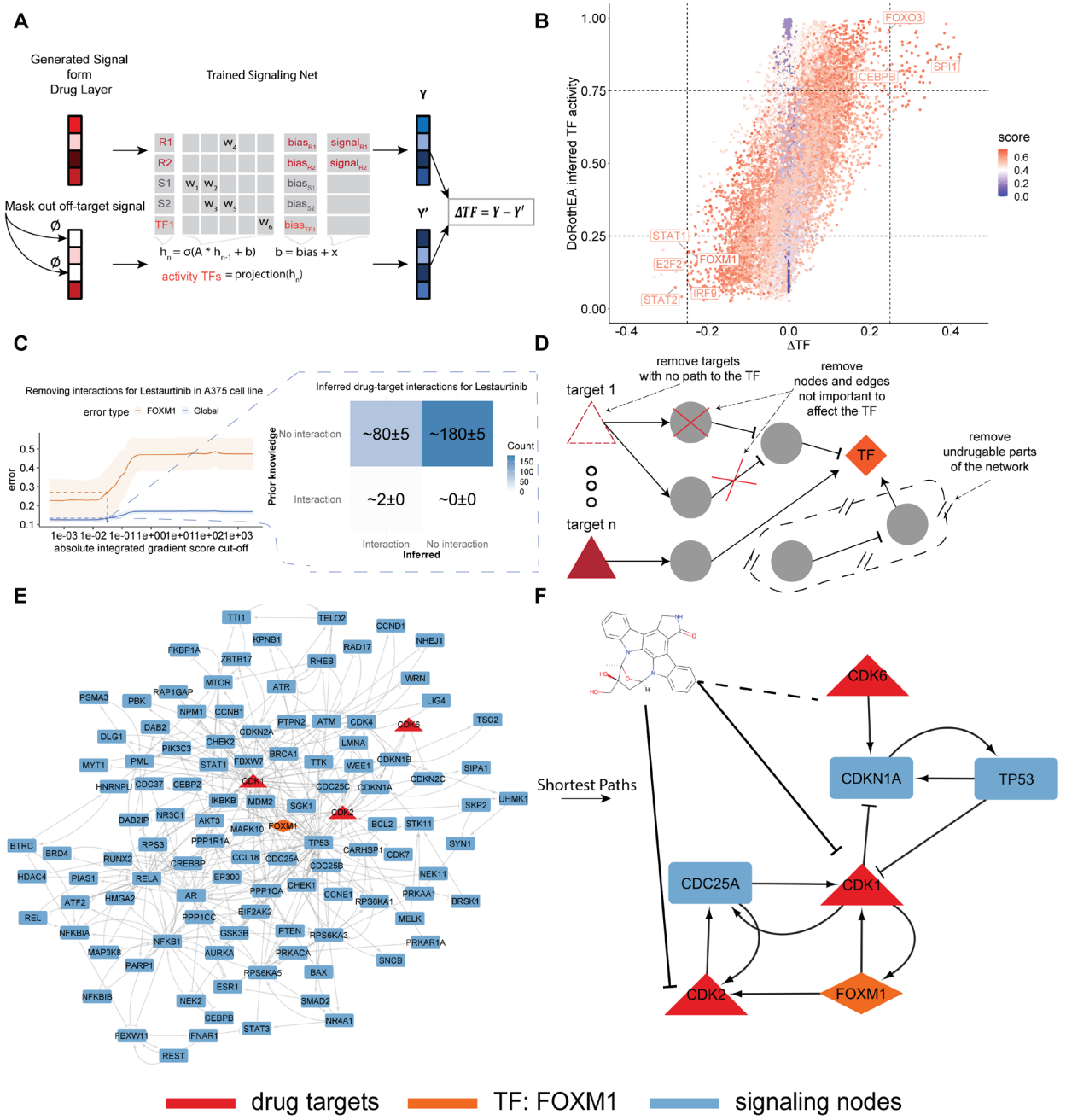
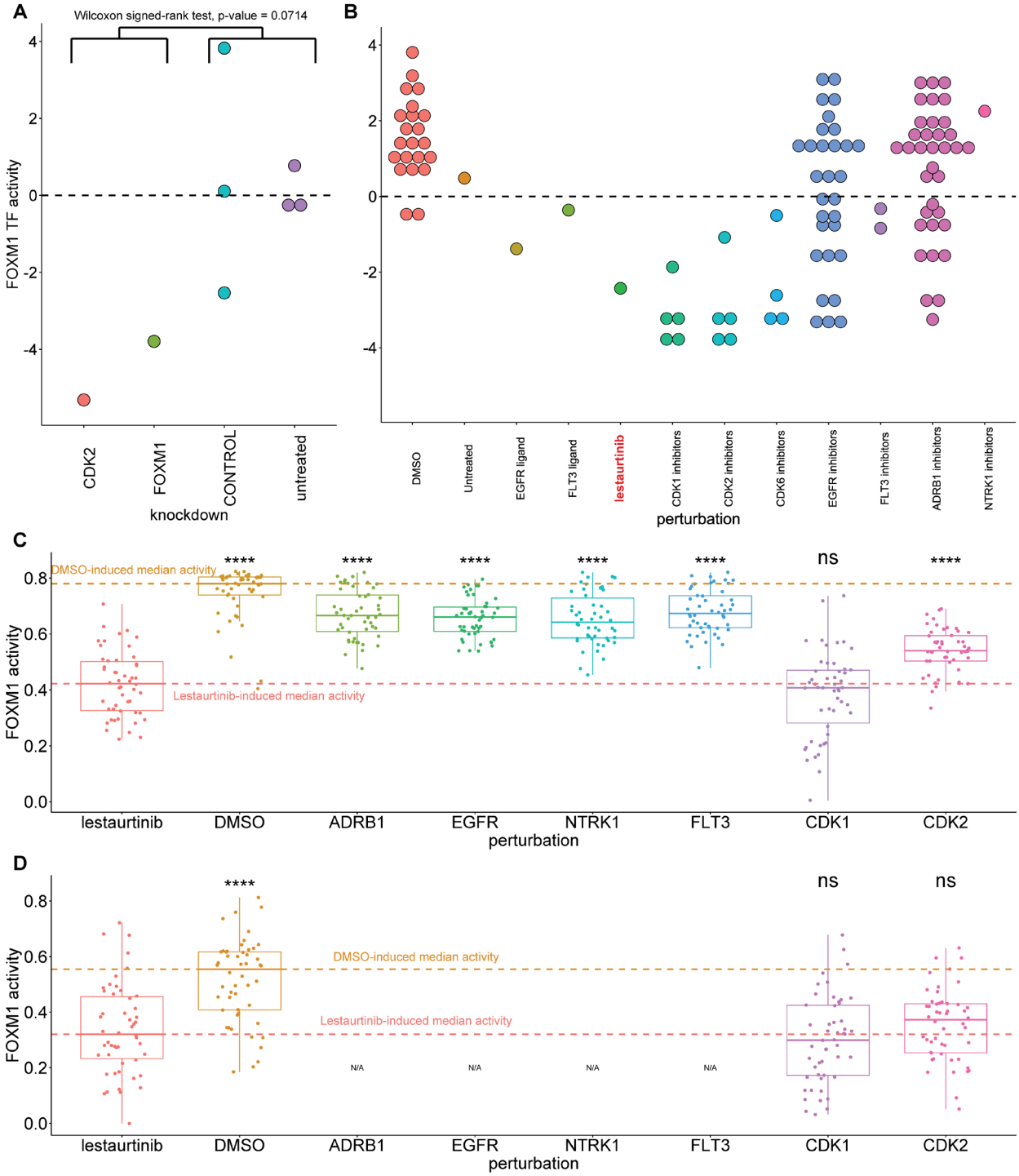


Figure 3: Process for interpreting off-target effects, with a case study for Lestaurtinib's effects on FOXM1. A) The difference between the model's predicted TF activity and the activity if the off-target signal is removed is used as a measure for the off-target effects on specific TFs. **B)** The activity of the TFs compared with the predicted off-target effects alongside a confidence score from the average performance in training and validation. **C)** Inferring the drug-target interactions using multiple models and the global error approach previously discussed. Here the example of Lestaurtinib is shown. **D)** The whole signaling network is trimmed by removing unimportant edges and nodes to control the TF of interest, stopping the process when there is no path from the inferred targets to the TF of interest. This process is repeated for every trained model and only frequently appearing edges and nodes are kept. **E)** The trimmed ensemble network explaining the off-target effect that leads Lestaurtinib to inhibit more FOXM1, via previously unknown drug-target interactions. **F)** A version of the trimmed network that only considers

874 the simplest paths that connect every target to FOXM1. Lestaurtinib, according to the model inhibits CDK1
875 and/or CDK2 kinases, while it interacts with an uncertain sign with CDK6.



876
877 **Figure 4: Validation of the predicted effects of Lestaurtinib on FOXM1 activity in the A375 cell line. A)**
878 Inferred activity after treatment with siRNA knockdowns of CDK2 and FOXM1 using public microarray
879 data. **B)** Inferred activity after treatment with ligands and inhibitors of Lestaurtinib targets, and CDKs in
880 the L1000 dataset. **C)** Predicted activity after an *in-silico* knockdown. **D)** Predicted FOXM1 activity using

881 the inferred sub-network explaining the MoA of the off-target effect of Lestaurtinib. Statistical
882 comparisons in C and D were performed relative to Lestaurtinib.