

Predicting of Gene Functions by Leveraging Biological Insights with Mechanistic Machine Learning



Preliminaries

Evolution of Gene Function

Mechanistic Machine Learning

Proof of Concept

George G. Vega Yon, Ph.D.

george.vegayon@utah.edu

Division of Epidemiology @ University of Utah

Dec 8th, 2022 @ Quinlan Lab

Collaborators: Paul Thomas, Paul Marjoram, Huaiyu Mi, Christopher Williams (USC), Alun Thomas (UofU)

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You can download the slides from <https://ggyv.cl/quinlanlab2022>

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But first...

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- ▶ Research Assistant Professor in Epidemiology since Nov. 2021.

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- ▶ Working with networks + programming since ~2010.

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whoami



George G. Vega Yon's GitHub Stats

★ Total Stars Earned:	247
⌚ Total Commits (2022):	2.4k
🍴 Total PRs:	111
❗ Total Issues:	228
👤 Contributed to:	33



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- ▶ Scientific software developer (R/C++)

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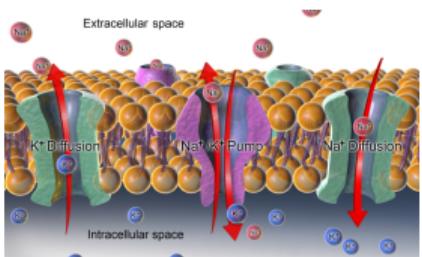
Proof of Concept

Gene Function

Encode the synthesis of genetic products that ultimately are related to a particular aspect of life, for example

Molecular function

Active transport



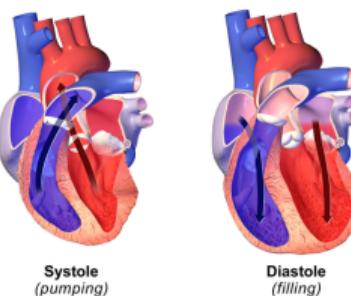
Cellular component

Mitochondria GO:0004016



Biological process

Heart contraction
GO:0060047



Gene Function: the Gene Ontology Project



GENEONTOLOGY
Unifying Biology

- The GO project has \sim 43,000 validated terms, \sim 7.4M annotations on \sim 5,200 species.

source: Statistics from <http://pantherdb.org/panther/summaryStats.jsp> and <http://geneontology.org/stats.html>

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- ▶ Only half of the human gene annotations are based on experimental evidence.

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- ▶ About \sim 700,000 annotations are on human genes.
- ▶ Only half of the human gene annotations are based on experimental evidence.
- ▶ About \sim 173,000 publications have used the GO.

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Predicting Gene Function: Current methods

Sequences, phylogenomics, and ML.

- ▶ **BLAST**:² Prediction by sequence homology (~ 105,000 citations).

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None of the ML-based methods relies on biological theory (mechanistic models).

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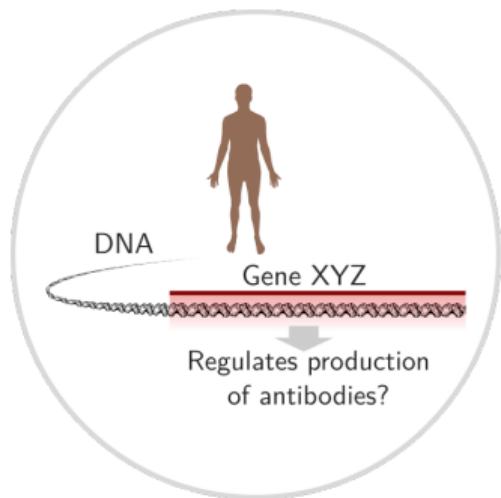
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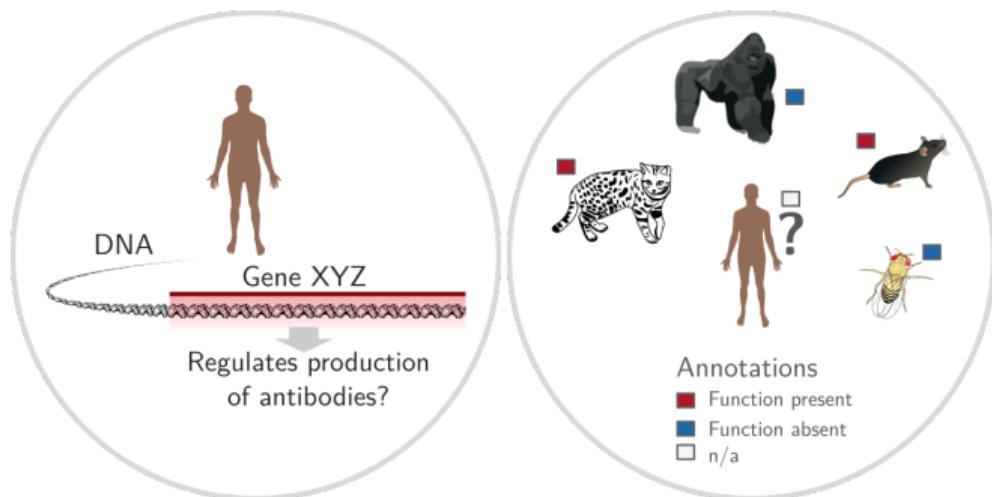
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Is gene *XYZ* involved in process *ABC*?



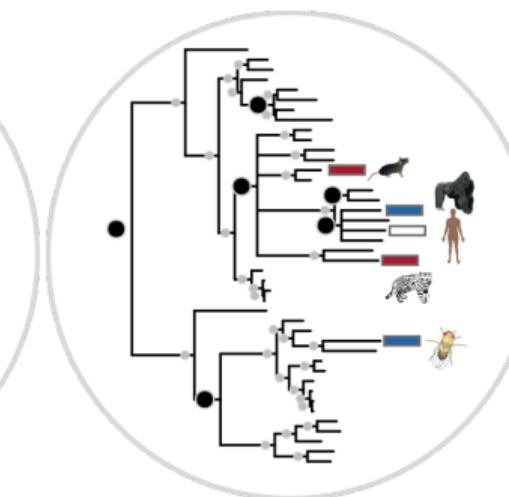
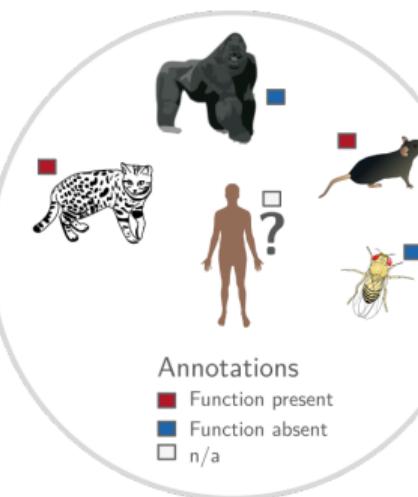
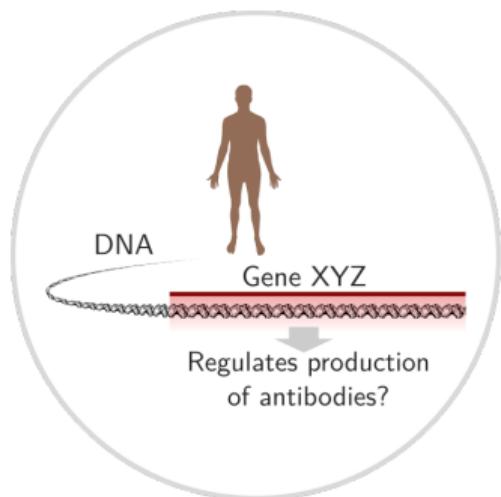
Complex to directly assess

Is gene XYZ involved in process ABC?



Complex to directly assess But we may know from other species

Is gene XYZ involved in process ABC?



Complex to directly assess

But we may know from other species

And we further know how these are *evolutionary* connected

Is the human gene **XYZ** involved in process **ABC**, given what we know about that for other *related* species?

Annotations

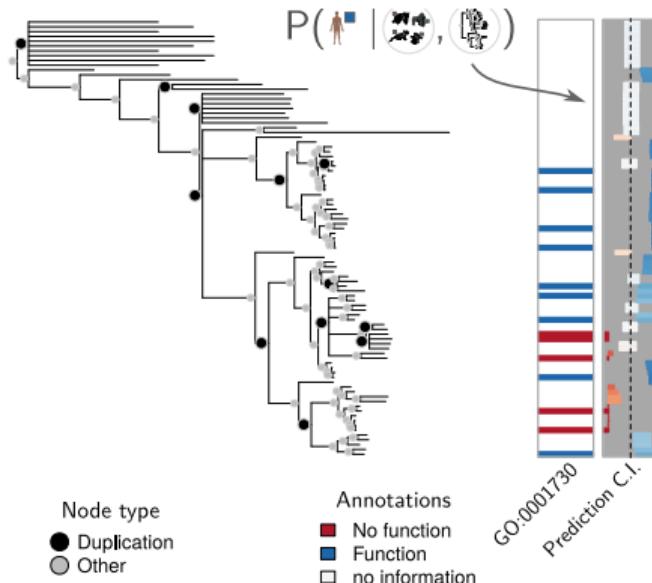
- Function present
- Function absent
- n/a

Evolution of Gene function (of one function)

Built a big model (lots of trees and annotations) called aphylo:

- ▶ Only two sources of data:

Phylogenetic tree
(pantherdb.org) and functional
annotations
(geneontology.org).



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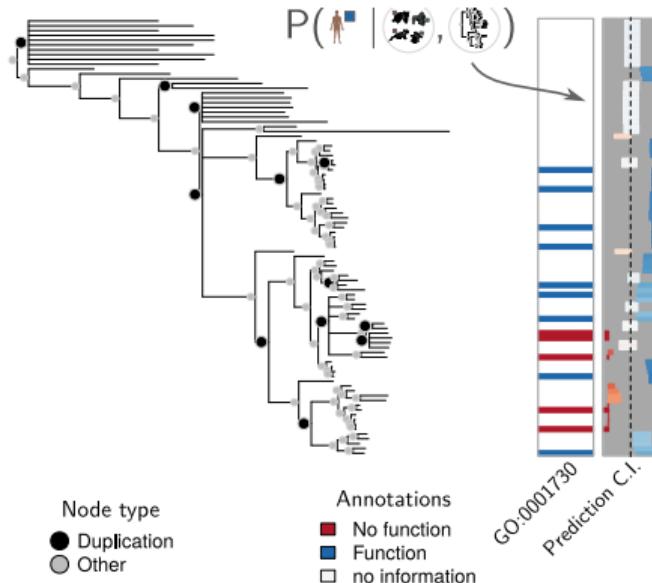
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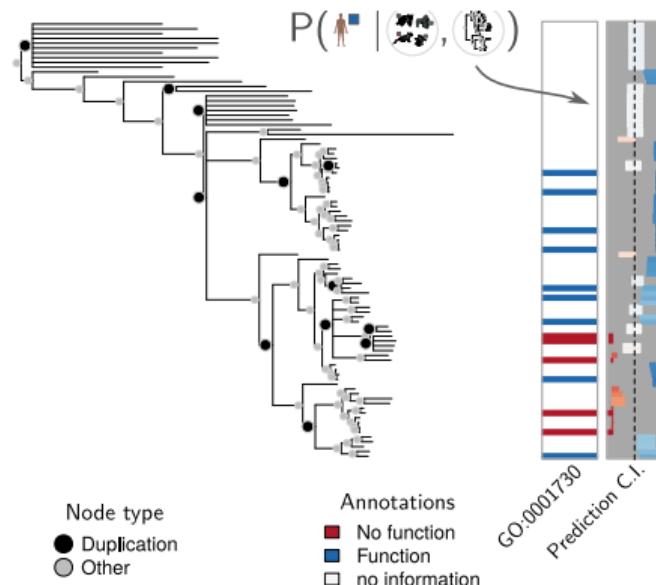
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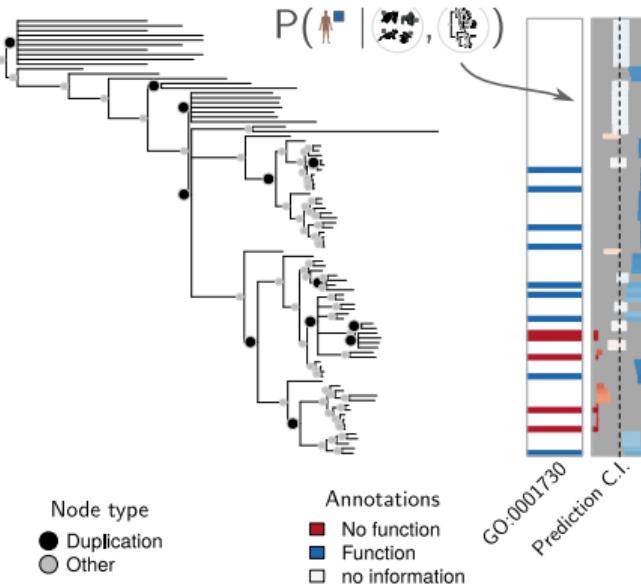
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(pantherdb.org) and functional annotations
(geneontology.org).
- ▶ Leverage negative annotation of GO terms (NOT).
- ▶ Use Felsenstein's tree pruning algorithm to compute tree likelihood.
- ▶ Fit pooled models featuring thousands of annotations in hundreds of trees (with split-second prediction capability).



... But what if we wanted to deal with multiple functions?

Evolution of Gene function (multiple functions)

Tapping into Evol. Theory

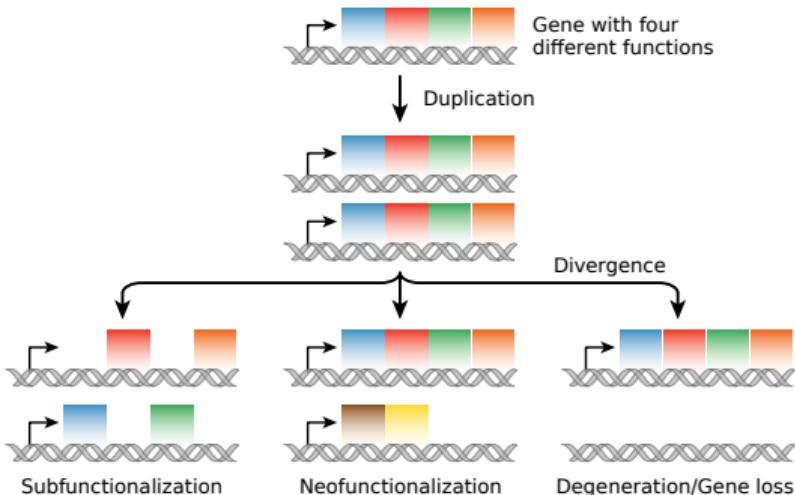


Figure: A key part of molecular innovation, gene duplication provides an opportunity for new functions to emerge (wikimedia)

Evolution of Gene function (multiple functions)

Tapping into Evol. Theory

- ▶ A fundamental part of Fun. Evol. is Duplication Events.
- ▶ Furthermore, knowing what happened to gene A (e.g., neofunctionalization) is highly informative to learn about the functional state of B.

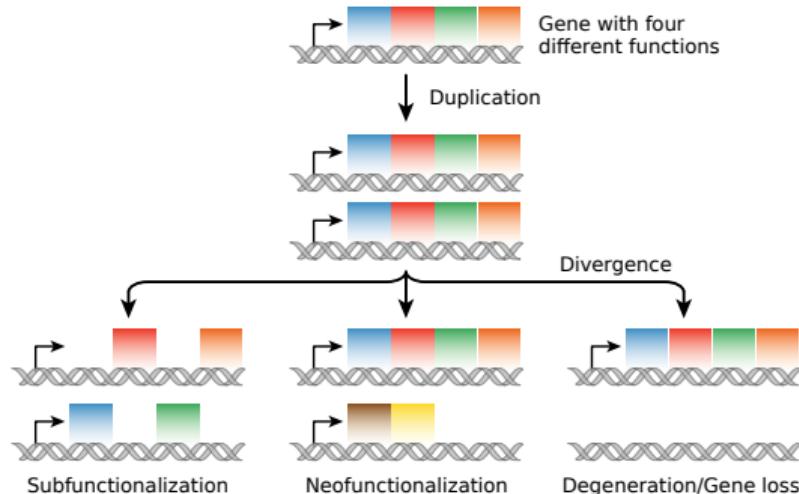


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Evolution of Gene function (multiple functions)

Tapping into Evol. Theory

- ▶ A fundamental part of Fun. Evolution is Duplication Events.
 - ▶ Furthermore, knowing what happened to gene A (e.g., neofunctionalization) is highly informative to learn about the functional state of B.
 - ▶ One way to model this is using a Markov Transition Model (as in SIFTER).

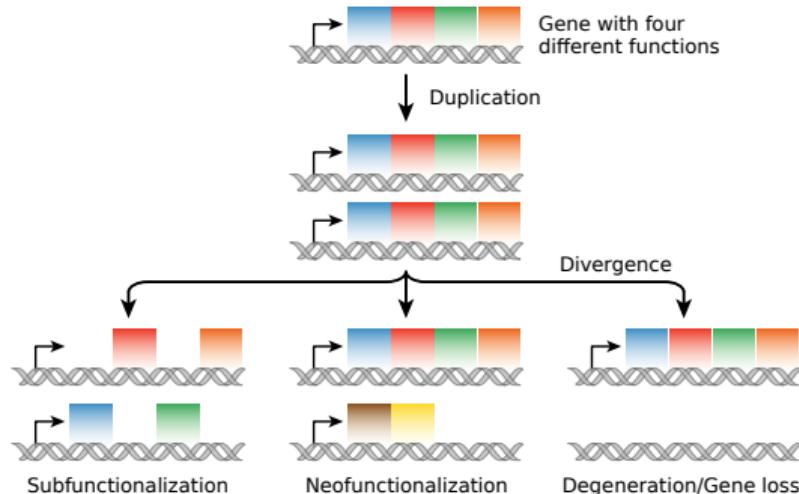
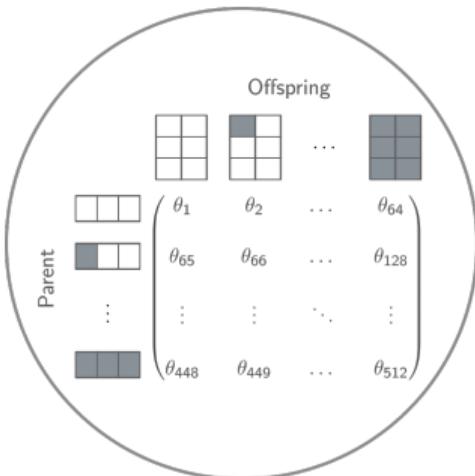


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Evolution of Gene function (multiple functions)

If we wanted to build a model with 3 functions, we would need to estimate...

Full Markov Transition Matrix



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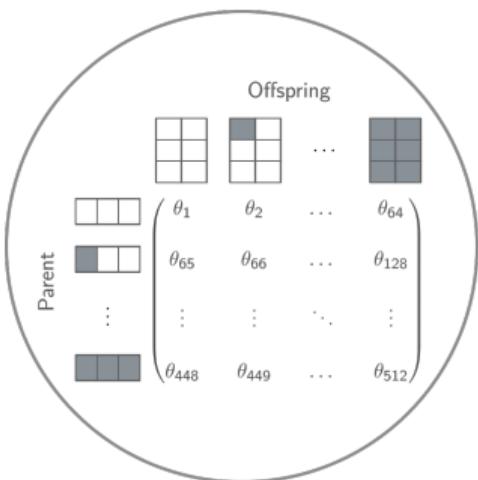
Proof of Concept

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Full Markov Transition Matrix

► 512 parameters



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Evolution of Gene Function

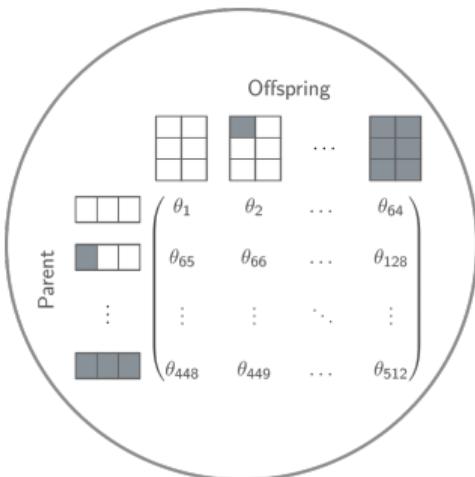
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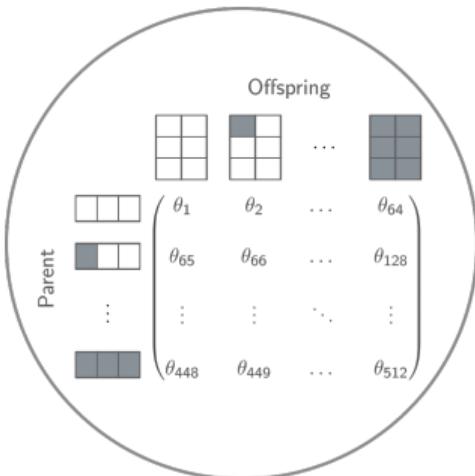


- ▶ 512 parameters
- ▶ Finding this many parameters is not easy.

Evolution of Gene function (multiple functions)

If we wanted to build a model with 3 functions, we would need to estimate...

Full Markov Transition Matrix



- ▶ 512 parameters
- ▶ Finding this many parameters is not easy.
- ▶ Even if you can, interpretation is awkward.

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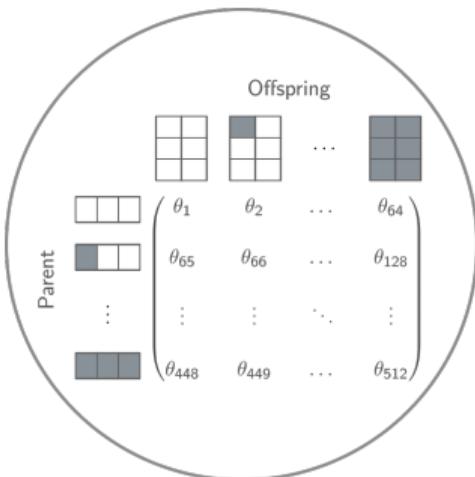
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Social Network Analysis may help us...

Exponential Random Graph Models (ERGMs)

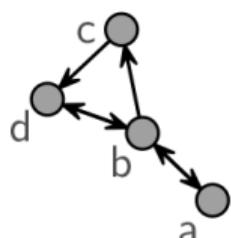
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Social Network



	a	b	c	d
a				
b				
c				
d				

Exponential Random Graph Models (ERGMs)

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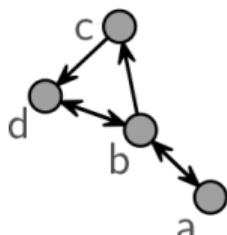
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Social Network

- ▶ Not about individual ties.



	a	b	c	d
a				
b				
c				
d				

Exponential Random Graph Models (ERGMs)

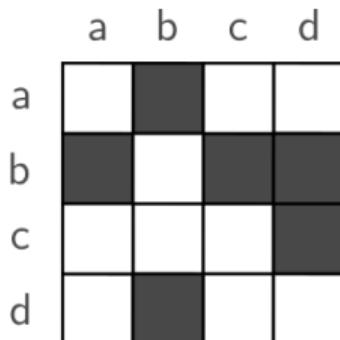
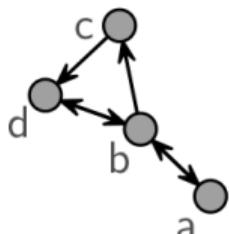
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Social Network



- ▶ Not about individual ties.
- ▶ Statistical inference on *motifs* (triangles, dyads, homophily, etc.)

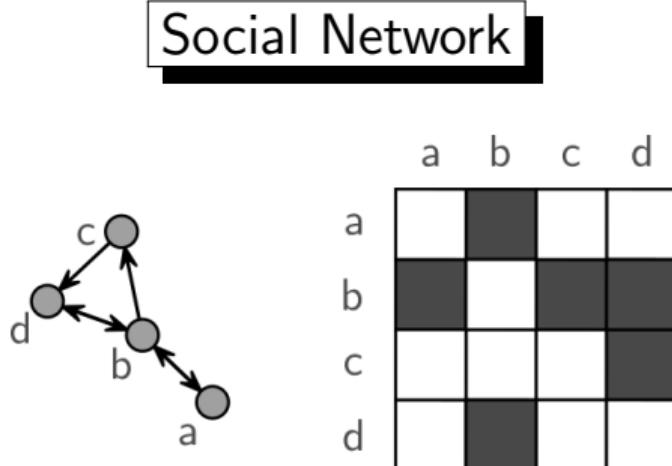
Exponential Random Graph Models (ERGMs)

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- ▶ Not about individual ties.
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- ▶ Literature about ERGMs is vast, a.k.a. a low-hanging fruit.

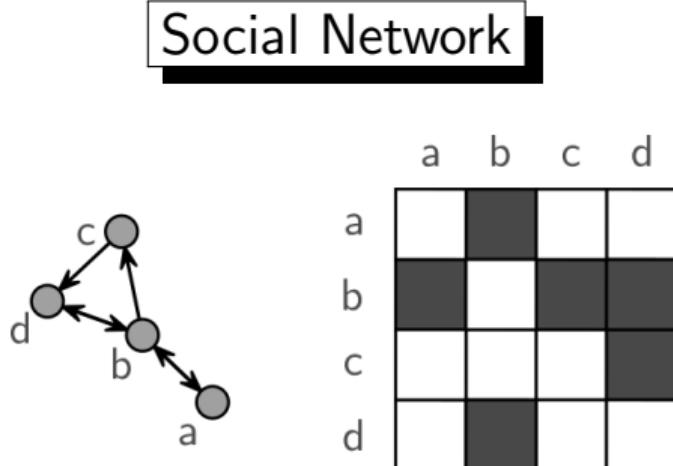
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Ultimately...

ERGM ≡ **Modeling binary arrays**

Exponential Random Graph Models (ERGMs)

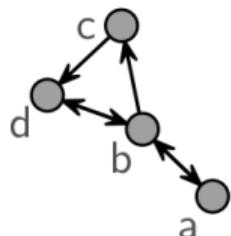
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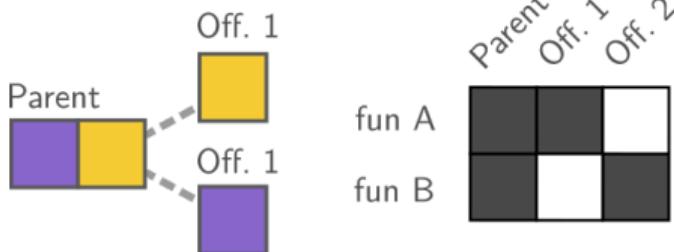
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Social Network



	a	b	c	d
a				
b				
c				
d				

Evolutionary Event

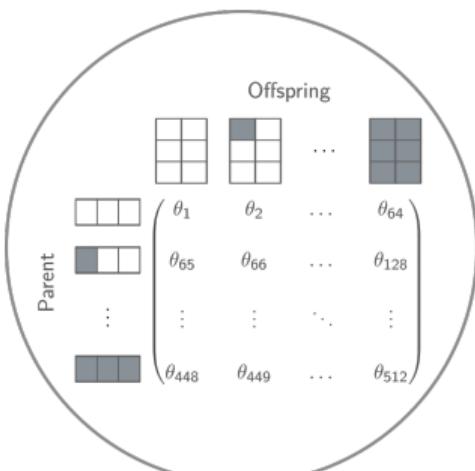


Social Networks are usually represented as **adjacency matrices**, and so can evolutionary events!

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Full Markov Transition Matrix

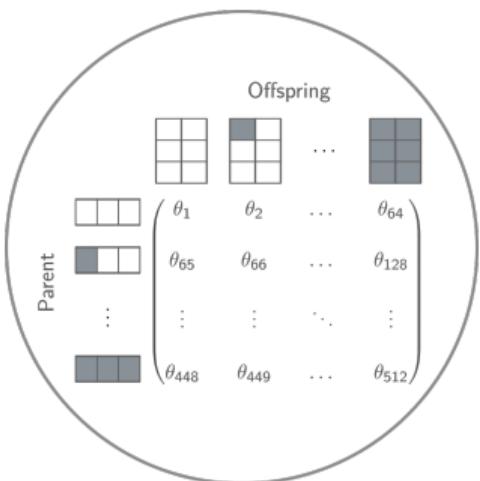


512 parameters

Evolution of Gene function (multiple functions) (cont.)

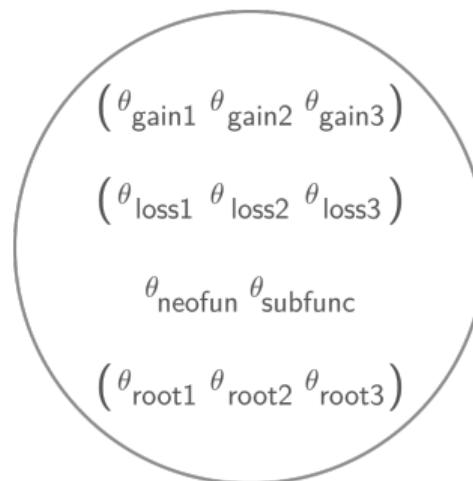
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512 parameters

Sufficient statistics



11 parameters (for example)

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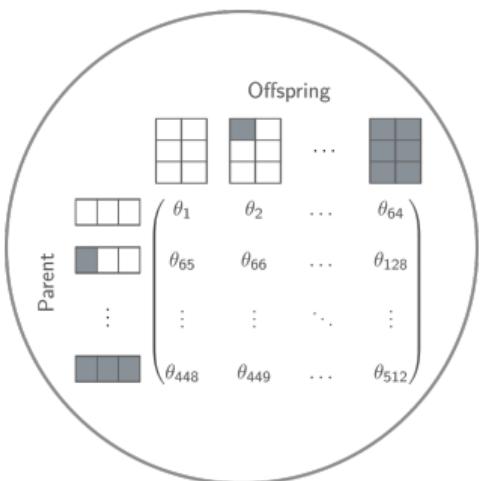
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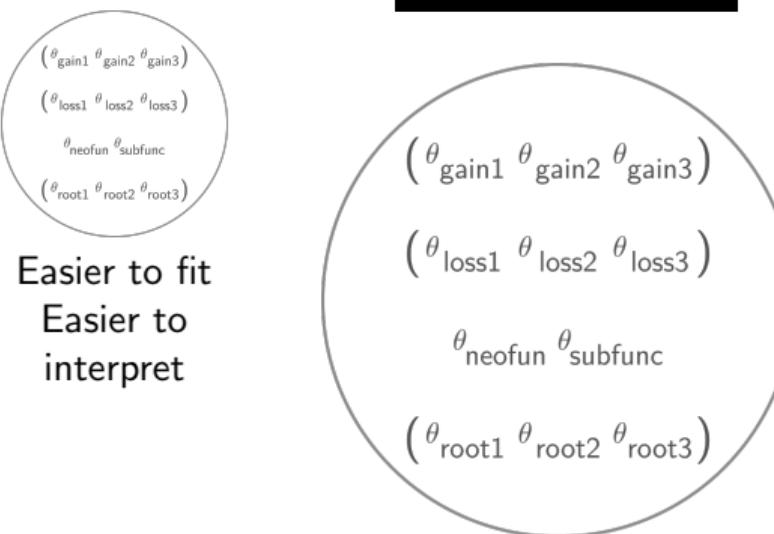
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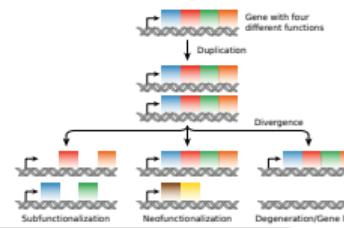
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Proof of Concept



Rep.	Description	Definition
	Gain of function	$(1 - x_p) \sum_{n:n \in Off} x_n$
	Loss of function	$x_p \sum_{n:n \in Off} (1 - x_n)$
	Subfunctionalization	$x_p^k x_p^j \sum_{n \neq m} x_n^k (1 - x_n^j) (1 - x_m^k) x_m^j$
	Neofunctionalization	$x_p^k (1 - x_p^j) \sum_{n \neq m} x_n^k (1 - x_n^j) (1 - x_m^k) x_m^j$
	Longest branch gains	$(1 - x_p^k) \mathbf{1} (x_m^k : m = \text{argmax}_n \text{blength}_n)$

Table: Example of sufficient statistics for evolutionary transitions.

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GEESE: GEne functional Evolution using SuficiEncy

I implemented what I just described in a C++ library with a companion R package called geese. The question is: How much do we earn by using these motifs?

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- ▶ Fitted both of them using MCMC.
- ▶ Used LOO cross-validation to compute aggregated AUCs and MAE.

GEESE for predicting gene function (cont.)

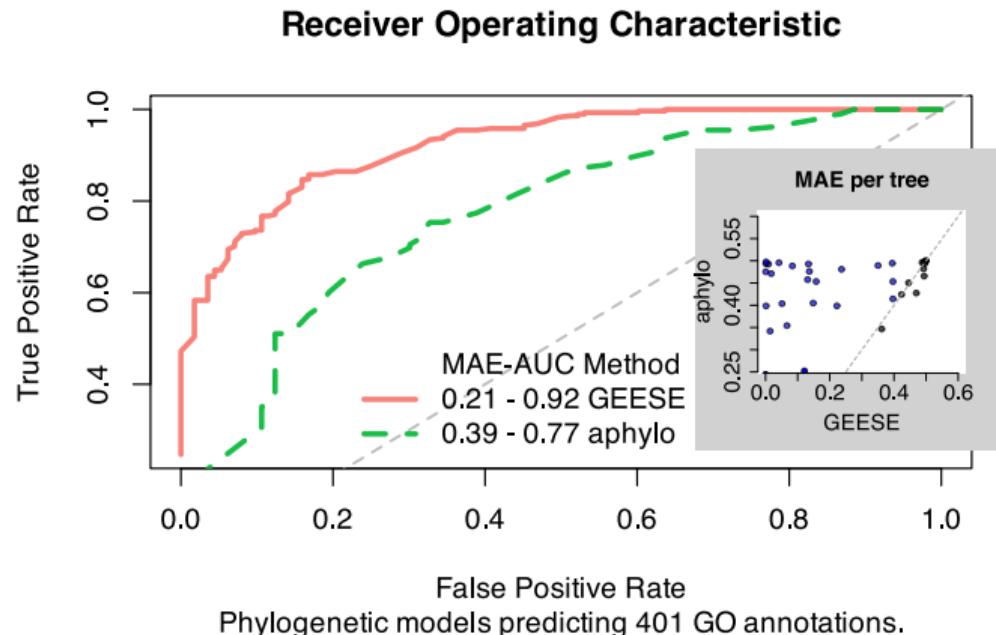
How much can we gain from a joint dist. model?

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Just controlling for preservation (having only one duplicate changing) significantly improves our predictions.

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Mechanistic Machine Learning: State-of-the-art

- ▶ After all the data pouring, attention to causal inference and mechanistic models is coming back^{3,14}
- ▶ Applications in Physics, Chemistry, Biomedical Imaging, and Biology^{17,11,7,1} show the benefits of combining the two approaches.

Mechanistic Models

- ▶ Inference driven (causality)
- ▶ Great for small datasets
- ▶ Not the most accurate

Machine Learning Models

- ▶ Data-driven (prediction)
- ▶ Lots of points to “learn”
- ▶ Great for big data

Important: Mechanistic Machine Learning **is not** domain-knowledge aided feature engineering. You need a whole other model to complement the ML algorithm.

Potential Strategies

- ▶ Use machine learning to learn the errors of a mechanistic model.
 - ▶ Add constraints to the ML algorithm based on a mechanistic model.
 - ▶ Add mechanistic predictions as a feature of a machine learning model.

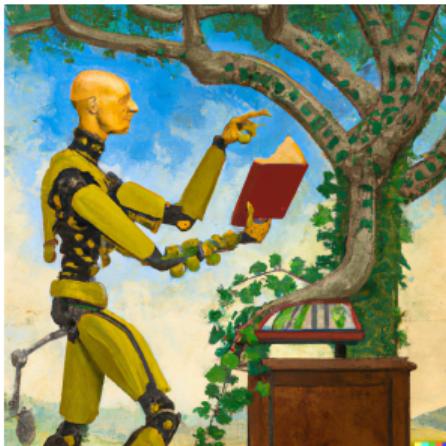


Figure: "A van Gogh-style painting of an android holding a large biology book in one hand and a computer in another, examining an evolutionary tree that, instead of leaves, have genes."—DALL-E's interpretation of my description ([link](#))

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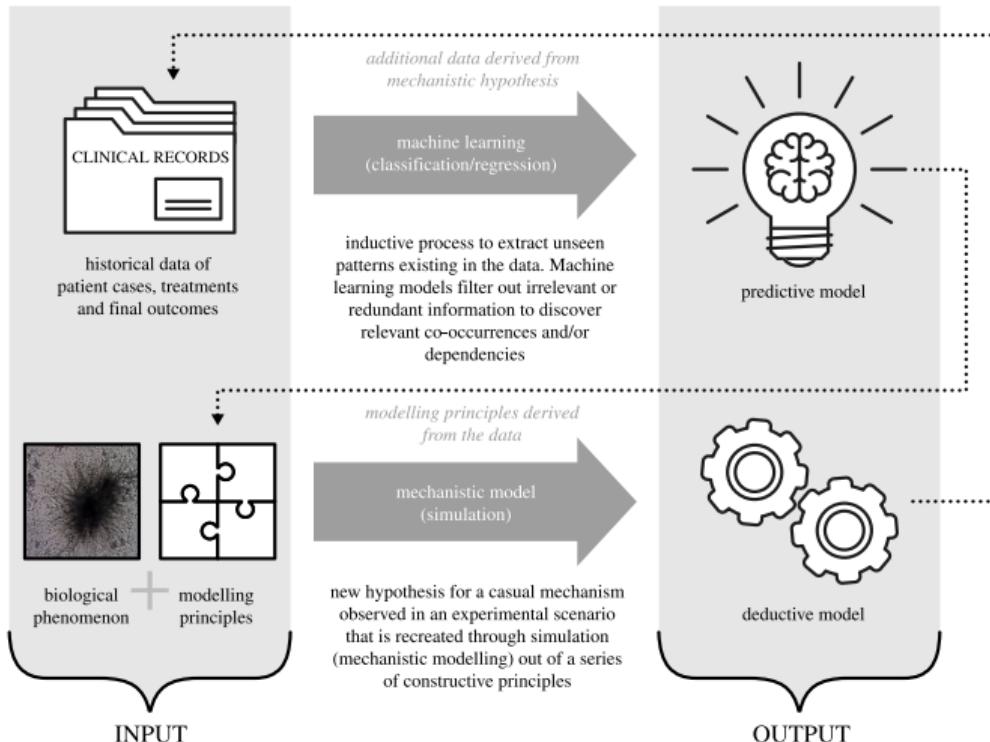


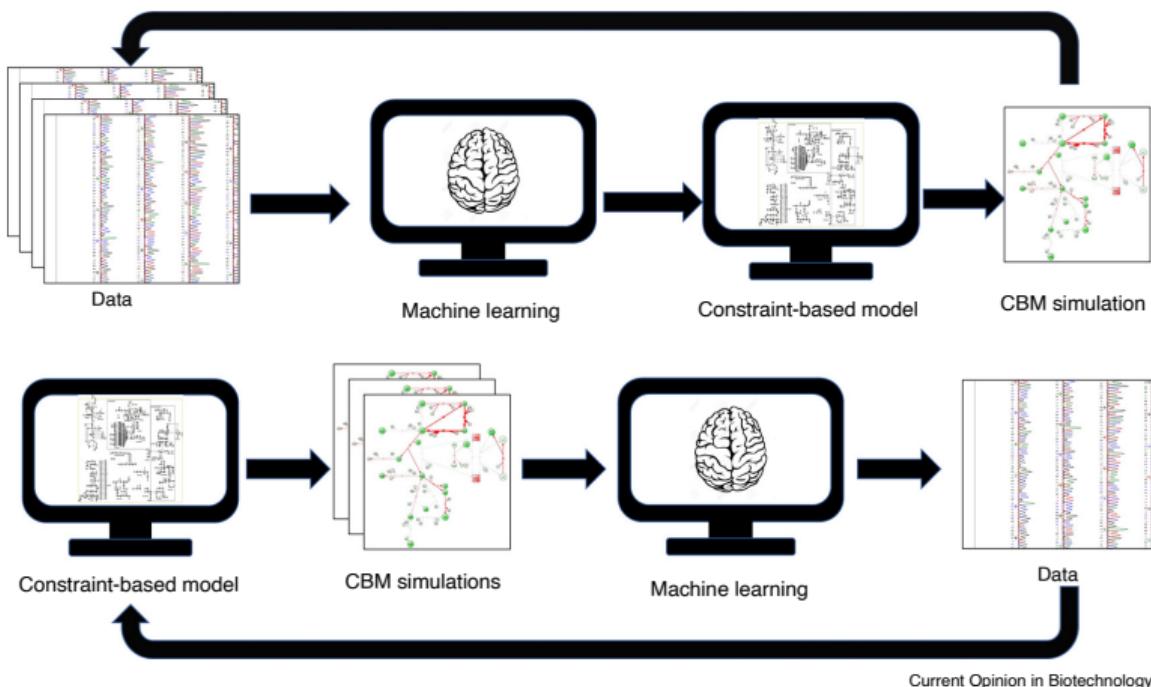
Figure: “The inputs and outputs from machine learning and mechanistic modelling approaches, and the potential for synergy between the two.” (Figure 1 reproduced directly from Baker et al. [3].

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Current Opinion in Biotechnology

Figure: “**Top:** Machine learning is applied to the input data to identify the important features for constructing reduced order constraint-based models; the CBM simulations can be iteratively matched with input data for convergence until the proper set of features are identified. **Bottom:** Machine learning is iteratively applied to CBM simulations to reconcile with experimental data. Interplay between the Top and Bottom parts can iteratively lead to convergence between CBM simulations, experimental data and machine learning based predictions.” (Figure 2 reproduced directly from Rana et al. [15])

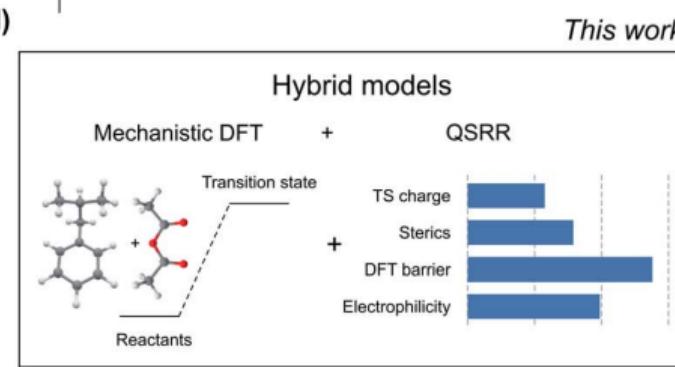
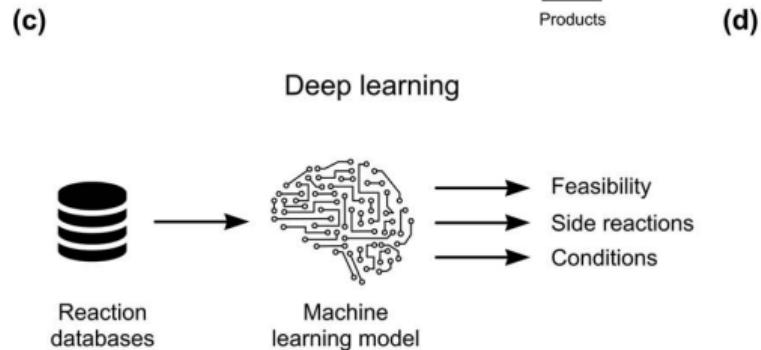
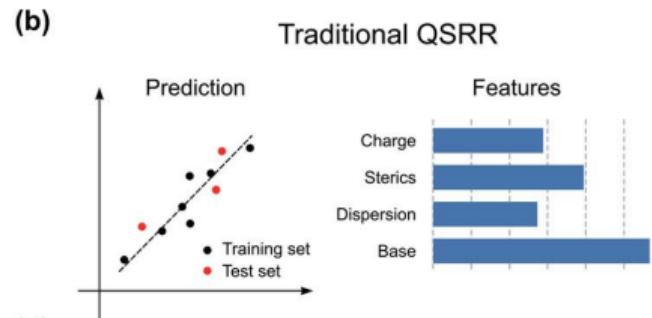
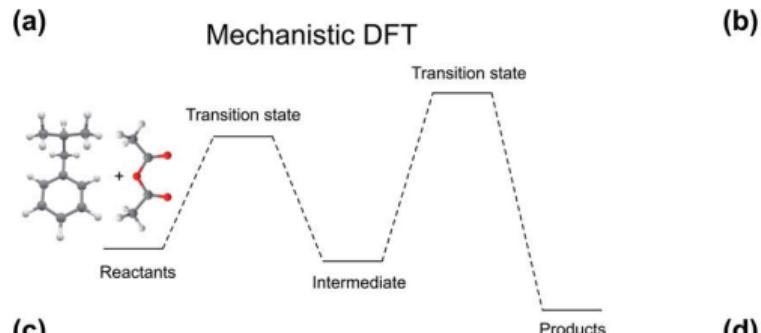


Figure: “Different types of quantitative reaction prediction approaches. Mechanistic DFT (a) and QSRR (b) are the current gold standard methods. Deep learning models (c) are emerging as an alternative. Hybrid models (d) combine mechanistic DFT modelling with traditional QSRR” (Figure 2 reproduced directly from Jorner et al. [11])

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Beyond GO and Trees... Bgee

The **Bgee** project “is a **database** for retrieval and **comparison of gene expression** patterns **across multiple animal species**. It provides an intuitive answer to the question ‘where is a gene expressed?’ and supports research in cancer and agriculture as well as evolutionary biology.” – Bastian et al. [4]

- ▶ Raw expression annotations.
- ▶ Standardized expression scores (so can compare across species/tissues).
- ▶ And also yes/no expression annotations based on the standardized scores.

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Beyond GO and Trees... Bgee (cont.)

Divergence across species in gene expression levels has been linked to evolutionary events,^{13,9} i.e., expression levels clustered phylogenies.

Thinking of different ways to use it as:

- ▶ As an additional feature for our model: “Given the phylo, observed annotations, **and expression levels in n tissues**, . . .”
- ▶ As 0/1 variable (expression is present/absent) to predict in our model: “Model the evolution of gene function **and expression**.”
- ▶ As part of a prediction model in, say, a Machine Learning Model.

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Data Feats

- ▶ Bgee 15 dataset: approx 7 billion annotations for 1.5 million genes.
- ▶ Our dataset: 1,484 predictions for 1,318 genes.
- ▶ Search by Gene name: 9,923,427 Bgee annotations.

What went into the blender

Data Feats

- ▶ Bgee 15 dataset: approx 7 billion annotations for 1.5 million genes.
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Final model

- ▶ 10 GO terms (in a full-Markov model, this is 1 MM params).
- ▶ 278 annotations for 256 genes.
- ▶ 10 GEESE predictions for each gene.
- ▶ 46 Bgee score for gene expression computed as **mean expression score by gene-genus**

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GO terms: GO:0004672, GO:0004713, GO:0004867, GO:0005730, GO:0005829, GO:0005886, GO:0006468, GO:0009408, GO:0015020, GO:0060070

Genus: Anguilla, Anolis, Astatotilapia, Astyanax, Bos, Branchiostoma, Caenorhabditis, Callithrix, Canis, Capra, Cavia, Coccocebus, Chlorocebus, Danio, Drosophila, Equus, Esox, Felis, Gadus, Gallus, Gasterosteus, Gorilla, Heterocephalus, Homo, Latimeria, Lepisosteus, Macaca, Manis, Meleagris, Microcebus, Monodelphis, Mus, Neolamprologus, Nothobranchius, Ornithorhynchus, Oryctolagus, Oryzias, Ovis, Pan, Papio, Poecilia, Rattus, Salmo, Scophthalmus,

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Mechanistic ML

We are comparing three models:



Phylogenetic based
predictions (evolution of
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We are comparing three models:



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Linear Prob. model using
expression as predictors.

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We are comparing three models:

GEESE

Bgee

GEESE + Bgee

Phylogenetic based
predictions (evolution of
gene function)

Linear Prob. model using
expression as predictors.

Linear Prob. model using
expression as predictors
and predictions made by
GEESE.

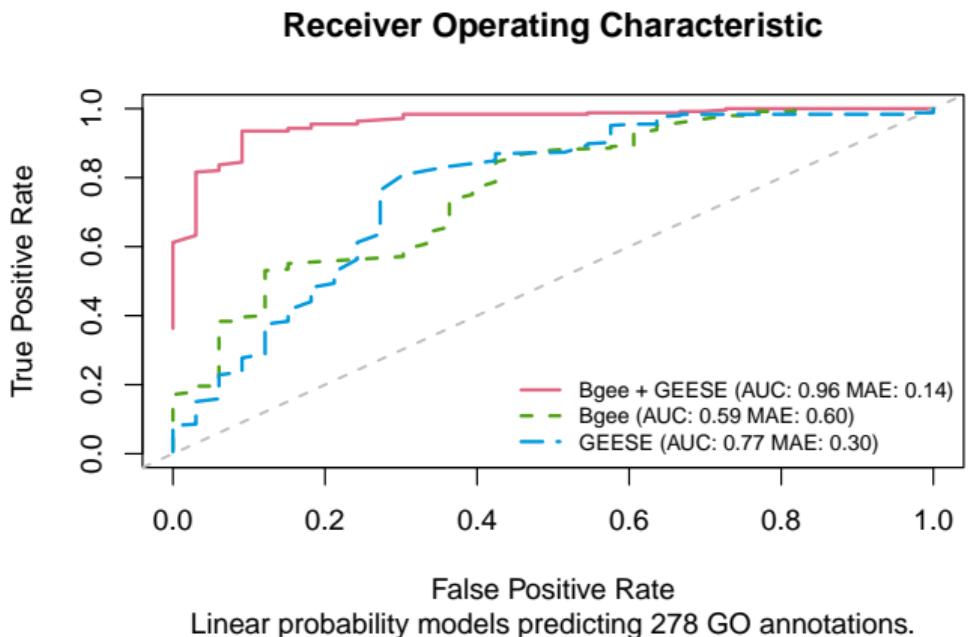
Mechanistic ML (prelim res.)

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Both AUC and MAE were computed only using predictions for which we knew the true value.

Discussion

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Gene function

- ▶ We are racing to discover what genes do.
- ▶ Experimental assessment is expensive (money and time,) → automatic annotations.
- ▶ Many ways to do it (seq. homology, evolutionary theory, ML, etc.)
- ▶ The best methods use ML (pattern discovery)... but none (AFAIK) are based on bio. theory.

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Evol. Model

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- ▶ We proposed an Evolutionary model of Gene Function.
 - ▶ This new model, GEESE, uses sufficiency to reduce “Markov complexity.”
 - ▶ We showed it really helps.

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- ▶ This new model, GEESE, uses sufficiency to reduce “Markov complexity.”
- ▶ We showed it really helps.

Mechanistic ML

- ▶ Mechanistic Machine Learning (mixing theory-based models with ML) promises improved predictions.
- ▶ I showed an application using gene expression (Bgee).
- ▶ Adding our mechanistic predictions (based on GEESE) boosted quality

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Discussion (cont.)

- This is the core of an R01 first submitted in Feb 2022.

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- ▶ This is the core of an R01 first submitted in Feb 2022.
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- ▶ We believe we are addressing both using gene expression data (Bgee) and Mechanistic ML.
- ▶ ...your thoughts?

Thank you!

Predicting of Gene Functions by Leveraging Biological Insights with Mechanistic Machine Learning



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George G. Vega Yon, Ph.D.

george.vegayon@utah.edu

Division of Epidemiology @ University of Utah

Dec 8th, 2022 @ Quinlan Lab

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Tree likelihoods: Felsenstein's Pruning algorithm

All possible transitions from \mathbf{x}_n

Transition Probability (ERGM)

$$\mathbb{P}(\tilde{D}_n \mid \mathbf{x}_n, \Theta) = \sum_{\mathbf{x}} \mathbb{P}(\mathbf{x} \mid \mathbf{x}_n) \prod_{m \in \mathcal{O}(n)} \mathbb{P}(\tilde{D}_m \mid \mathbf{x}_m)$$

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Model Parameters

Vector of Sufficient Statistics

$\mathbb{P}(x \mid x_n) = \frac{\exp\{\Theta^t s(x, x_n)\}}{\sum_{x'} \exp\{\Theta^t s(x', x_n)\}}$

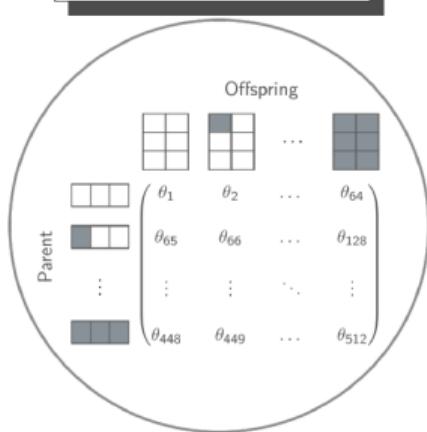
Normalizing Constant

the *lingua franca* of SNA

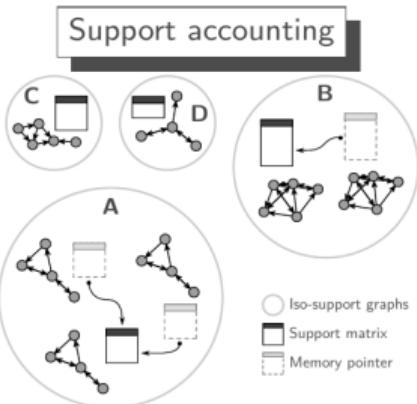
... I implemented this (and more) on **barry**

Some computational features of **barry**

Constrain support set



Support accounting



Reduced peeling sequence

