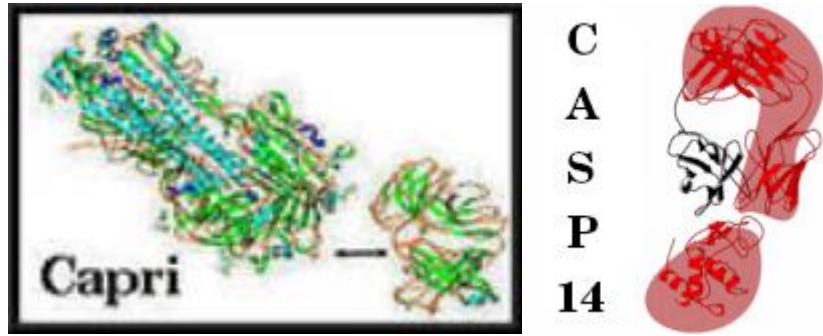


生物统计学： 生物信息中的概率统计模型

2020年秋



有关信息

- 授课教师：宁康
 - Email: ningkang@hust.edu.cn
 - Office: 华中科技大学东十一楼504室
 - Phone: 87793041, 18627968927
- 课程网页
 - <http://www.microbioinformatics.org/teach/#>
 - QQ群: 182996651



2020生物统计学



扫一扫二维码，加入群聊。



课程安排

- 生物背景和课程简介
- 传统生物统计学及其应用
- 生物统计学和生物大数据挖掘
 - Hidden Markov Model (HMM)及其应用
 - Markov Chain
 - HMM理论
 - HMM和基因识别 (Topic I)
 - HMM和序列比对 (Topic II)
 - 进化树的概率模型 (Topic III)
 - Motif finding中的概率模型 (Topic IV)
 - EM algorithm
 - Markov Chain Monte Carlo (MCMC)
 - 基因表达数据分析 (Topic V)
 - 聚类分析-Mixture model
 - Classification-Lasso Based variable selection
 - 基因网络推断 (Topic VI)
 - Bayesian网络
 - Gaussian Graphical Model
 - 基因网络分析 (Topic VII)
 - Network clustering
 - Network Motif
 - Markov random field (MRF)
 - Dimension reduction及其应用 (Topic VIII)
- 面向生物大数据挖掘的深度学习

研究对象：
生物序列，
进化树，
生物网络，
基因表达
...

方法：
生物计算与生物统计

第8-1章:蛋白质相互作用 的实验方法和预测

- Experimental methods
- Prediction of protein-protein interactions

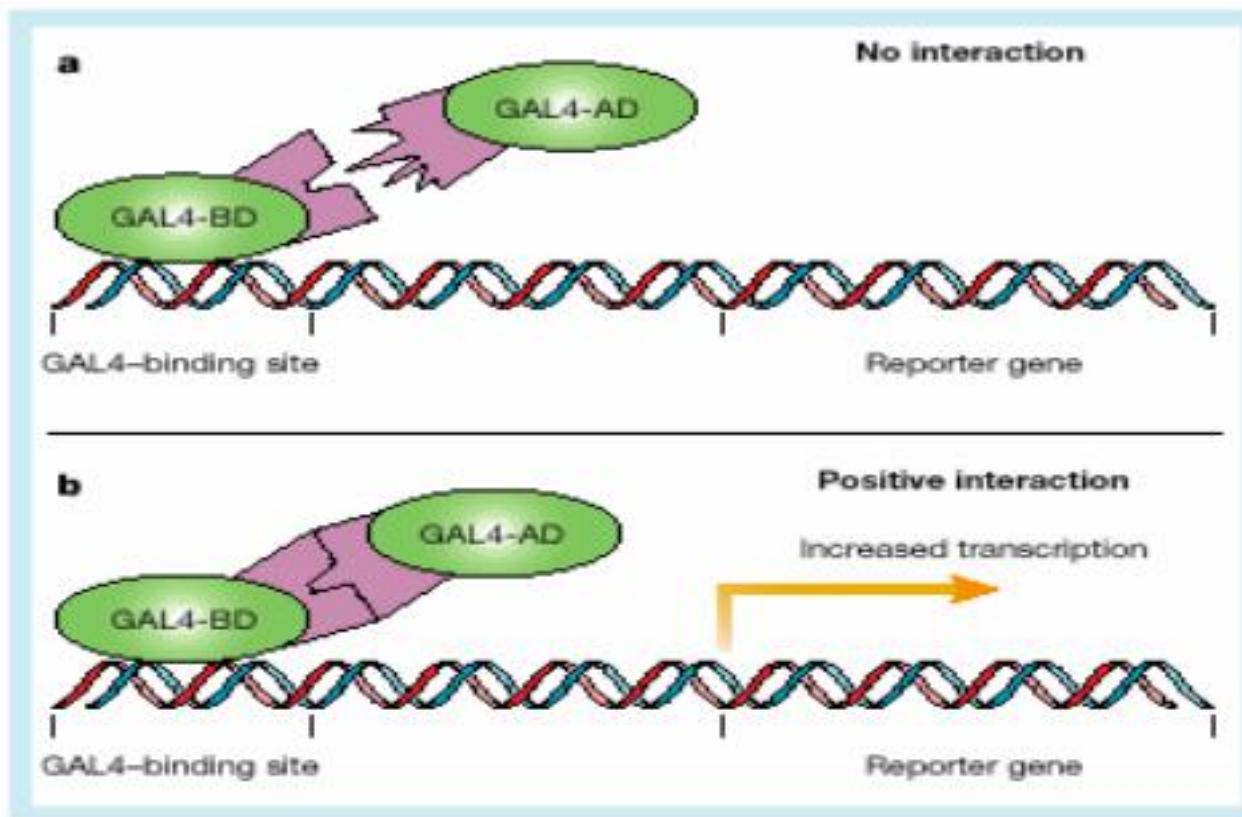
Part I: Experimental Methods

- Physical interaction
 - Yeast two hybrid system
 - TAP-mass spectrometry
- Genetic interaction
 - SGA
 - EMAP

Protein-protein interactions (Experimental methods)

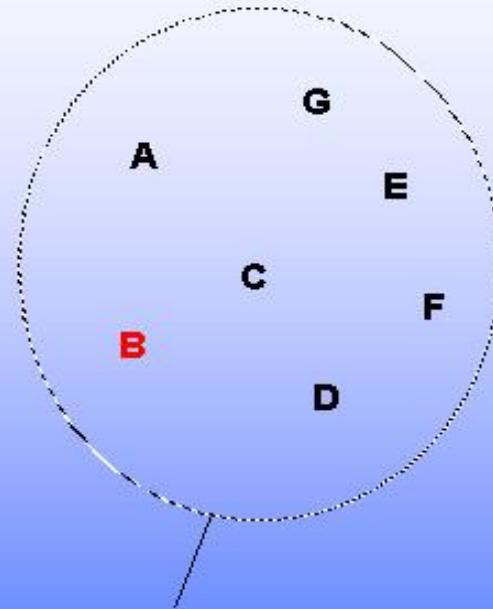
- Co-immunoprecipitation.
- Two-hybrid system (Uetz et al. 2000, Ito et al. 2000, 2001).
- Purified Complex by mass spectrometry
 - TAP: Tandem affinity purification (Gavin et al. 2002).
 - HMS-PCI: high-throughput mass spectrometric protein complex identification (Ho et al. 2002).

Mechanism of two-hybrid system



From: Nature 405, June 15, 2000, 837-846.

mass spec



**protein pulled down
with epitope-tagged
protein B**

Mass spectrometry

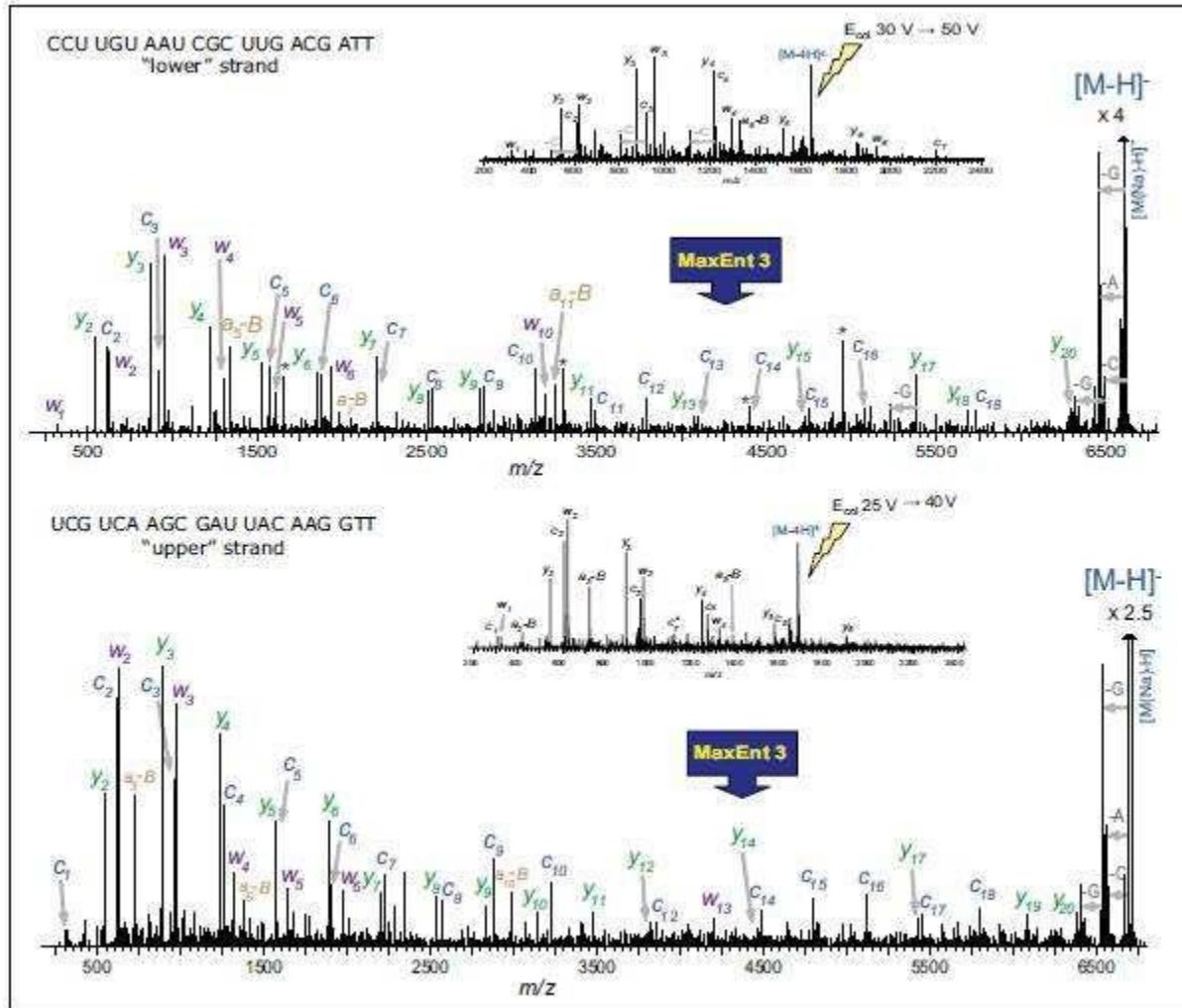


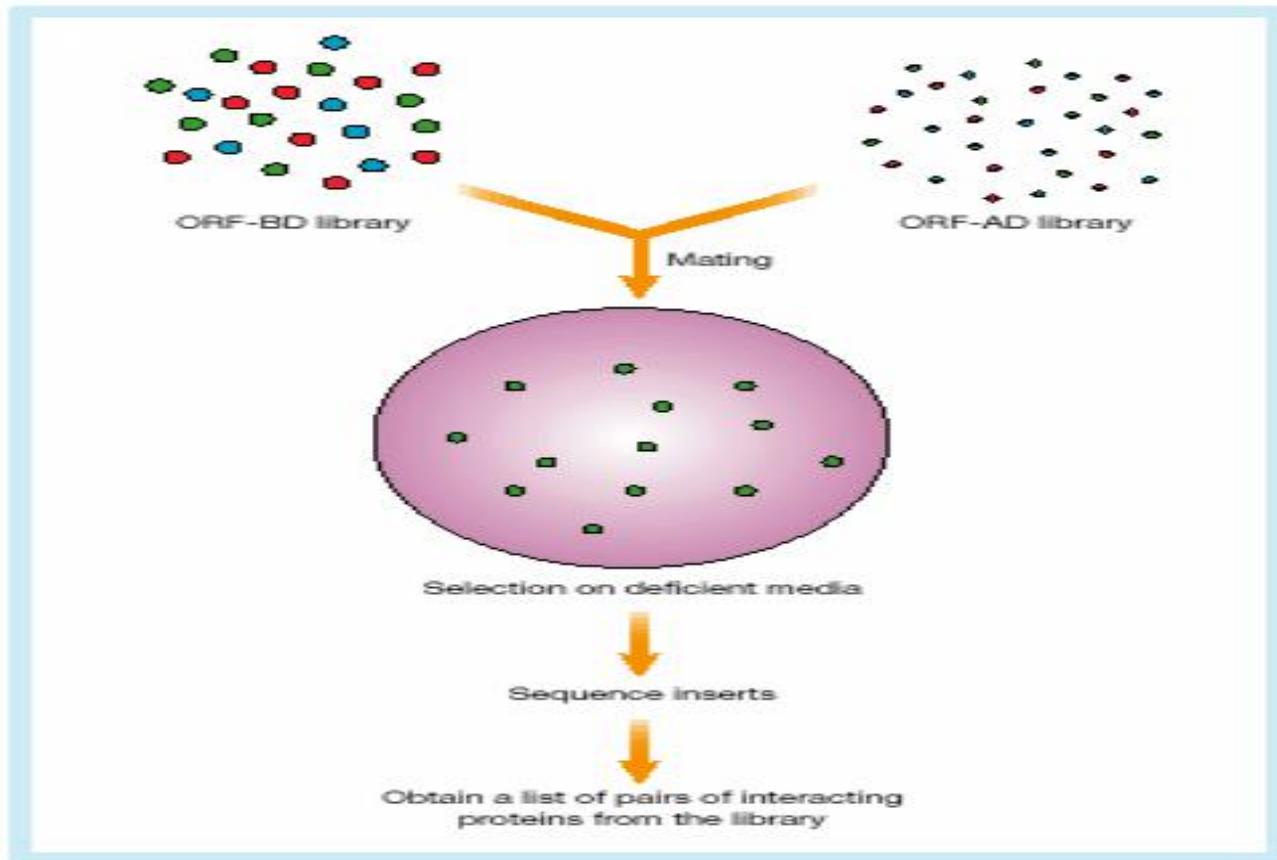
图2.21 核苷酸RNA寡核苷酸的MaxEnt3去卷积MS/MS图谱。星号为谐波峰(去卷积的结果)

Matrix method (two hybrid)



From: TRENDS in Genetics Vol.17, No.6, June 2001.

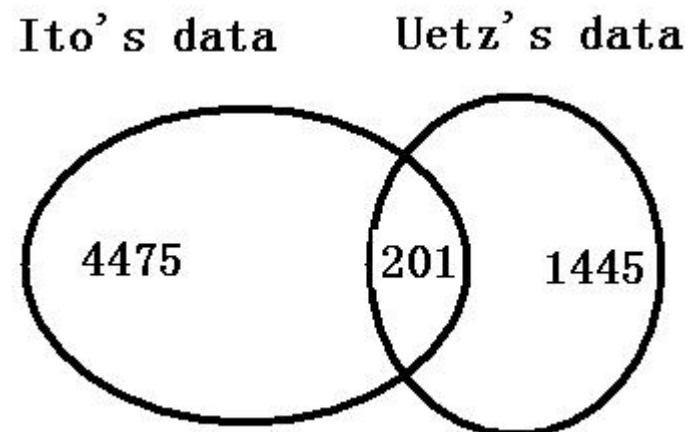
Interaction Sequence Tags (ISTs)



From: Nature 405, June 15, 2000, 837-846.

Two data sets from yeast two hybrid system

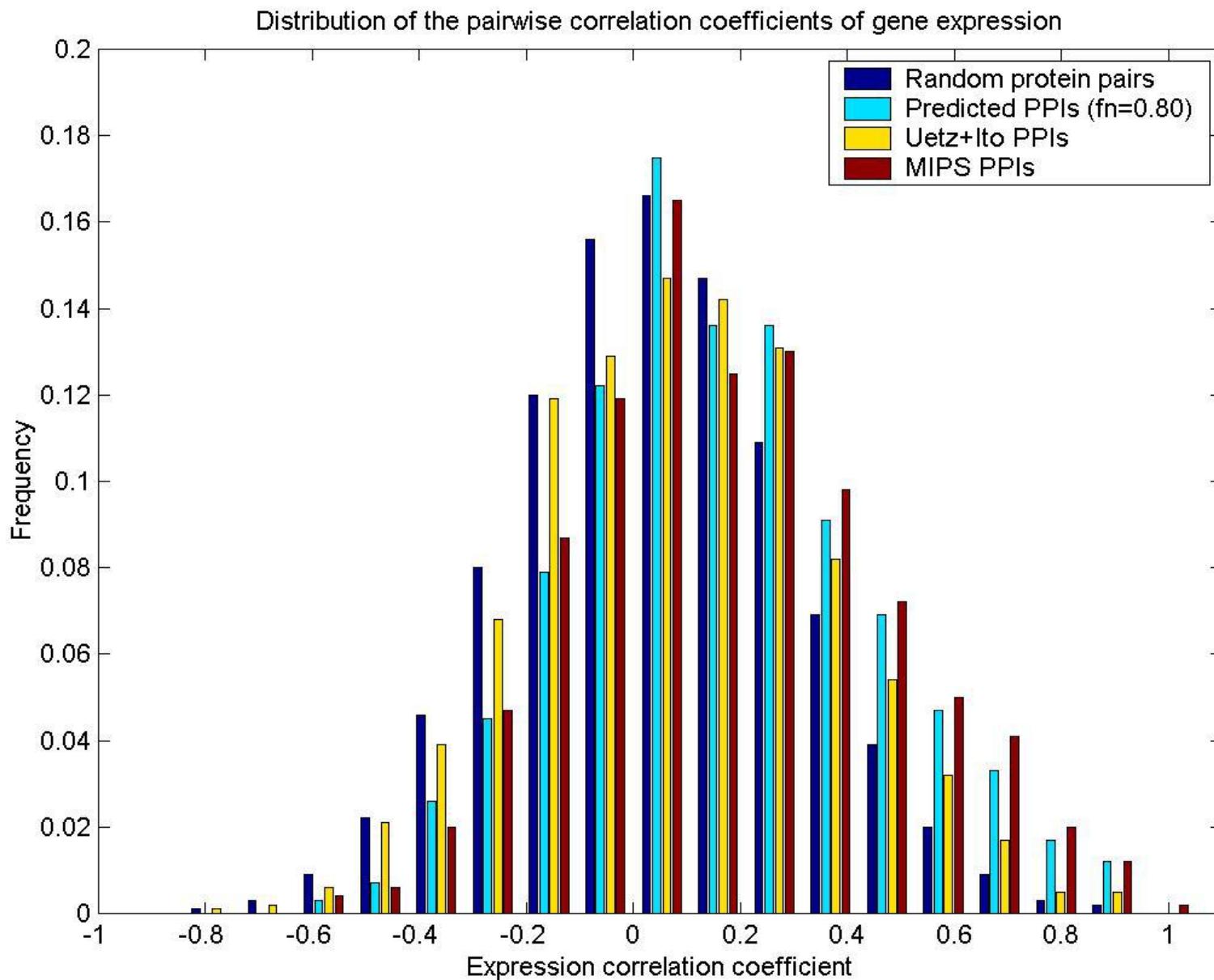
- Uetz's data (Uetz et al. 2000).
- Ito's data (Ito et al. 2000, 2001).

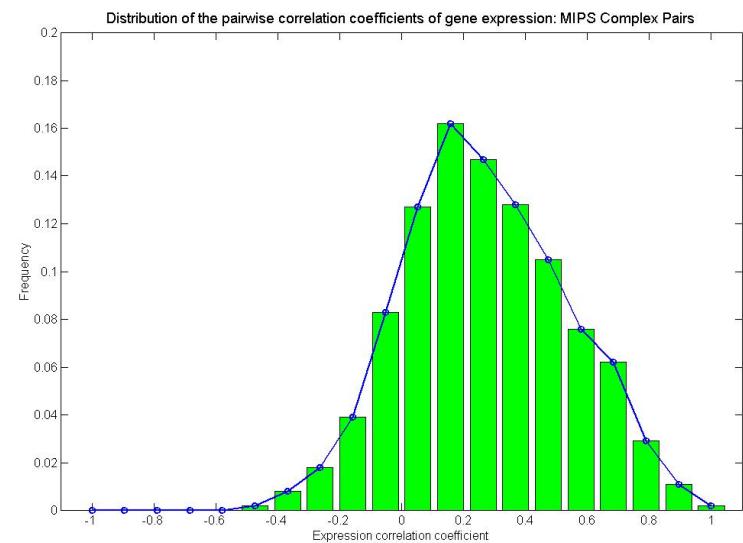
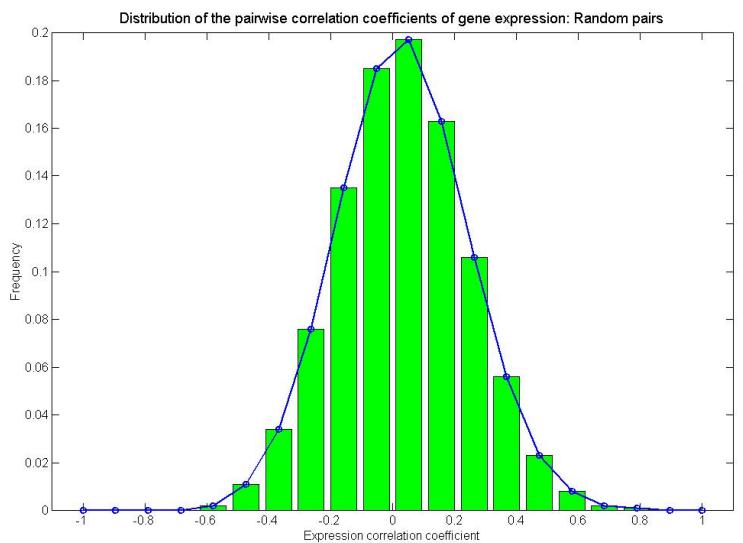


Possible Errors in 2-hybrid system

- False positive.
 - Possible mutation during PCR-amplifying.
 - Stochastic activation of reporter gene.
- False negative.
 - Membrane protein, post-translational modification protein, those self-activating reporter genes (Removed in experiment).
 - Weak interactions.

The size of interactome for yeast (5-50/protein)



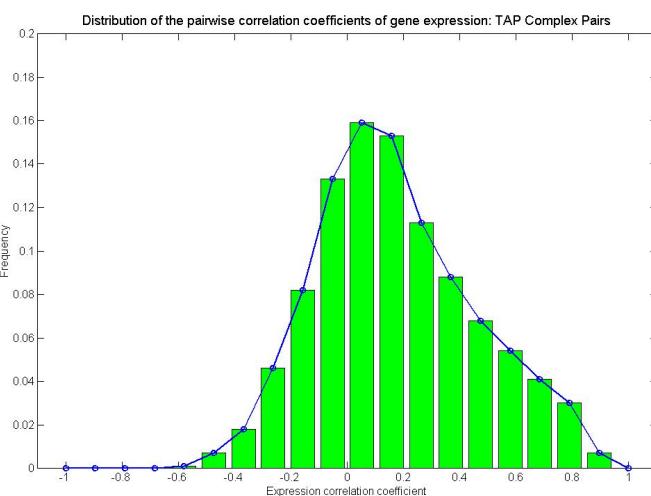


Non-interaction

$1 - \alpha$

Real interaction

α'



Observed interaction data

MLE of the reliability

- Likelihood function

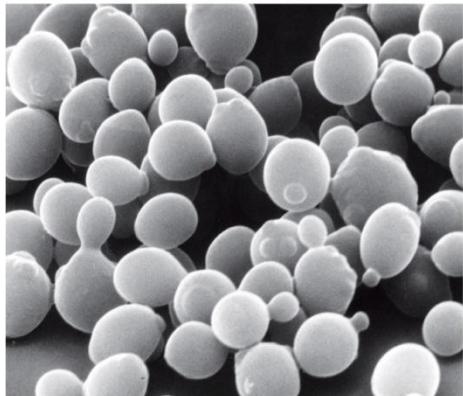
$$L(\alpha) = \prod_{k=1}^K (\alpha p_k + (1 - \alpha) q_k)^{n_k}$$

- Precision of the estimation

$$Var(\hat{\alpha}) = \frac{1}{\sum_{k=1}^K n_k \frac{(p_k - q_k)^2}{(\hat{\alpha} p_k + (1 - \hat{\alpha}) q_k)^2}}$$

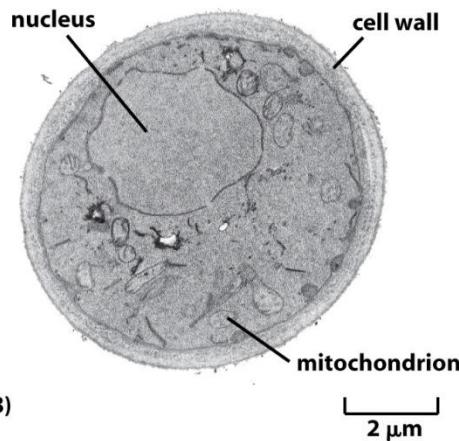
Budding Yeast

Saccharomyces Cerevisiae



(A)

10 μm



(B)

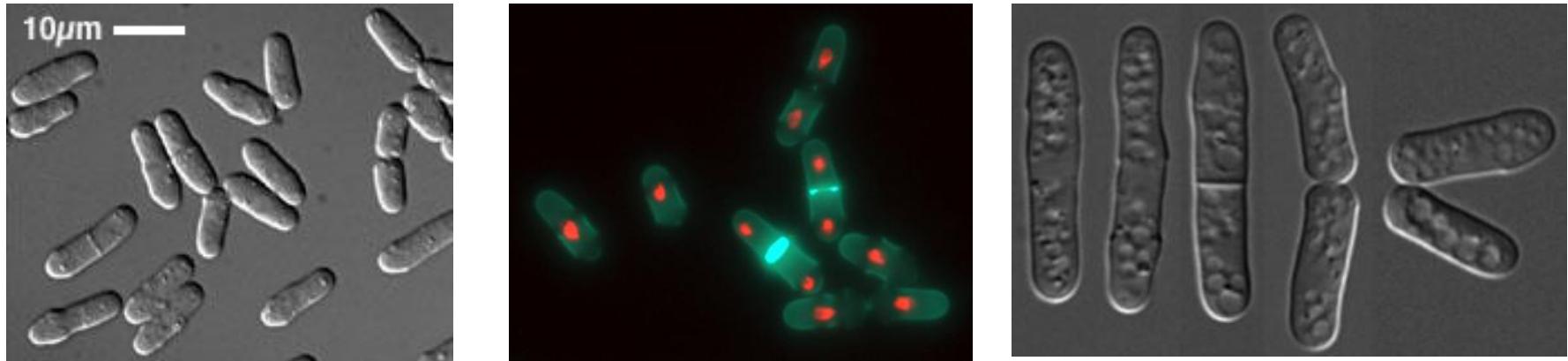
2 μm



- a and α mating type, cell cycle
- 6300 genes (1997)
- Genome-wide single mutants analysis (2000~)

Fission yeast

Schizosaccharomyces Pombe



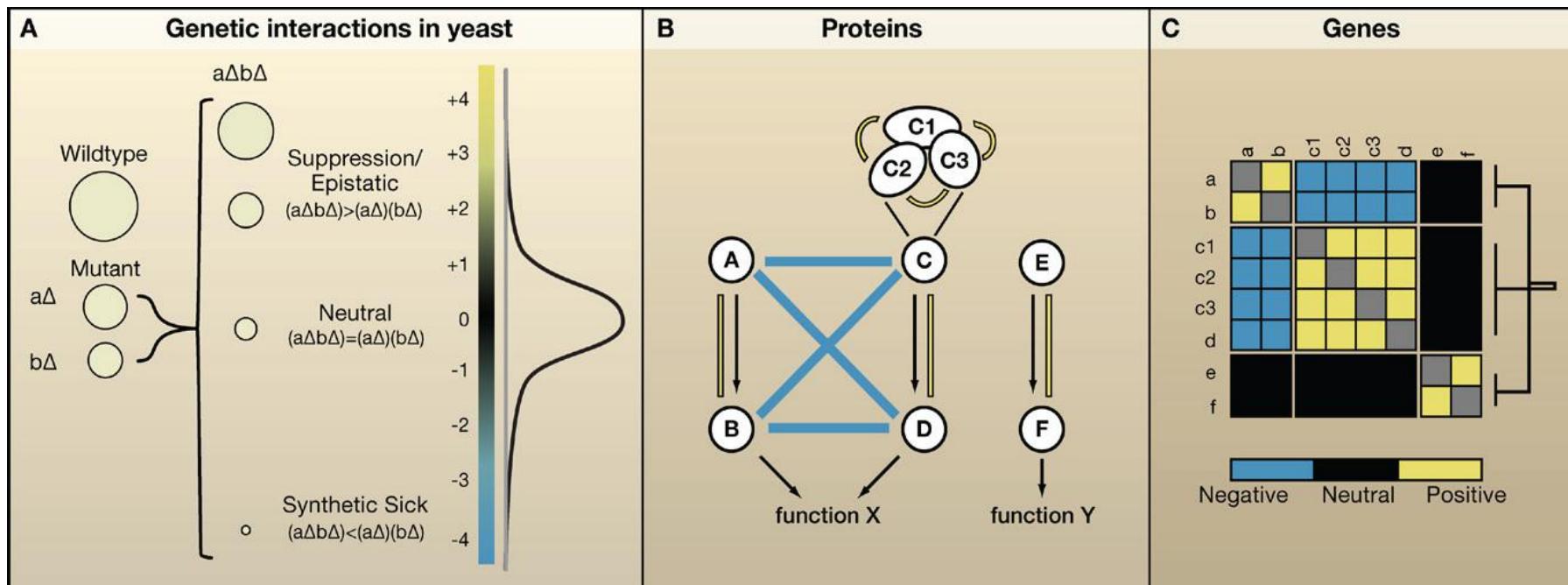
- 1000 million years separation from budding yeast;
- 13.8 Mb genome size, 4824 genes (open reading frames, OPF);
- 3 chromosomes, no genome-wide duplications; h+ and h- mating types;
- Cell cycle: 10% G1, 10% S, 70% G2 and 10% M phases.
- Genome-wide single mutants analysis (2010~)

more similar to metazoans than *S. cerevisiae*

- *cell cycle* regulation in G2/ M phase,
- gene regulation by the RNAi pathway
- the widespread presence of introns in genes

What's Genetic Interaction

- Genetic interactions between two loci can be mapped by measuring how the phenotype of an organism lacking both genes (double mutant) differs from that expected when the phenotypes of the single mutations are combined
- Null model: $F(\Delta AB) = F(\Delta A) * F(\Delta B)$

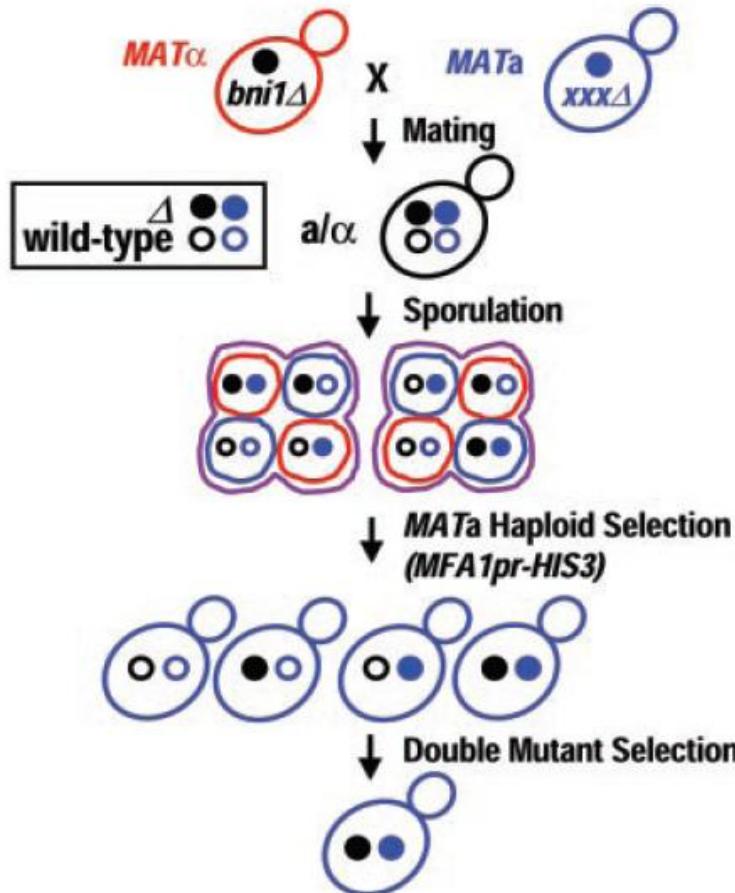


Identification of Genetic Interactions

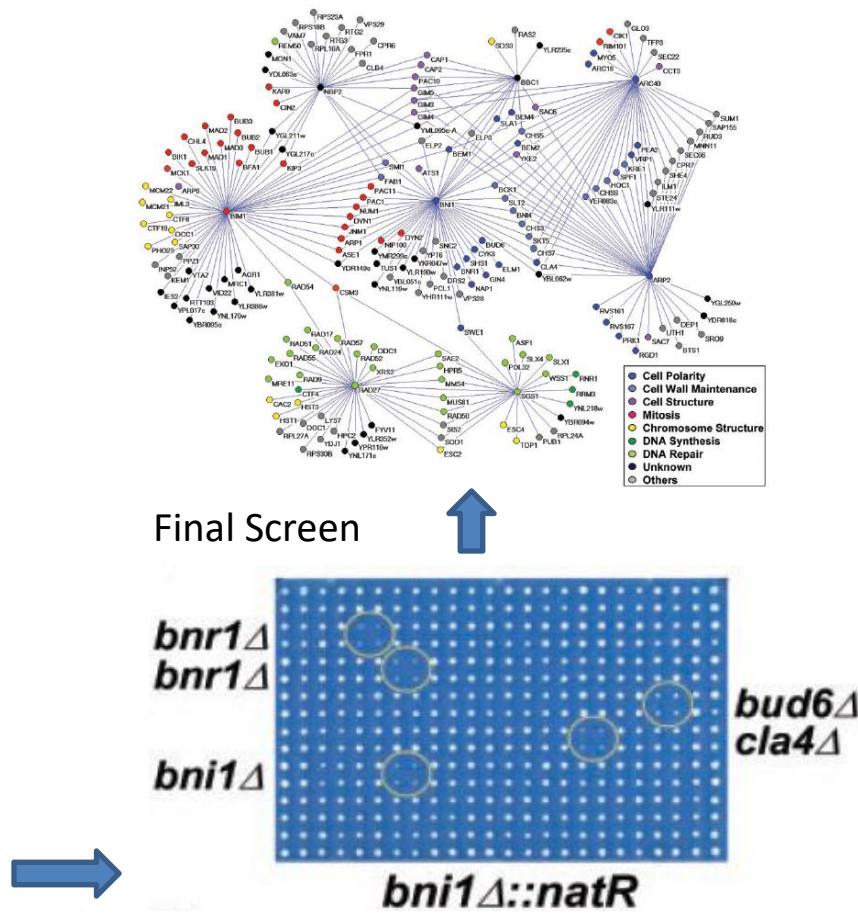
- Synthetic Gene Array (SGA) (Tong, et al. 2001)
- Diploid based Synthetic Lethality Analysis on Microarrays (dSLAM) (Pan, X., et al. 2004)

Synthetic Gene Array (SGA)

Synthetic genetic array methodology



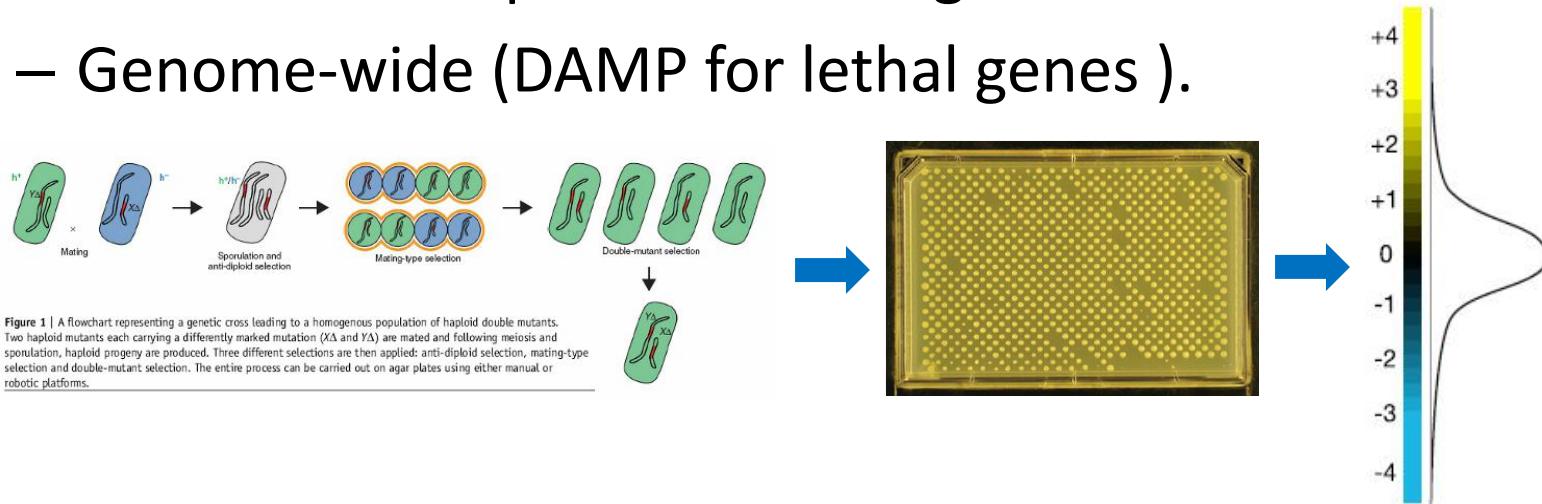
Genetic Interaction Network



Amy Hin Yan Tong, et al. *Science*, 2001.

EMAP is the Extension of SGA

- EMAP: Epistatic Miniarrray Profiles (Maya Schuldiner, et al. 2005. *Cell*)
- Quantitative measurement of phenotype (colony size)
 - Measure both positive and negative interactions.
 - Genome-wide (DAMP for lethal genes).

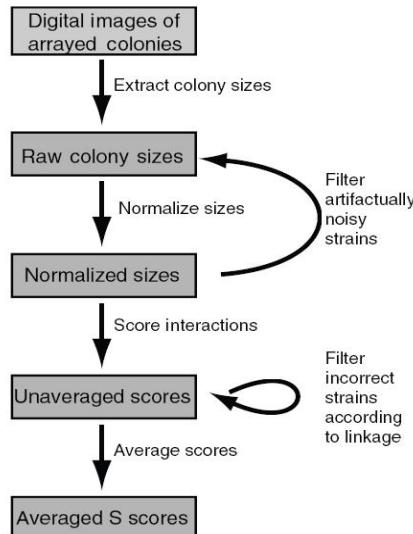


EMAP S-score

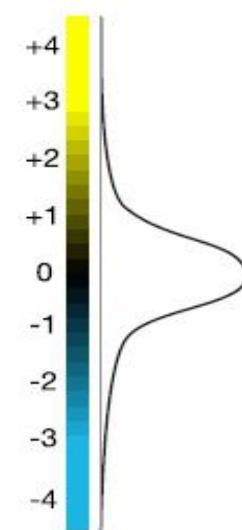
- Quantitative measure: $\epsilon = W_{ab} - W_a W_b$, $W_a = w/w_{wild}$.

No interaction	Synthetic sick/Lethality	Synthetic alleviating
$\epsilon = 0$	$\epsilon < 0$	$\epsilon > 0$

– T-Test with null hypothesis $\epsilon = 0$



$$S_0 = \frac{\mu_{ab} - w_a \mu_b}{\sqrt{n_1 S_{ab}^2 + n_2 w_a^2 S_b^2}}$$



PPI databases

- MIPS: Munich Information center for Protein Sequences (<http://mips.gsf.de>)
- DIP: Database of Interacting Proteins (<http://dip.doe-mbi.ucla.edu>)
- BIND: Biomolecular Interaction Network Database (<http://www.bind.ca>)
- GRID: General Repository for Interaction Datasets (<http://biodata.mshri.on.ca/grid>)
- MINT: Molecular Interaction Database (<http://cbm.bio.uniroma2.it/mint/>)

Further Reading

- For more experimental methods and databases, please read the following review paper
 - Shoemaker BA, Panchenko AR (2007) Deciphering Protein–Protein Interactions. Part I. Experimental Techniques and Databases. *PLoS Comput Biol* 3(3): e42. doi:10.1371/journal.pcbi.0030042.

Protein-protein interactions (Computational Methods)

- Gene fusion method (A.Enright 1999. E.Maccote 1999)
- Phylogenetic profile method (M.Pellegrini 1999, D.Eisenberg, 1999).
- Gene cluster method (R.Overbeek, 1999).
- Highly co-expressed gene pairs.

Part II: Predicting Protein-protein Interactions

- Some computational methods
- Predicting protein-protein interaction from domains
 - Association method
 - MLE method

Rosetta Stone Method

The Rosetta Stone method for detecting functional linkage

General concept

Rosetta Stone in organism 1 A1 B1
Protein A in organism 2 A
Protein B in organism 2 B

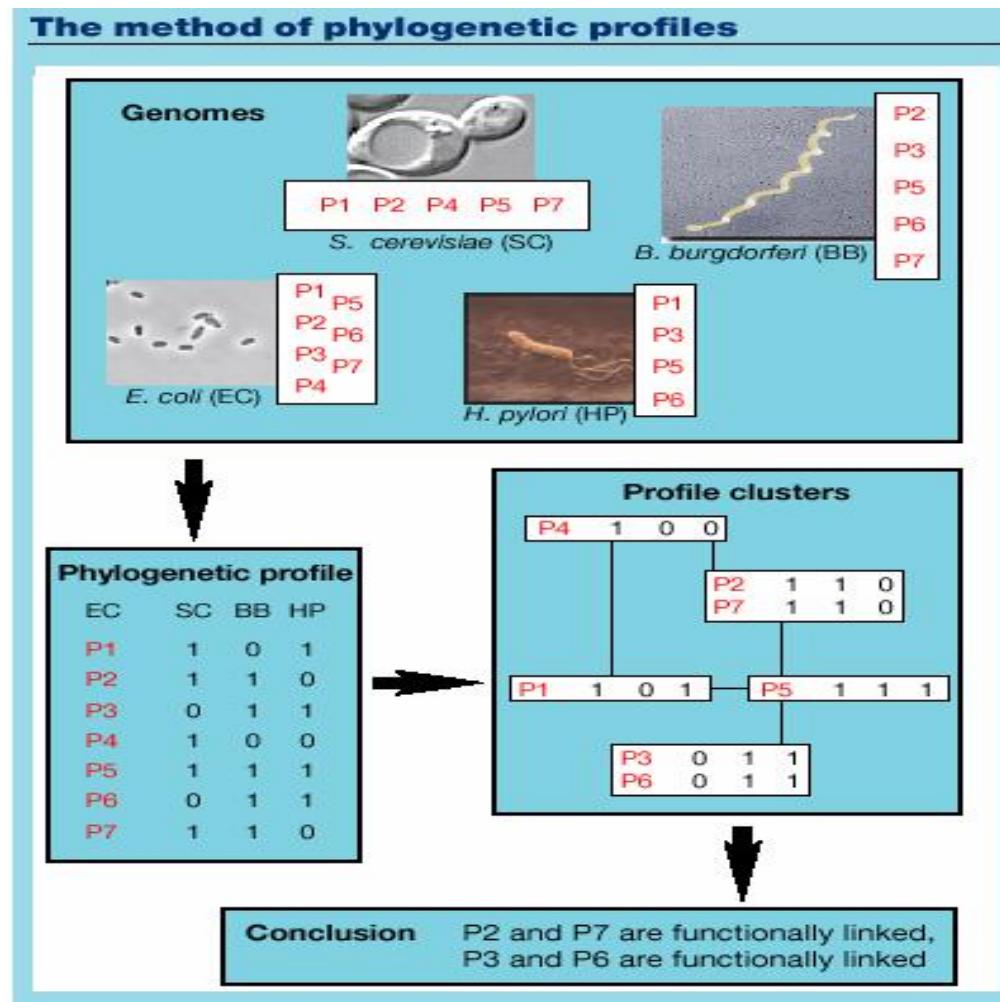
C. elegans

Ade 5,7,8
Yeast Pur2
Yeast Pur3

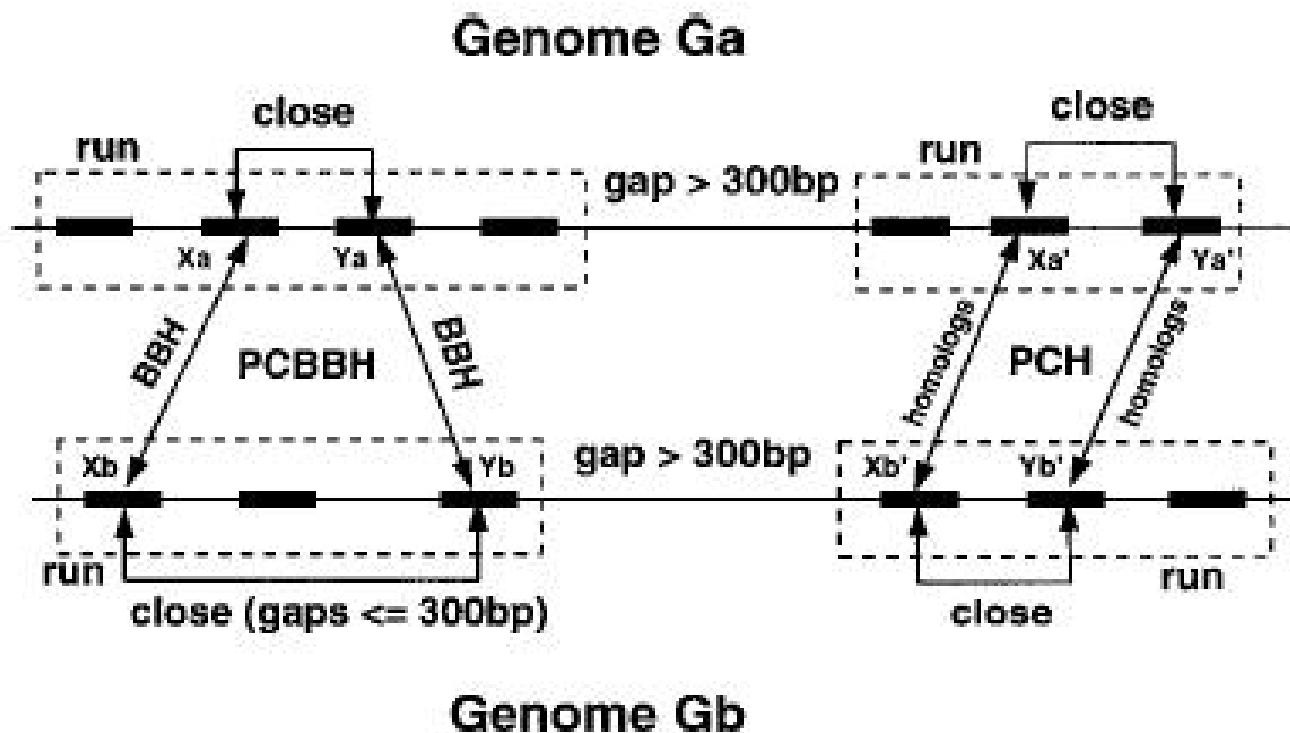
E. coli TrpC

Yeast TrpG
Yeast TrpF

Phylogenetic Profiles Method

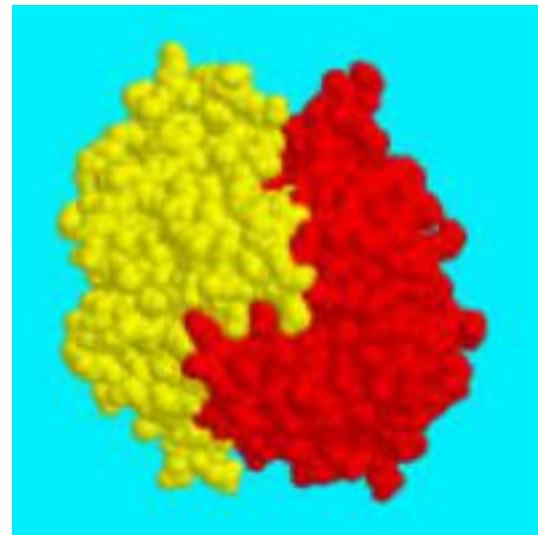


Using Gene Clusters to Infer Functional Coupling



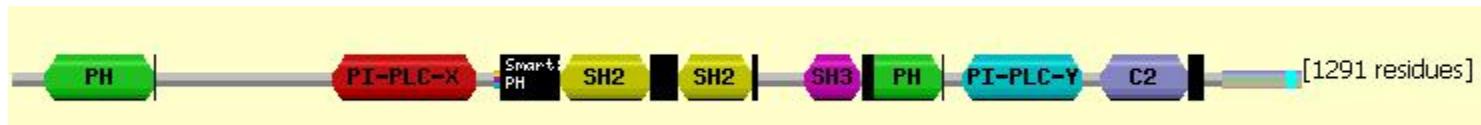
From: R.Overbeek, PNAS 96, 2896-2901, 1999.

Structure of Proteins



Predicting PPIs from Domains

- Domains are treated as elementary unit of function.
- Domains are responsible for the generation of interactions.
- Understanding protein-protein interaction at the domain level.



Domain Databases

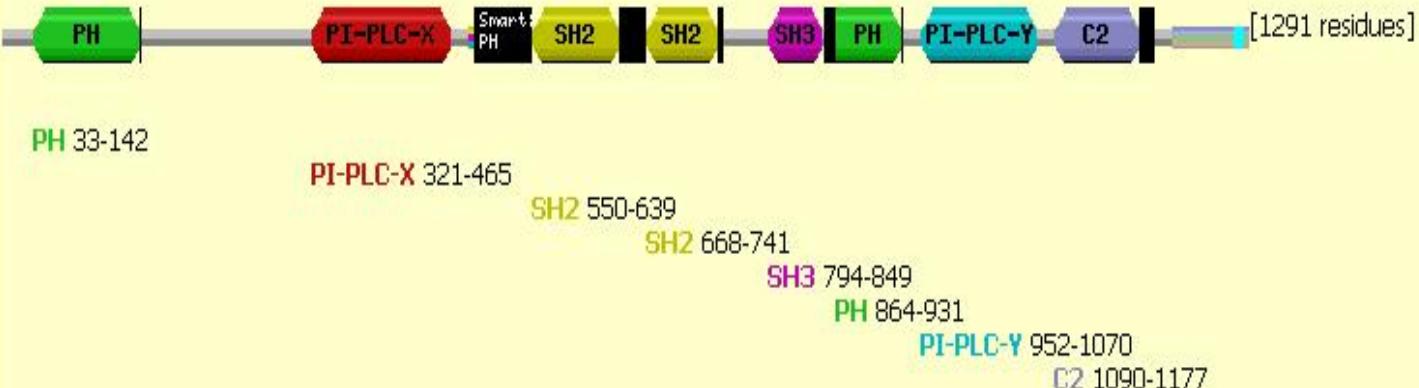
- Pfam, domain classification by HMM.
- Prodom.
- PRINTS, fingerprint information of protein sequences.
- SMART, mobile domain.
- BLOCKs, multiple alignment blocks.
- Interpro.

[Home](#) | [Keyword Search](#) | [Protein Search](#) | [Browse Pfam](#) | [DNA Search](#) | [Taxonomy](#) | [ftp](#) | [Help](#) | [SwissPfam](#)

SwissPfam entry for PIG1_BOVIN

Description from Swissprot for PIG1_BOVIN :

1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase gamma 1(ec 3.1.4.11) (plc-gamma-1) (phospholipase c-gamma-1) (plc-ii)(plc-148)


Key


Source	Domain	Start	End
Pfam	PH	33	142
Pfam	PI-PLC-X	321	465

Overlapping Domains: Change the domain order using the ^ and v buttons. View the changes by clicking the 'Change order' button.

high priority

Piwi

[Edit Wikipedia article](#)

Piwi (or PIWI) genes were identified as regulatory proteins responsible for stem cell and germ cell differentiation.^[4] Piwi is an abbreviation of *p*-element Induced *W*impy testis in Drosophila.^[5] Piwi proteins are highly conserved RNA-binding proteins and are present in both plants and animals.^[6] Piwi proteins belong to the Argonaute/Piwi family and have been classified as nuclear proteins. Studies on Drosophila have also indicated that Piwi proteins have slicer activity conferred by the presence of the Piwi domain.^[7] In addition, Piwi associates with Heterochromatin protein 1, an epigenetic modifier, and piRNA-complementary sequences. These are indications of the role Piwi plays in epigenetic regulation. Piwi proteins are also thought to control the biogenesis of piRNA as many Piwi-like proteins contain slicer activity which would allow Piwi proteins to process precursor piRNA into mature piRNA.

Contents

[\[hide\]](#)

- 1 Protein structure and function
- 2 Human Piwi proteins
- 3 Role in germline cells
- 4 Role in RNA interference
- 5 piRNAs and transposon silencing
- 6 References
- 7 External links

Protein structure and function

The structure of several Piwi and Argonaute proteins (Ago) have been solved. Piwi proteins are RNA-binding proteins with 2 or 3 domains: The N-terminal PAZ domain binds the 3'-end of the guide RNA; the middle MID domain binds the 5'-phosphate of RNA; and the C-terminal PIWI domain acts as an RNase H endonuclease that can cleave RNA.^{[8][9]} The small RNA partners of Ago proteins are microRNAs (miRNAs). Ago proteins utilize miRNAs to silence genes post-transcriptionally or use small-interfering RNAs (siRNAs) in both transcription and post-transcription silencing mechanisms. Piwi proteins interact with piRNAs (28–33 nucleotides) that are longer than miRNAs and siRNAs (~20 nucleotides), suggesting that their functions are distinct from those of Ago proteins.^[8]

Human Piwi proteins

Presently there are four known human Piwi proteins—PIWI-like protein 1, PIWI-like protein 2, PIWI-like protein 3 and PIWI-like protein 4. Human Piwi proteins all contain two RNA binding domains, PAZ and Piwi. The four PIWI-like proteins have a spacious binding site within the PAZ domain which allows them to bind the bulky 2'-OCH₃ at the 3' end of piwi-interacting RNA.^[10]

One of the major human homologues, whose upregulation is implicated in the formation of tumours such as seminomas, is called hiwi (for human in wi).^[11]

Homologous proteins in mice have been called miwi (for mouse in wi).^[12]

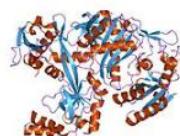
Role in germline cells

PIWI proteins play a crucial role in fertility and germline development across animals and ciliates. Recently identified as a polar granule component, PIWI proteins appear to control germ cell formation so much so that in the absence of PIWI proteins there is a significant decrease in germ cell formation. Similar observations were made with the mouse homologs of PIWI, MILI, MIWI and MIWI2. These homologs are known to be present in spermatogenesis. Miwi is expressed in various stages of spermatocyte formation and spermatid elongation where Miwi2 is expressed in Sertoli cells. Mice deficient in either Mili or Miwi-2 have experienced spermatogenic stem cell arrest and those lacking Miwi-2 underwent a degradation of spermatogonia.^[13] The effects of piwi proteins in human and mouse germlines seems to stem from their involvement in translation control as Piwi and the small noncoding RNA, piwi-interacting RNA (piRNA), have been known to co-fractionate polysomes. The piwi-piRNA pathway also induces heterochromatin formation at centromeres,^[14] thus affecting transcription. The piwi-piRNA pathway also appears to protect the genome. First observed in Drosophila, mutant piwi-piRNA pathways led to a direct increase in dsDNA breaks in ovarian germ cells. The role of the piwi-piRNA pathway in transposon silencing may be responsible for the reduction in dsDNA breaks in germ cells.

Role in RNA interference

The piwi domain^[15] is a protein domain found in piwi proteins and a large number of related nucleic acid-binding proteins, especially those that bind and cleave RNA. The function of the domain is double stranded-RNA-guided hydrolysis of single stranded-RNA that has been determined in the argonaute family of related proteins.^[1] Argonautes, the most well-studied family of nucleic-acid binding proteins, are RNase H-like enzymes that carry out the catalytic functions of the RNA-induced silencing complex (RISC). In the well-known cellular process of RNA interference, the argonaute protein in the RISC complex can bind both small interfering RNA (siRNA) generated from exogenous double-stranded RNA and microRNA (miRNA)

Piwi domain

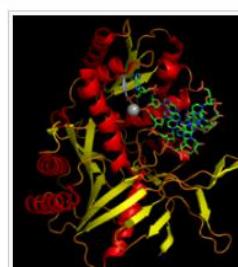


Structure of the Pyrococcus furiosus Argonaute protein.^[1]

Identifiers

Symbol	Pivi
Pfam	PF02171
InterPro	IPR003165
PROSITE	PS50822
CDD	cd02826

Available protein structures: [\[show\]](#)



The piwi domain of an argonaute protein with bound siRNA, components of the RNA-induced silencing complex that mediates gene silencing by RNA interference.



Key: █ PAZ domain █ Piwi domain

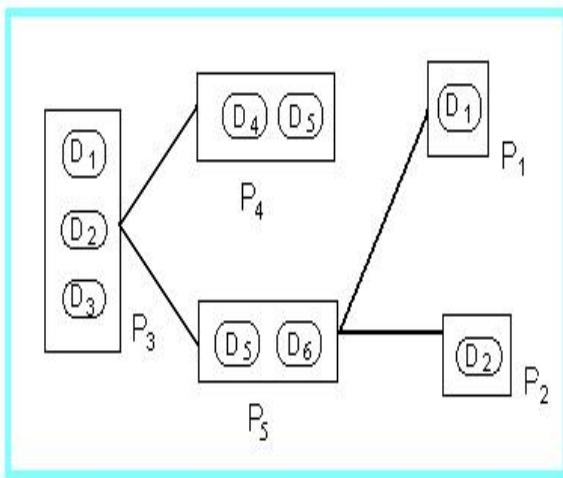
All human Piwi proteins and argonaute proteins have the same RNA binding domains, PAZ and Piwi.^[2]

Association-A simple method

$$V(D_{ij}) = \frac{\#\{\text{Interacted protein pairs contain } D_{ij}\}}{\#\{\text{All protein pairs contain } D_{ij}\}}$$

More observed PPIs for one domain pair will give higher probability of interaction for that domain pair.

Simple Example



By association method:

$$D_{34} = D_{35} = D_{36} = D_{26} = D_{16} = 1.0$$

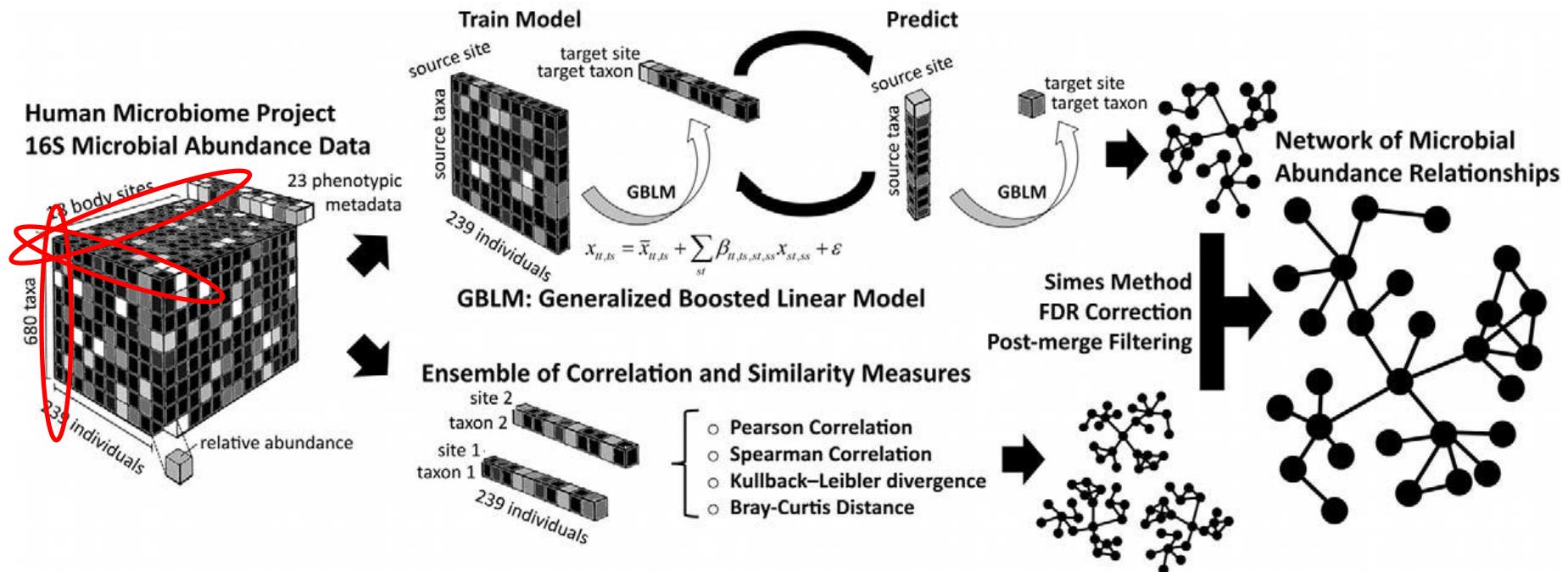
$$D_{15} = D_{25} = 0.75, D_{14} = D_{24} = 0.5$$

Others are 0.0.

$$D_{15}: \{P_{34}, P_{35}, P_{15}\} / \{P_{34}, P_{35}, P_{15}, P_{14}\} = 0.75$$

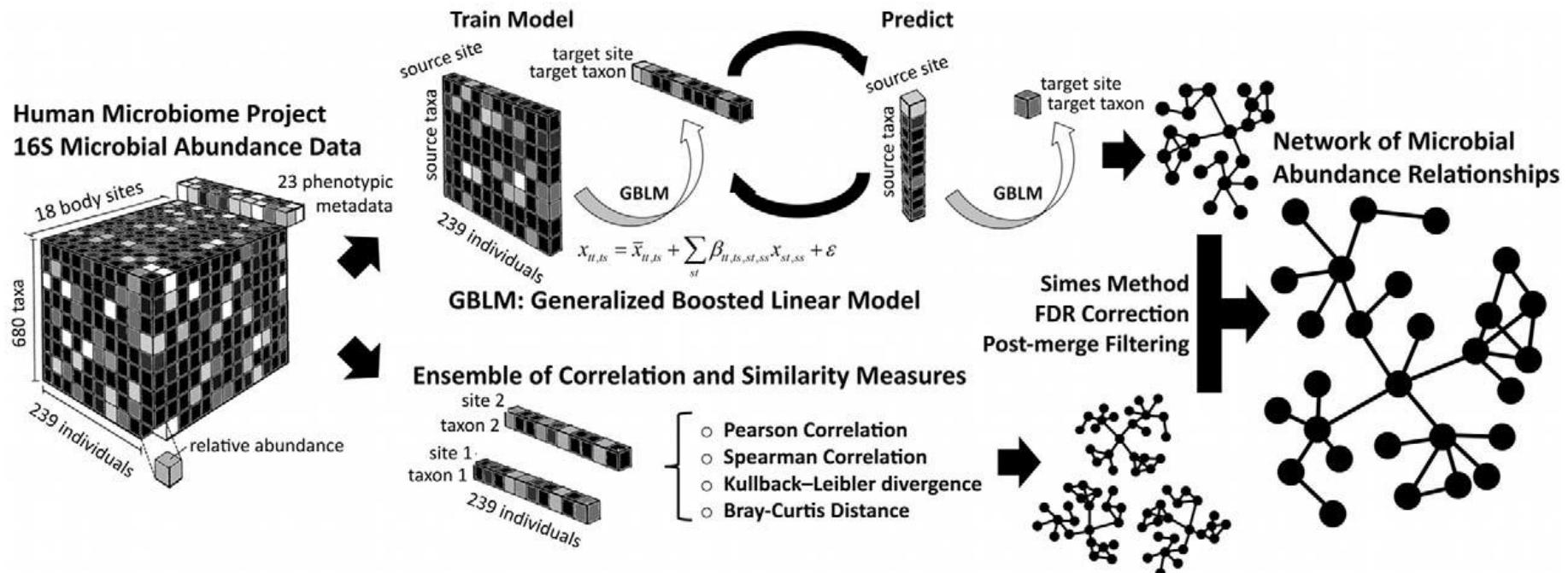
More complicated example

Generalized Boosted Linear Models (GBLM): 广义线性模型



More complicated example

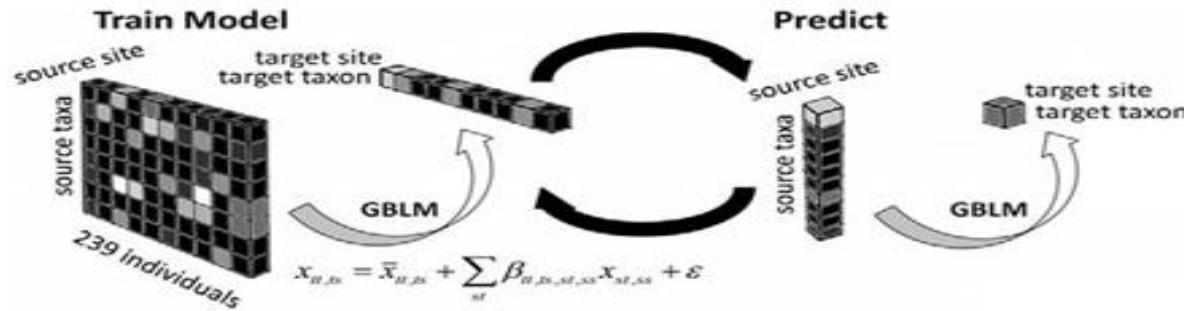
Generalized Boosted Linear Models (GBLM): 广义线性模型



Ensemble scoring

More complicated example

Generalized Boosted Linear Models (GBLM): 广义线性模型



$$x_{tt,ts} = \bar{x}_{tt,ts} + \sum_{st} \beta_{tt,ts,st,ss} x_{st,ss}$$

$$\text{logit}(x_{tt,ts}) = \bar{x}_{tt,ts} + \sum_{st} \beta_{tt,ts,st,ss} x_{st,ss}$$

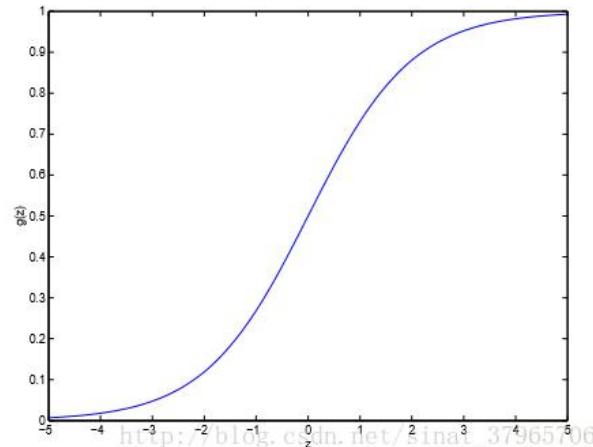
Huttenhower, et al., *PLoS Computational Biology*, 2013

More complicated example

Generalized Linear Models (GLM): 广义线性模型

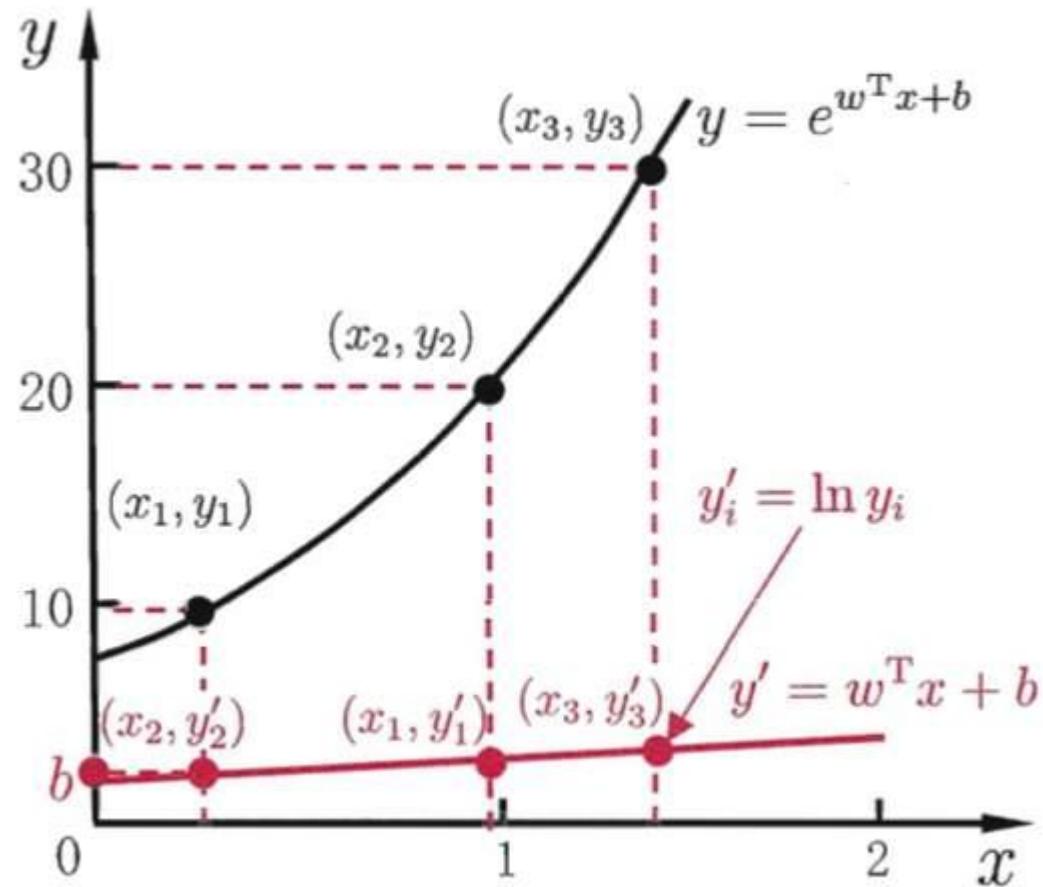
广义线性模型的核心体现在：

- y 服从指数族分布(包括高斯分布，伯努利分布，多项式分布，泊松分布， beta 分布.....)，且同个样本的 y 必须服从同个分布
- 接着在具体分布中比较与指数分布族之间的参数关系，最重要的就是具体分布的参数(Φ)和指数分布参数(η)之间的关系



More complicated example

Generalized Linear Models (GLM): 广义线性模型



Limitation of Association Method

- For multiple-domain proteins, this method computes the value for a certain domain pair ignoring the value of other domain-domain pairs. So it's a local one.
- This method cannot deal with possible error of the data.

Probabilistic Model

- Domain-domain interactions are independent, which means that the event that two domains interact or not does not depend on other domains.
- Two proteins interact if and only if at least one pair of domains from the two proteins interact.

Yeast Data

- Interactions (Uetz's and Ito's interaction data).
- Domain: Pfam (Pfam-A, Pfam-B).
- Proteins: SGD, N=6359.

Protein Interaction Data Sources

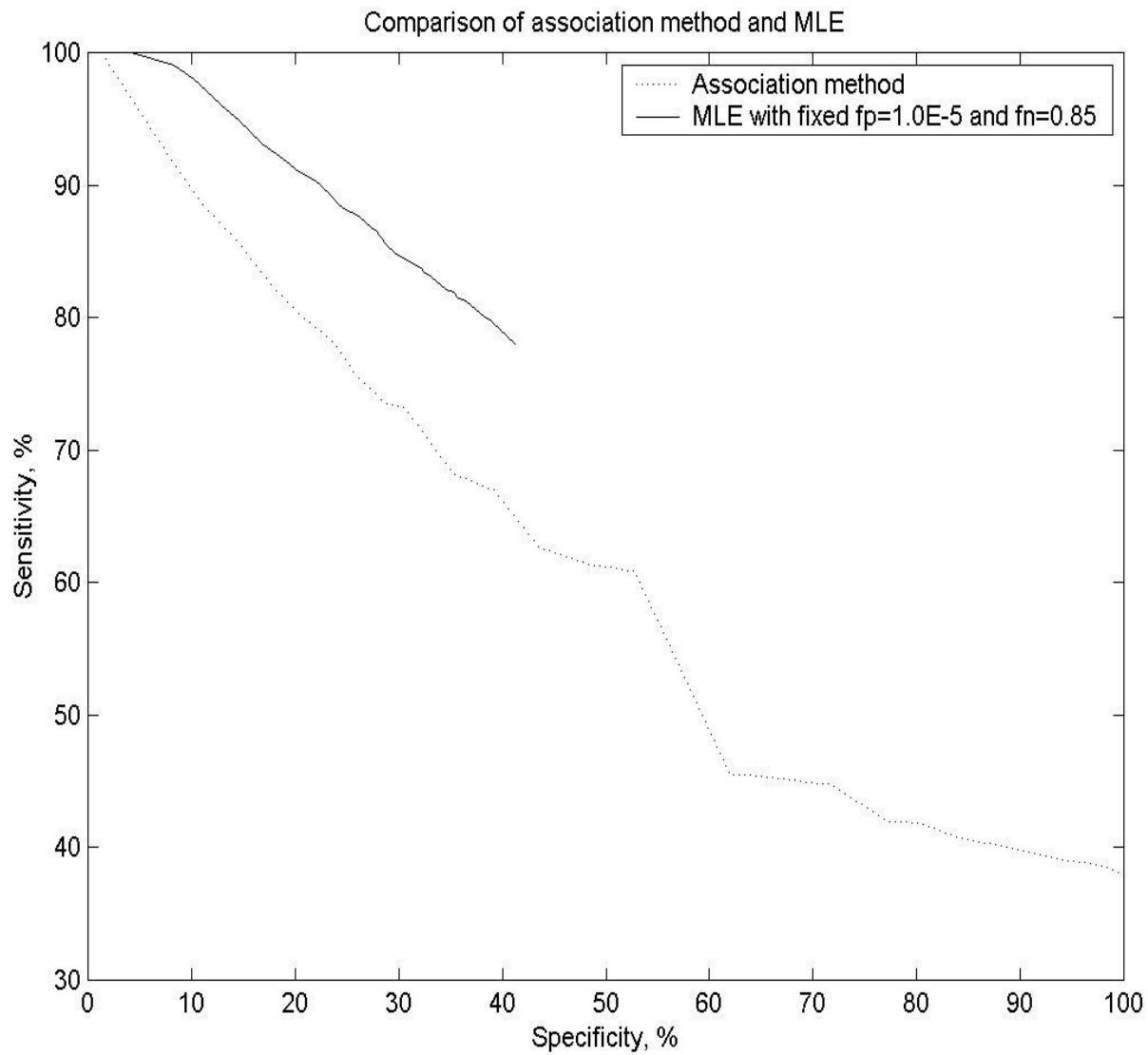
	Proteins	Pfam domains	Super - domains	PPI
Uetz	1337	1330	313	1445
Ito	3277	2776	909	4475
Uetz+Ito	3729	3124	1007	5719
Overlap	855	964	215	201

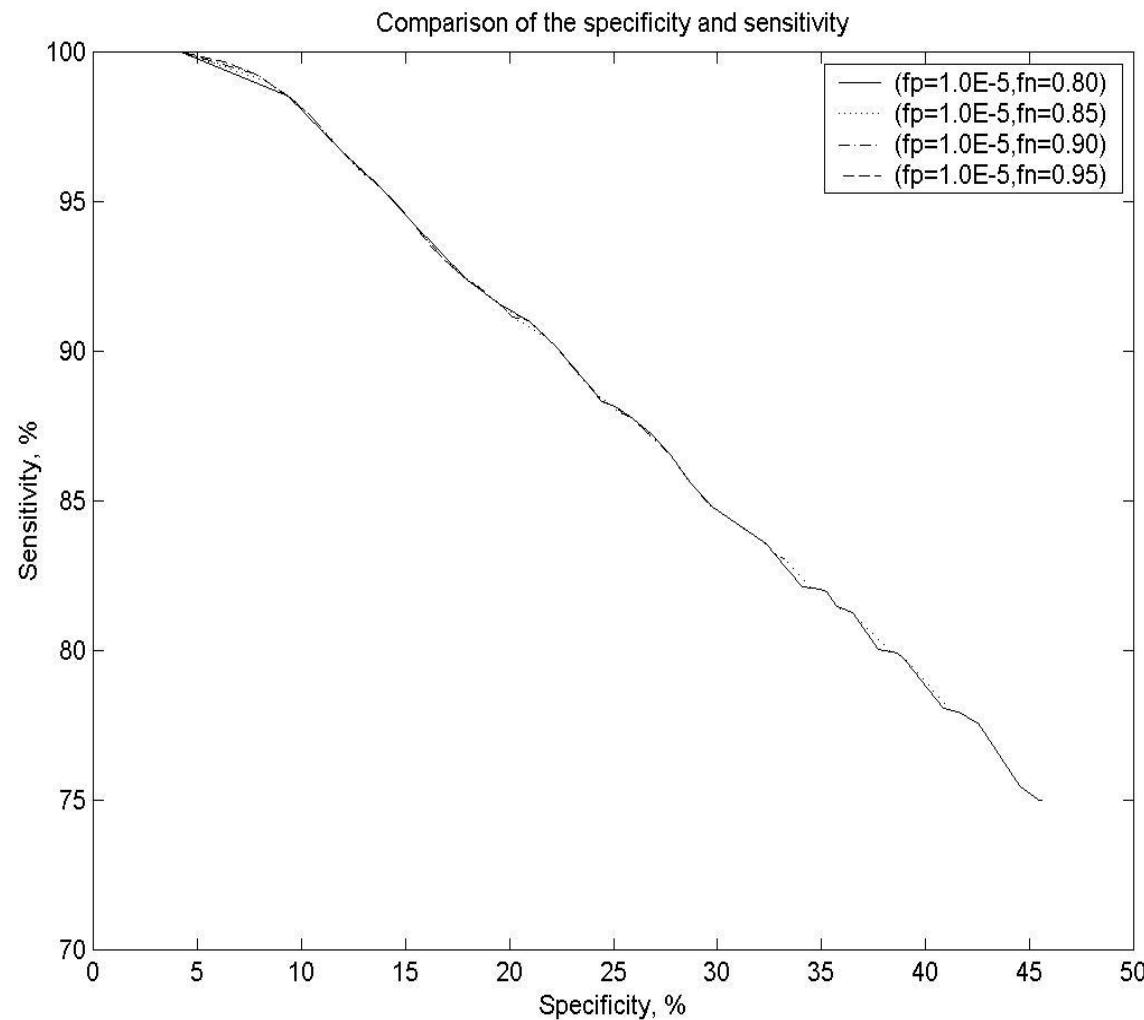
Measure the Accuracy

- Specificity and sensitivity.
- Verification by MIPS physical interactions (as TRUE interactions).
- Relationship between protein-protein interactions and expression data.

$$SP = \frac{\text{number of matches with observation}}{\text{number of prediction}}$$

$$SN = \frac{\text{number of match with observation}}{\text{number of observation}}$$





Verification by Known PPIs

- MIPS physical interaction. (Totally 2570 PPIs, 1414 PPIs not overlapping with our training set).
- Compare with random matching.
 - Fold number
 - Larger fold number imply more reliable prediction

$$\# \text{Fold} = \frac{\#\{\text{Our prediction matched to MIPS}\}}{\#\{\text{Expectation of random pairs matched to MIPS}\}}$$

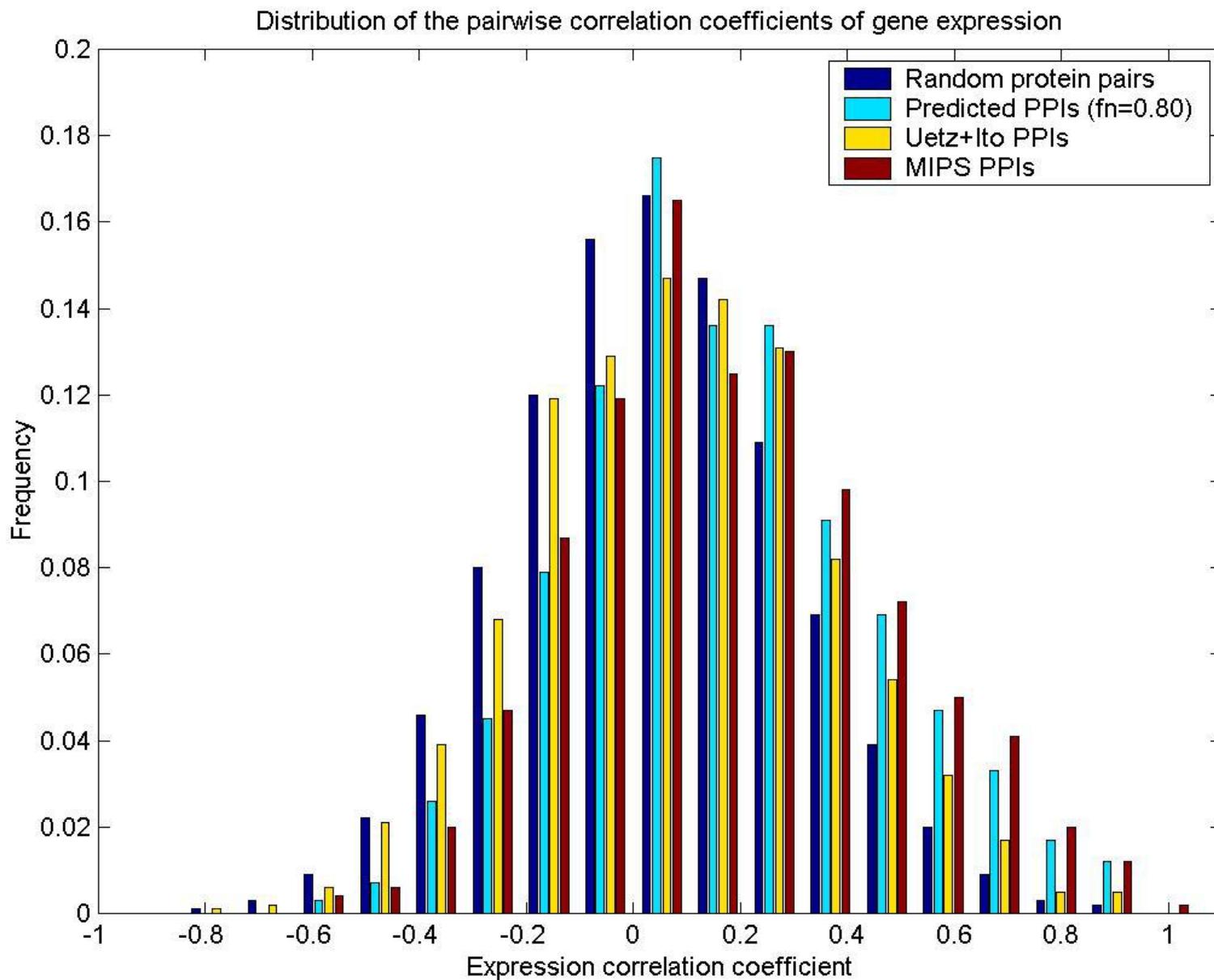
Think about FDR again...

Matching with MIPS PPIs

Prob	#Predict	#Train	#MIPS		#Fold
All	20221620	5719	2570	1414	1.00
>0.00	136463	5719	1265	109	11.92
>=0.20	26908	5238	1093	53	34.97
>=0.40	19360	5018	1035	48	47.85
>=0.60	14725	4775	971	47	67.53
>=0.80	12734	4647	932	43	76.02
>=0.97	10824	4461	886	40	89.88
5					

Interaction Data Correlated With Gene Expression Data

- Interacted proteins seems to have high expression correlation
 - A. Grigorieve *Nucleic Acid Res.* 29, 2001;
 - H. Ge et al. *Nature Genetics* 29, 2001;
 - R. Jansen et al. *Genome Res.* 12, 2002.
- Expression data (M. Eisen, 1998); 2465 Yeast ORFs with 79 data points/ORF.
- Pearson correlation coefficient.



Statistics of Pairwise Correlation of Gene Expression

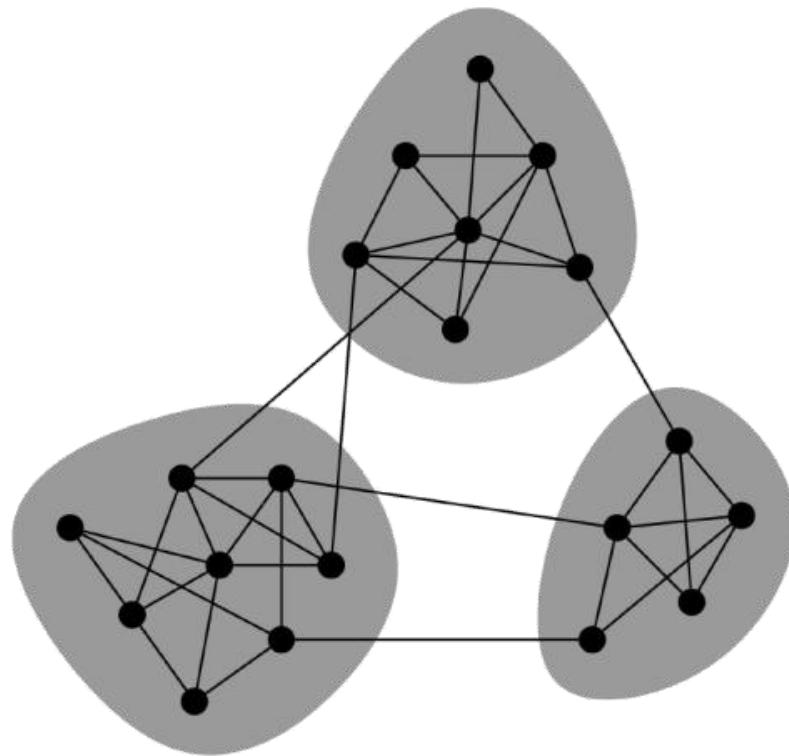
pairs	# pairs	mean	std	T-score	p-value	$R^* > 0.5$
All ORFs	3036880	0.0428	0.2473	0.0000	5.000e-01	3.84%
≥ 0.20	6392	0.0514	0.2550	2.7984	2.575e-03	4.79%
≥ 0.40	4433	0.0510	0.2538	2.2232	1.311e-02	4.96%
≥ 0.60	3318	0.0598	0.2579	3.9644	3.715e-05	5.42%
≥ 0.80	2756	0.0626	0.2622	4.2196	1.238e-05	5.88%
≥ 0.975	2266	0.0628	0.2637	3.8482	6.002e-05	5.87%
Uetz+Ito	1307	0.0586	0.2587	2.3213	1.015e-02	5.20%
MIPS	1106	0.1109	0.2767	9.1619	2.706e-20	8.23%

$$T = \frac{\mu_1 - \mu_2}{\sqrt{\frac{1}{n_1} + \frac{1}{n_2}} \sqrt{\frac{(n_1-1)S_1^2 + (n_2-1)S_2^2}{n_1+n_2-2}}}$$

第8-3章： Network Module

- Definition
- Module detection
- Bayesian approach
- Markov clustering algorithm

Network Modular



Modularity

- Suppose we are given a candidate division of the vertices into some number of groups. The modularity of this division is defined to be the fraction of the edges that fall within the given groups minus the expected such fraction if edges were distributed at random.

[http://en.wikipedia.org/wiki/Modularity_\(networks\)](http://en.wikipedia.org/wiki/Modularity_(networks))

Modularity

- A_{ij} : adjacency matrix
- k_i : degree
- m : total number of edges

$$Q = \frac{1}{2m} \sum_{ij} (A_{ij} - \frac{k_i k_j}{2m}) \delta(c_i, c_j)$$

Modularity

- For two class problem, let $s_i=1$ if node i belongs to group 1 and $s_i=-1$ if it belongs to group 2,

$$\delta(c_i, c_j) = \frac{1}{2}(s_i s_j + 1)$$

$$Q = \frac{1}{4m} \sum_{ij} S^T B S$$

$$B = (B_{ij}), B_{ij} = A_{ij} - \frac{k_i k_j}{2m}$$

$$S = (s_1, \dots, s_n)^T$$

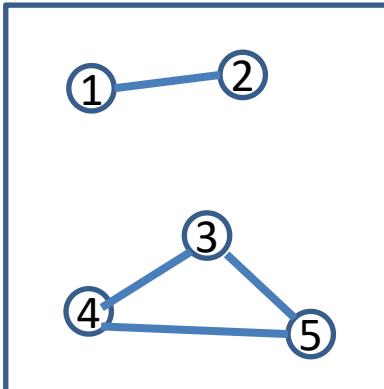
Example

$$A = \begin{pmatrix} 0 & 1 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 1 \\ 0 & 0 & 1 & 0 & 1 \\ 0 & 0 & 1 & 1 & 0 \end{pmatrix} \quad m = 4, k_1 = k_2 = 1 \\ k_3 = k_4 = k_5 = 2$$





$$B = \frac{1}{8} \begin{pmatrix} -1 & 7 & -2 & -2 & -2 \\ 7 & -1 & -2 & -2 & -2 \\ -2 & -2 & -4 & 4 & 4 \\ -2 & -2 & 4 & -4 & 4 \\ -2 & -2 & 4 & 4 & -4 \end{pmatrix}$$



Spectrum Method

- The largest eigenvectors will give the best grouping, positive entries corresponding to one class, and negative ones corresponding to another class.
- This can be achieved by power method

$$\lim_{k \rightarrow +\infty} \frac{A^k e}{e^T A^k e} = w$$

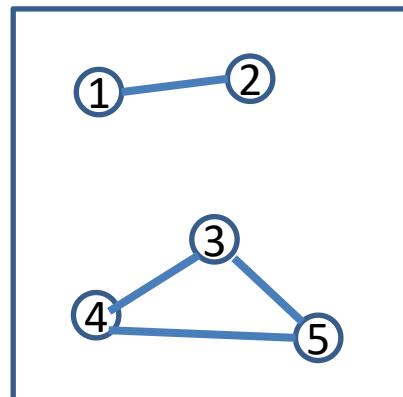
where $e = (1, 1, \dots, 1)^T$

Example

- 对于上述矩阵B, 可以计算出最大特征值为10, 对应的特征向量

$$v = (-0.55, -0.55, 0.37, 0.37, 0.37)$$

- 于是我们对节点的划分为{1,2}; {3,4,5}



优化方法

- 既然现在有一个衡量划分“好坏”的量 Q , 那么一般的优化方法都可以使用;
 - 1. 给定初始划分
 - 2. 对于划分的某种修正, 计算 Q 的改变量
 - 3. 依据一定的原则考虑是否接受这种修正, 重复步骤2, 直到某种收敛条件满足。
- Greedy方法
- 模拟退火方法

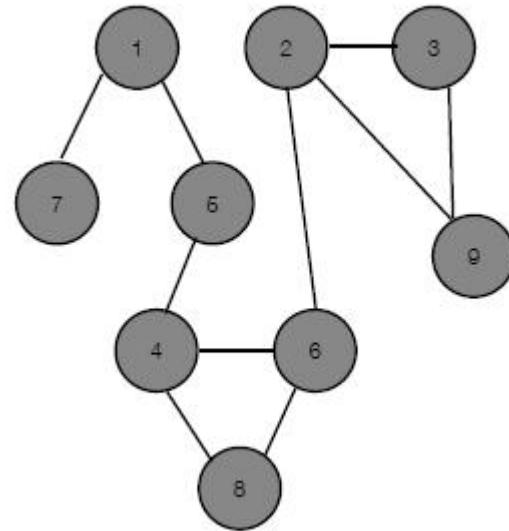
A Bayesian Approach to Network Modularity

Slides for this part are mainly from
Hofman's talk

www.jakehofman.com/talks/apam_20071019.pdf

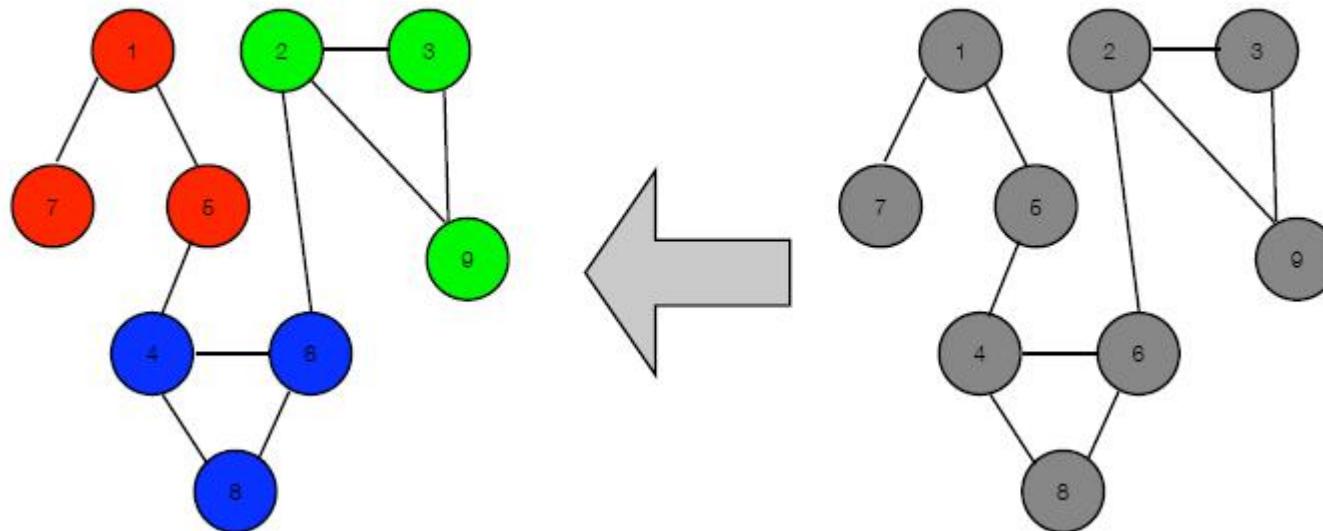
Overview: Modular Networks

- Given a network
 - Assign nodes to modules?
 - Determine number of modules(scale/complexity)?



Overview: Modular Networks

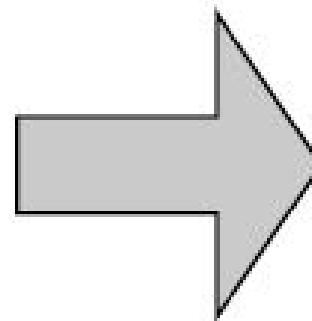
- With a generative model of modular networks, rules of probability tell us how to calculate model parameters (e.g. number of modules & assignments)



Generative Models

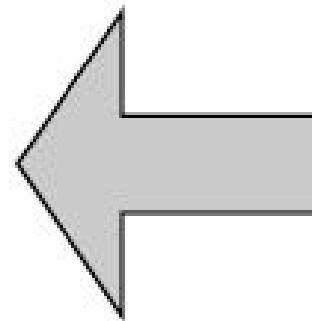
Know model
(parameters,
assignment
variables,
complexity)

Generate
synthetic data



Infer model
(parameters,
latent variables,
complexity)

Observe real
data



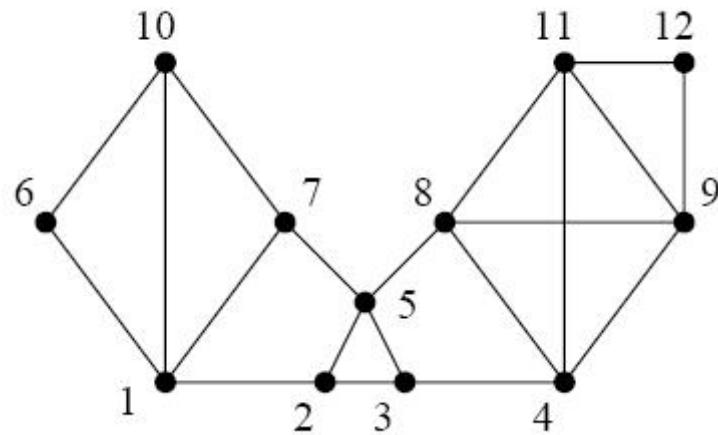
Markov Clustering Algorithm

van Dongen. A cluster algorithm for
graphs. Information Systems, 2000

K-length Path

- Basic idea: dense regions in sparse graphs corresponding with regions in which the number of k-length path is relatively large.
- Random walks can also be used to detect clusters in graphs, the idea is that the more closed is a subgraph, the largest the time a random walker need to escape from it.

K-path Clustering



5	2	1	0	2	3	3	0	0	4	0	0
2	4	3	1	3	1	2	1	0	1	0	0
1	3	4	2	3	0	1	2	1	0	1	0
0	1	2	5	2	0	0	4	4	0	4	2
2	3	3	2	5	0	2	2	1	1	1	0
3	1	0	0	0	3	2	0	0	3	0	0
3	2	1	0	2	2	4	1	0	3	0	0
0	1	2	4	2	0	1	5	4	0	4	2
0	0	1	4	1	0	0	4	5	0	5	3
4	1	0	0	1	3	3	0	0	4	0	0
0	0	1	4	1	0	0	4	5	0	5	3
0	0	0	2	0	0	0	2	3	0	3	3

Matrix manipulation: $(N+I)^2$

Markov Clustering

- Expansion: Through matrix manipulation (power), one obtains a matrix for a n-steps connection.
- Inflation: Enhance intercluster passages by raising the elements to a certain power and then normalize

Markov Clustering Algorithm

- Iteratively running two operators

- Inflation:

$$(T_r M)_{ij} = \frac{M_{ij}^r}{\sum_i M_{ij}^r} \quad \text{Column normalization}$$

- Expansion:

$$\text{Expand}(M) = M^k$$

MCL Running

0.380	0.087	0.027	--	0.077	0.295	0.201	--	--	0.320	--	--	--
0.047	0.347	0.210	0.017	0.150	0.019	0.066	0.012	--	0.012	--	--	--
0.014	0.210	0.347	0.056	0.150	--	0.016	0.046	0.009	--	0.009	--	--
--	0.027	0.087	0.302	0.062	--	--	0.184	0.143	--	0.143	0.083	
0.058	0.210	0.210	0.056	0.406	--	0.083	0.046	0.009	0.019	0.009	--	
0.142	0.017	--	--	--	0.295	0.083	--	--	0.184	--	--	
0.113	0.069	0.017	--	0.062	0.097	0.333	0.012	--	0.147	--	--	
--	0.017	0.069	0.175	0.049	--	0.016	0.287	0.143	--	0.143	0.083	
--	--	0.017	0.175	0.012	--	--	0.184	0.288	--	0.288	0.278	
0.246	0.017	--	--	0.019	0.295	0.201	--	--	0.320	--	--	
--	--	0.017	0.175	0.012	--	--	0.184	0.288	--	0.288	0.278	
--	--	--	0.044	--	--	--	0.046	0.120	--	0.120	0.278	

$\Gamma_2 M^2$, M defined in Figure 8

MCL Running

$$\begin{pmatrix} 0.448 & 0.080 & 0.023 & -- & 0.068 & 0.426 & 0.359 & -- & -- & 0.432 & -- & -- \\ 0.018 & 0.285 & 0.228 & 0.007 & 0.176 & 0.006 & 0.033 & 0.005 & -- & 0.007 & -- & -- \\ 0.005 & 0.223 & 0.290 & 0.022 & 0.173 & -- & 0.010 & 0.017 & 0.003 & 0.001 & 0.003 & 0.001 \\ -- & 0.018 & 0.059 & 0.222 & 0.040 & -- & 0.001 & 0.187 & 0.139 & -- & 0.139 & 0.099 \\ 0.027 & 0.312 & 0.314 & 0.028 & 0.439 & 0.005 & 0.054 & 0.022 & 0.003 & 0.010 & 0.003 & 0.001 \\ 0.116 & 0.007 & 0.001 & -- & 0.004 & 0.157 & 0.085 & -- & -- & 0.131 & -- & -- \\ 0.096 & 0.040 & 0.013 & -- & 0.037 & 0.083 & 0.197 & 0.001 & -- & 0.104 & -- & -- \\ -- & 0.012 & 0.042 & 0.172 & 0.029 & -- & 0.002 & 0.198 & 0.133 & -- & 0.133 & 0.096 \\ -- & 0.001 & 0.015 & 0.256 & 0.009 & -- & -- & 0.266 & 0.326 & -- & 0.326 & 0.346 \\ 0.290 & 0.021 & 0.002 & -- & 0.017 & 0.323 & 0.260 & -- & -- & 0.316 & -- & -- \\ -- & 0.001 & 0.015 & 0.256 & 0.009 & -- & -- & 0.266 & 0.326 & -- & 0.326 & 0.346 \\ -- & -- & 0.001 & 0.037 & 0.001 & -- & -- & 0.039 & 0.069 & -- & 0.069 & 0.112 \end{pmatrix}$$

$$\Gamma_2(\Gamma_2 M^2 \cdot \Gamma_2 M^2)$$

MCL Running

0.807	0.040	0.015	--	0.034	0.807	0.807	--	--	0.807	--	--
--	0.090	0.092	--	0.088	--	--	--	--	--	--	--
--	0.085	0.088	--	0.084	--	--	--	--	--	--	--
--	0.001	0.001	0.032	0.001	--	--	0.032	0.031	--	0.031	0.031
--	0.777	0.798	--	0.786	--	0.001	--	--	--	--	--
0.005	--	--	--	--	0.005	0.005	--	--	0.005	--	--
0.003	0.001	--	--	0.001	0.003	0.003	--	--	0.003	--	--
--	--	0.001	0.024	--	--	--	0.024	0.024	--	0.024	0.024
--	--	0.002	0.472	0.001	--	--	0.472	0.472	--	0.472	0.472
0.185	0.005	0.001	--	0.004	0.185	0.184	--	--	0.185	--	--
--	--	0.002	0.472	0.001	--	--	0.472	0.472	--	0.472	0.472
--	--	--	0.001	--	--	--	0.001	0.001	--	0.001	--

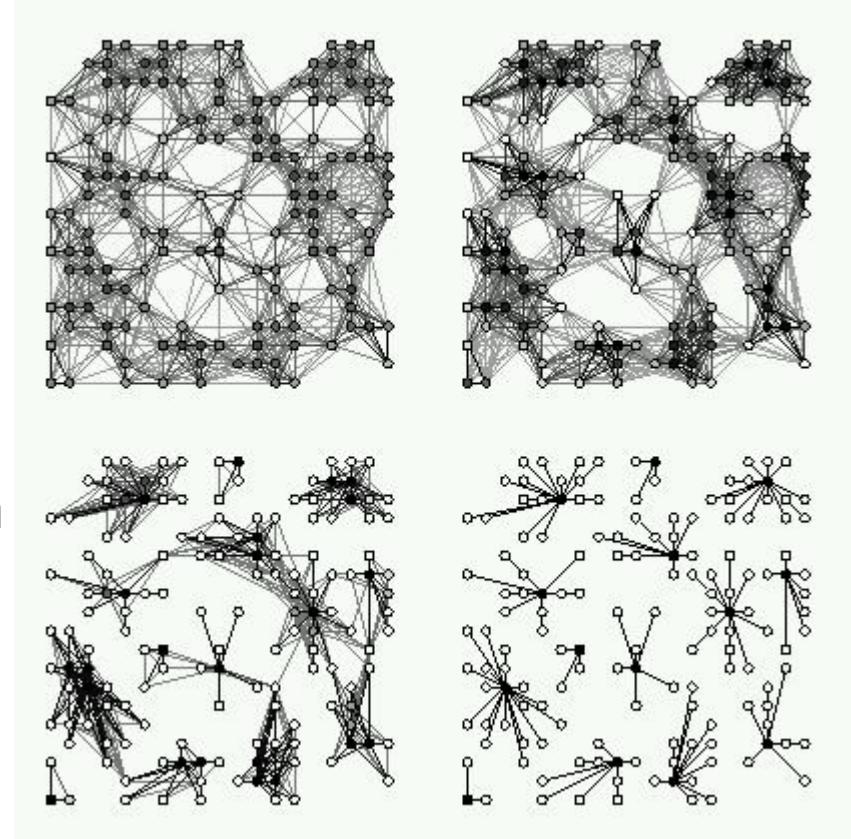
$(\Gamma_2 \circ Squaring)$ iterated four times on M

MCL Running

A Heuristic for MCL

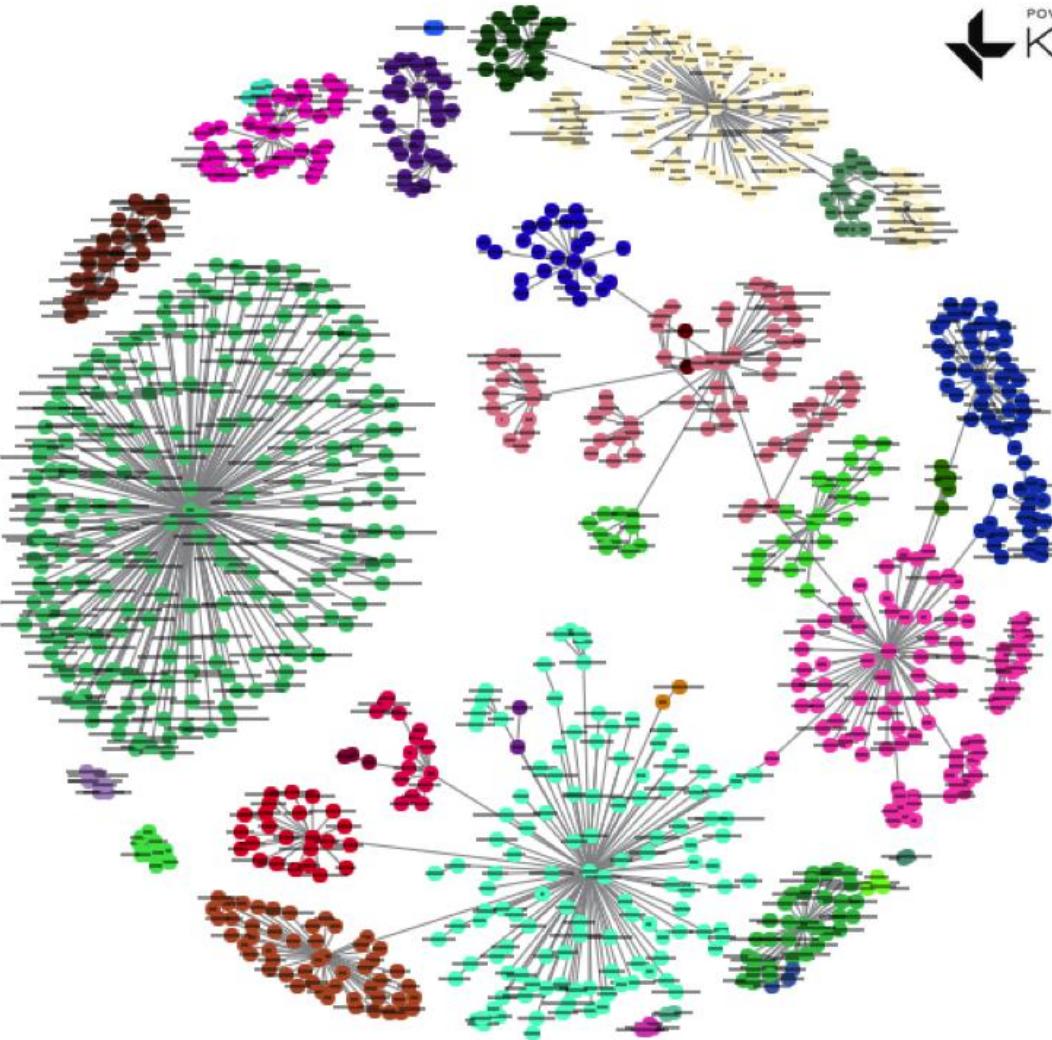
We take a random walk on the graph described by the similarity matrix

After each step we weaken the links between distant nodes and strengthen the links between nearby nodes



Graphic from van Dongen, 2000

Clustering examples



POWERED BY
KeyLines

STRING

[Search](#)[Download](#)[Help](#)[My Data](#)

- [Protein by name](#) >
- [Protein by sequence](#) >
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- [Protein families \("COGs"\)](#) >
- [Examples](#) >
- [Random entry](#) >

SEARCH

Single Protein by Name / Identifier

Protein Name: (examples: #1 #2 #3)

Organism:

auto-detect ▼

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STITCH

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SEARCH

Single Item by Name / Identifier

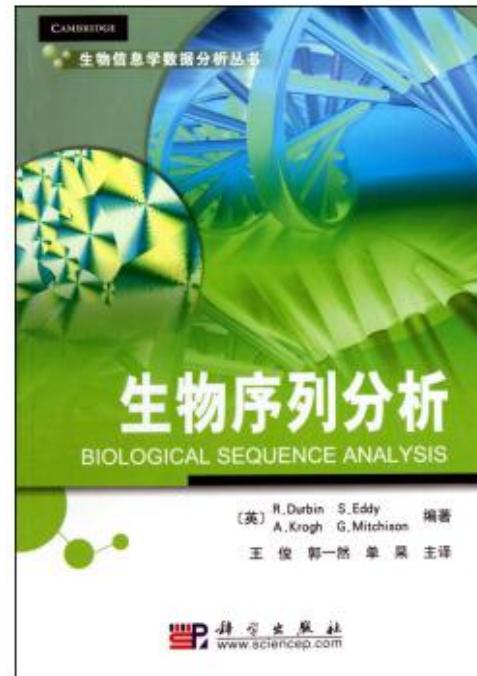
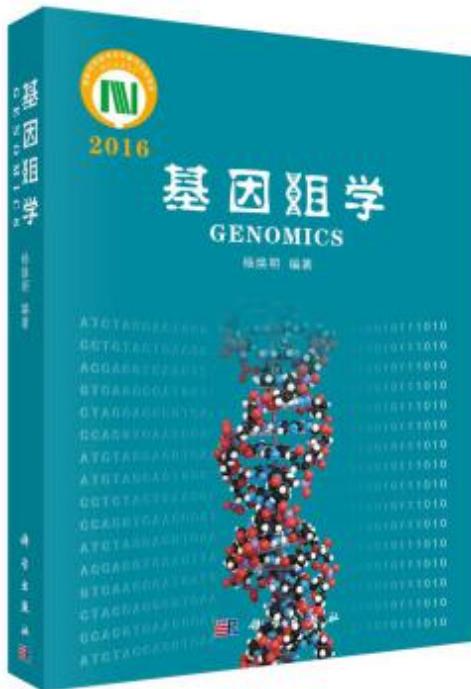
Item Name: (examples: #1 #2 #3)

Organism:

auto-detect ▼

SEARCH

References



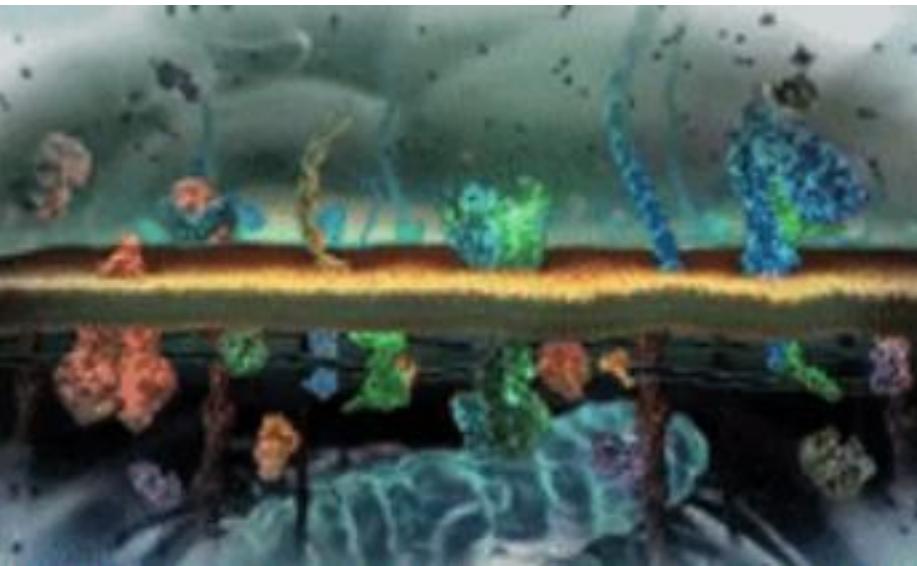
补充知识

- 蛋白质3D结构预测
- AlphaFold2（利用AI攻克蛋白质3D结构预测问题）

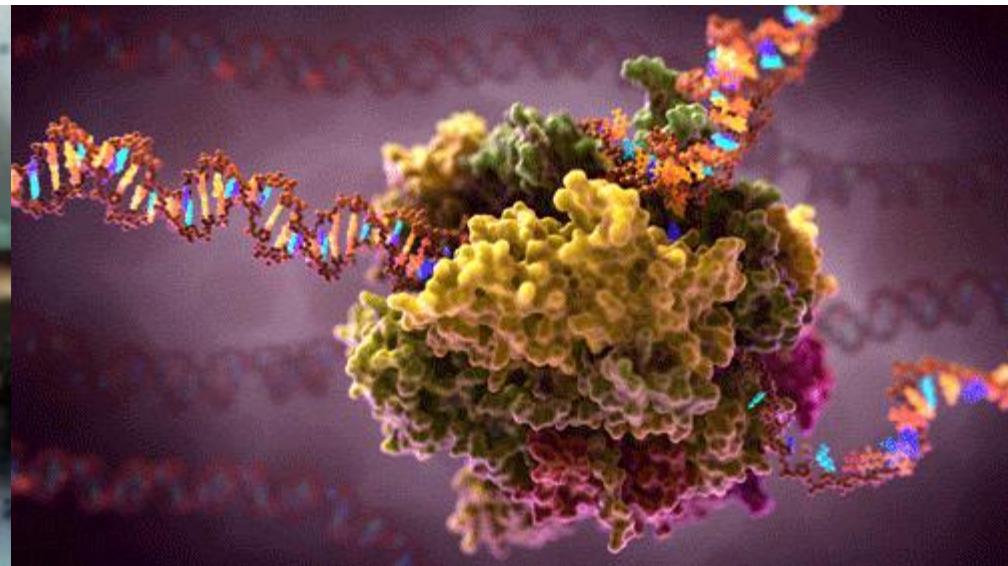
Protein 3D structure

眼见为实

Overview



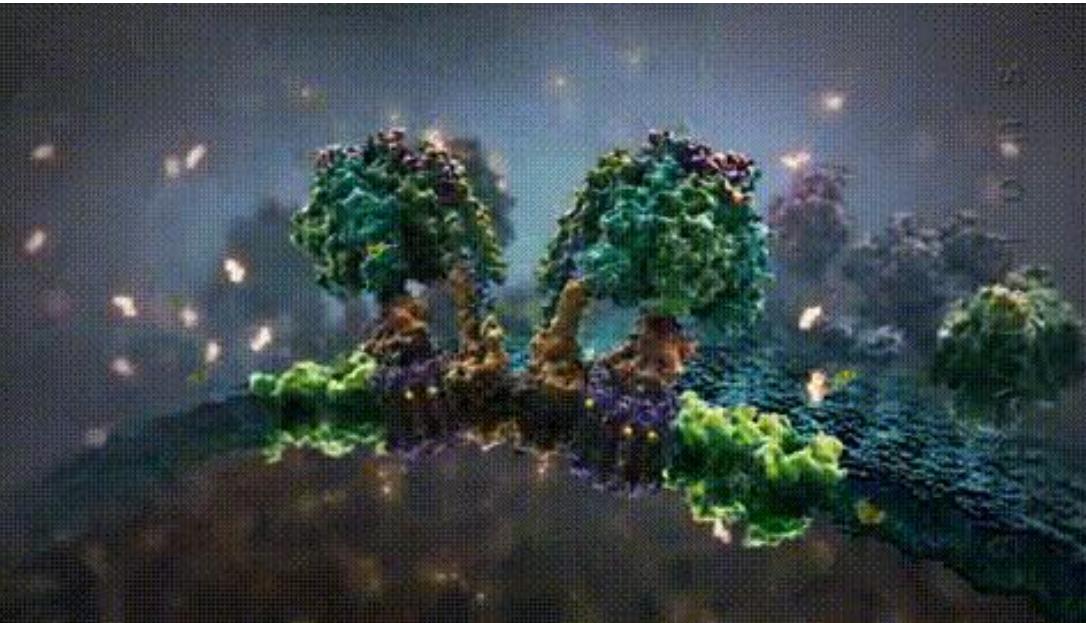
Ribosome



Protein 3D structure

眼见为实

ATP

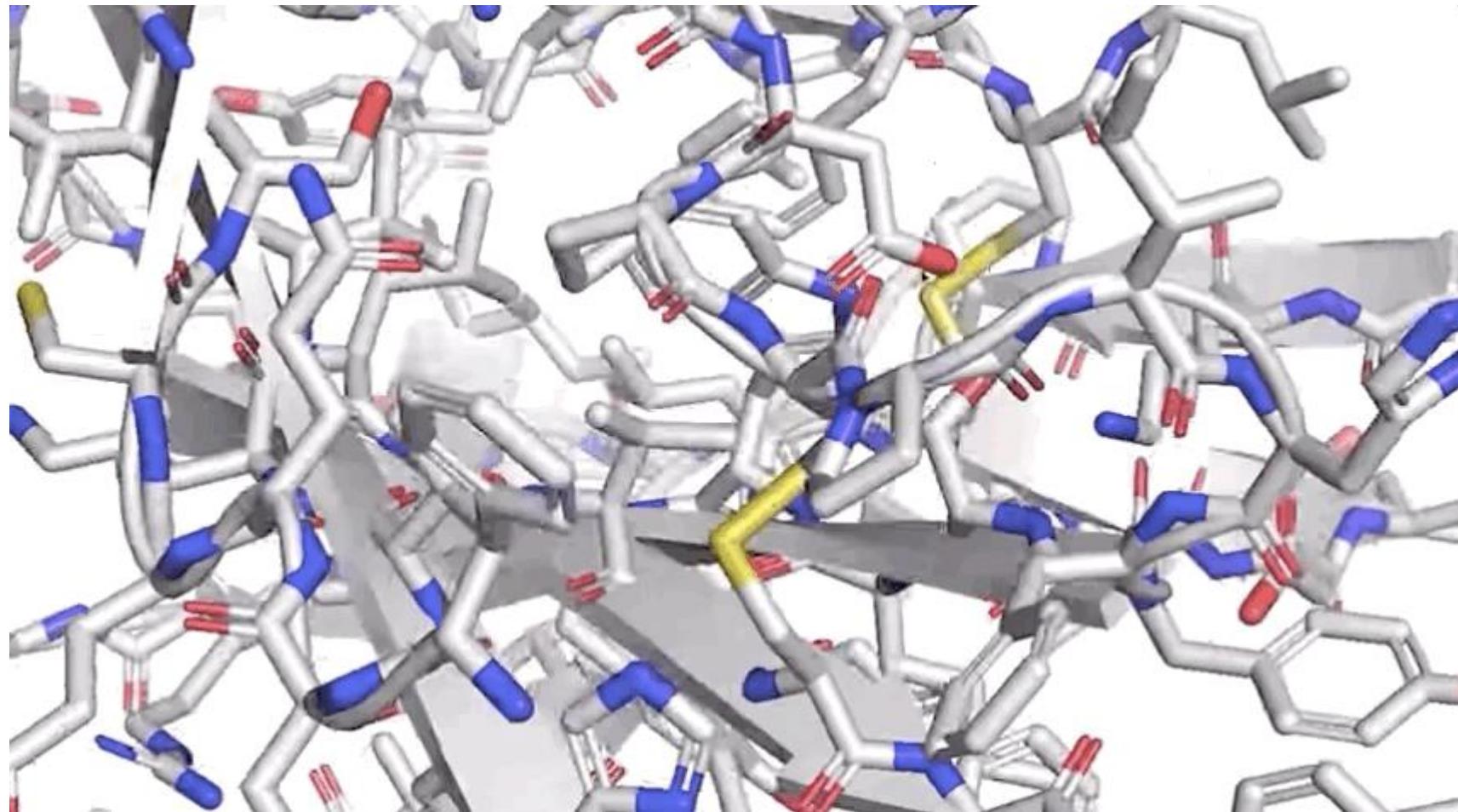


Transportation



Protein 3D structure

眼见为实

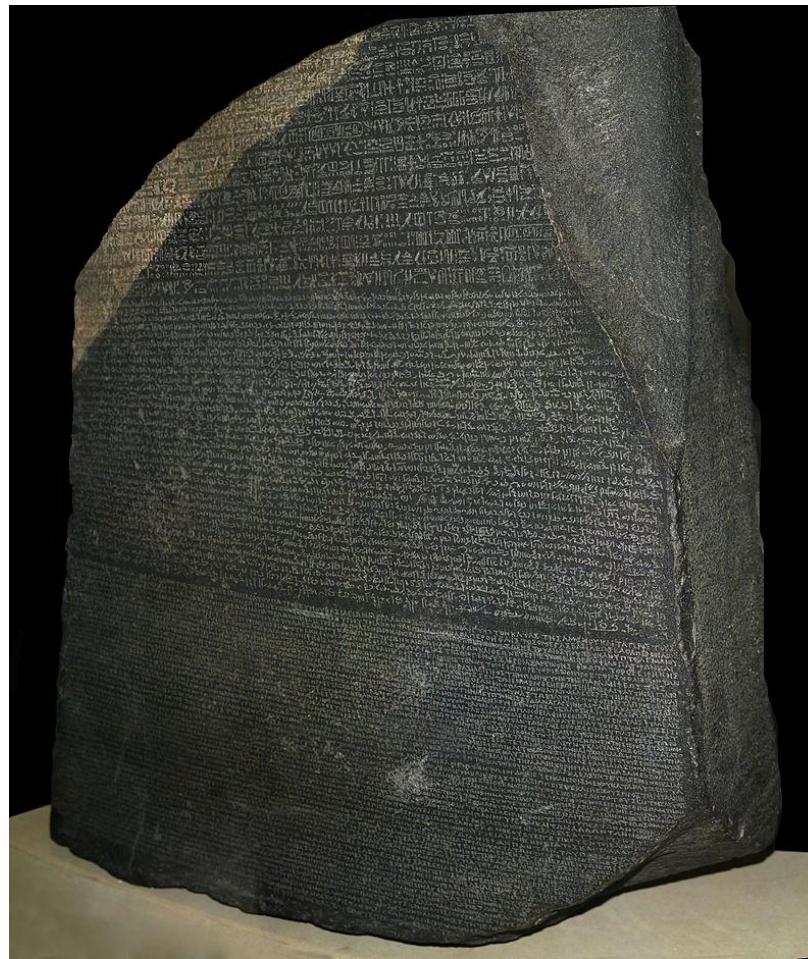


Protein 3D structure

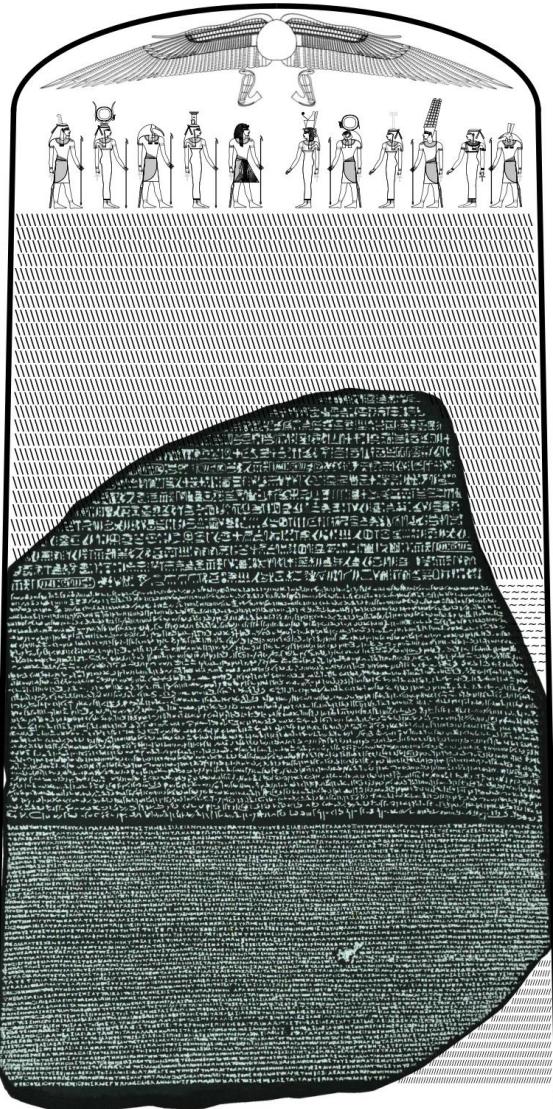
眼见为实



Rosetta stone



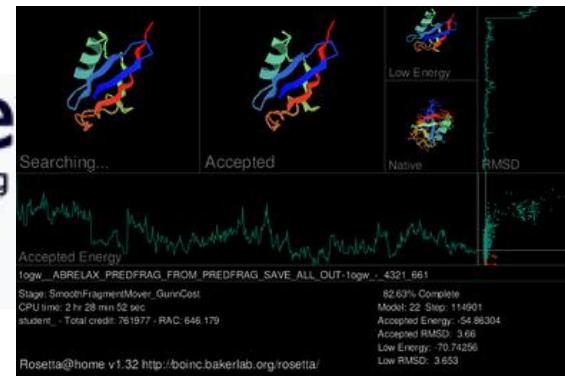
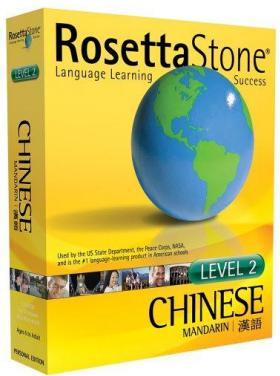
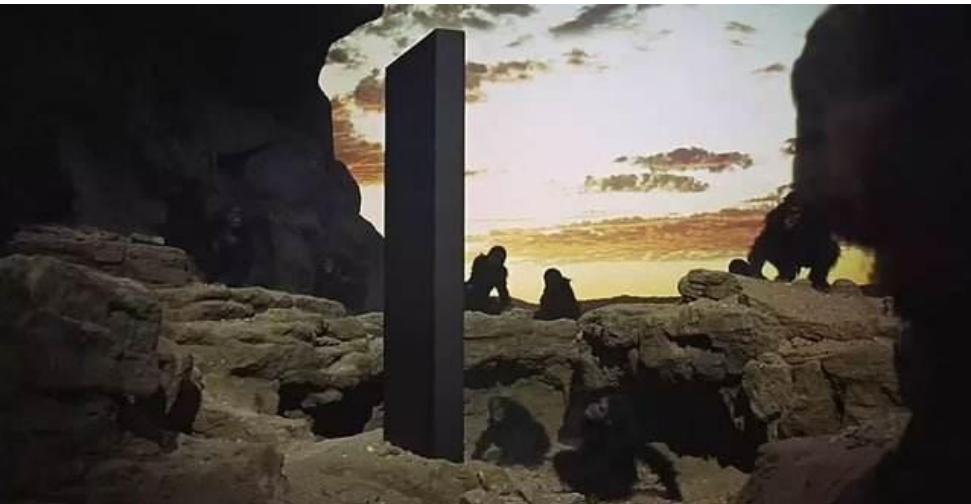
Rosetta stone



*Tableau des Signes Phonétiques
des écritures hiéroglyphique et Démotique des anciens Egyptiens*

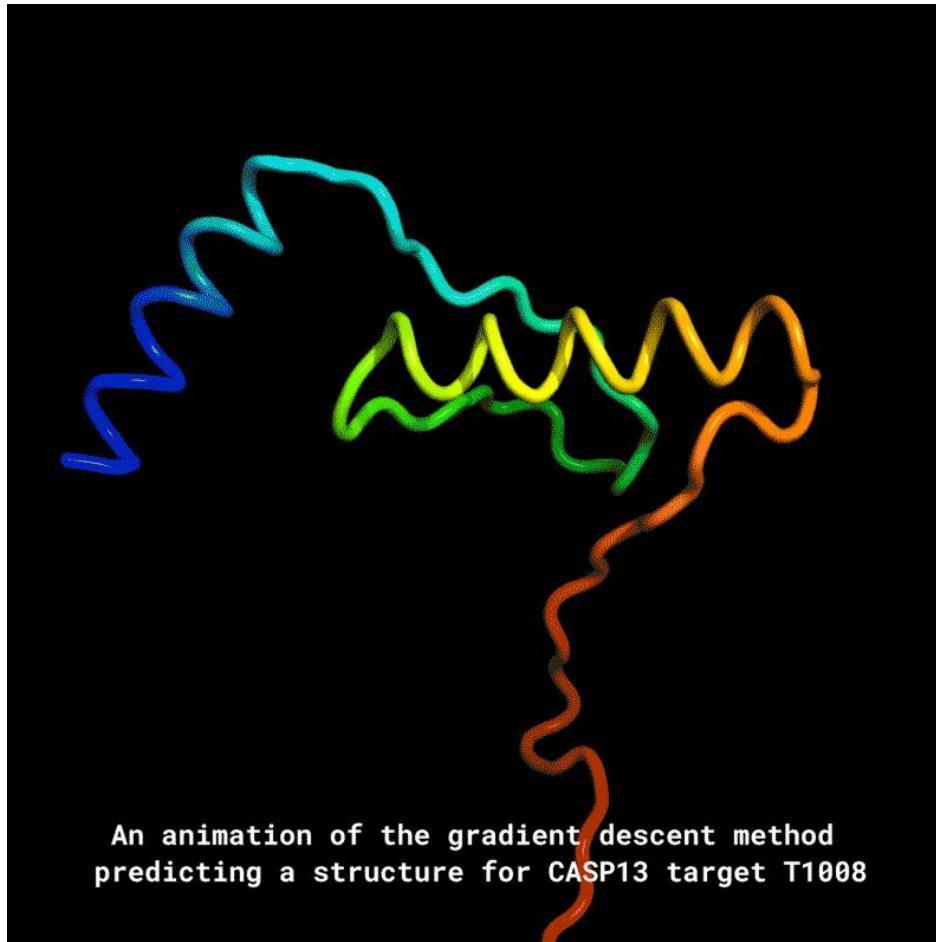
Lettres grecques	Signes Démotiques	Signes hiéroglyphiques
A	ւ.ւ.	𓏏 𓏏 𓏏 𓏏 𓏏 𓏏 𓏏 𓏏 𓏏 𓏏 𓏏 𓏏
B	ւ.ւ.	𓏏 𓏏 𓏏 𓏏 𓏏 𓏏 𓏏 𓏏 𓏏 𓏏 𓏏 𓏏
Γ	κ.━	━ ━
Δ	◀.◀.	━ ━
Ε	ι.	ἴ
Ζ		
Η	III JII. ցI. յII.	III III III III ցI ցI յII յII ցI ցI
Θ		
Ι	ս. ս.	ս ս ս ս ս ս ս ս ս ս ս ս
Կ	ւ.ւ.ւ.ւ.ւ.ւ.	ւ ւ ւ ւ ւ ւ ւ ւ ւ ւ ւ ւ ւ
Լ	Վ.Վ.Վ.	Վ Վ Վ Վ Վ Վ Վ Վ Վ Վ Վ Վ
Մ	Ջ.Ջ.	Ջ Ջ Ջ Ջ Ջ Ջ Ջ Ջ Ջ Ջ Ջ Ջ
Ն	Չ.Չ.━.━.	Չ Չ ━ ━ Չ Չ ━ ━ Չ Չ ━ ━
Շ	Ճ.	Ճ Ճ Ճ Ճ Ճ Ճ Ճ Ճ Ճ Ճ Ճ Ճ
Օ	Ր.Ր.Ր.Ր.	Ր Ր Ր Ր Ր Ր Ր Ր Ր Ր Ր Ր
Ո	Հ.Հ.Հ.Հ.	Հ Հ Հ Հ Հ Հ Հ Հ Հ Հ Հ Հ
Ռ	Ռ.Ռ.Ռ.Ռ.	Ռ Ռ Ռ Ռ Ռ Ռ Ռ Ռ Ռ Ռ Ռ Ռ
Շ	Շ.Շ.Շ.Շ.	Շ Շ Շ Շ Շ Շ Շ Շ Շ Շ Շ Շ
Տ	Հ.Հ.Հ.Հ.	Հ Հ Հ Հ Հ Հ Հ Հ Հ Հ Հ Հ
ՙ	Հ	Հ Հ Հ Հ Հ Հ Հ Հ Հ Հ Հ Հ
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ՏՕ.		Հ Հ Հ Հ Հ Հ Հ Հ Հ Հ Հ Հ

Rosetta stone



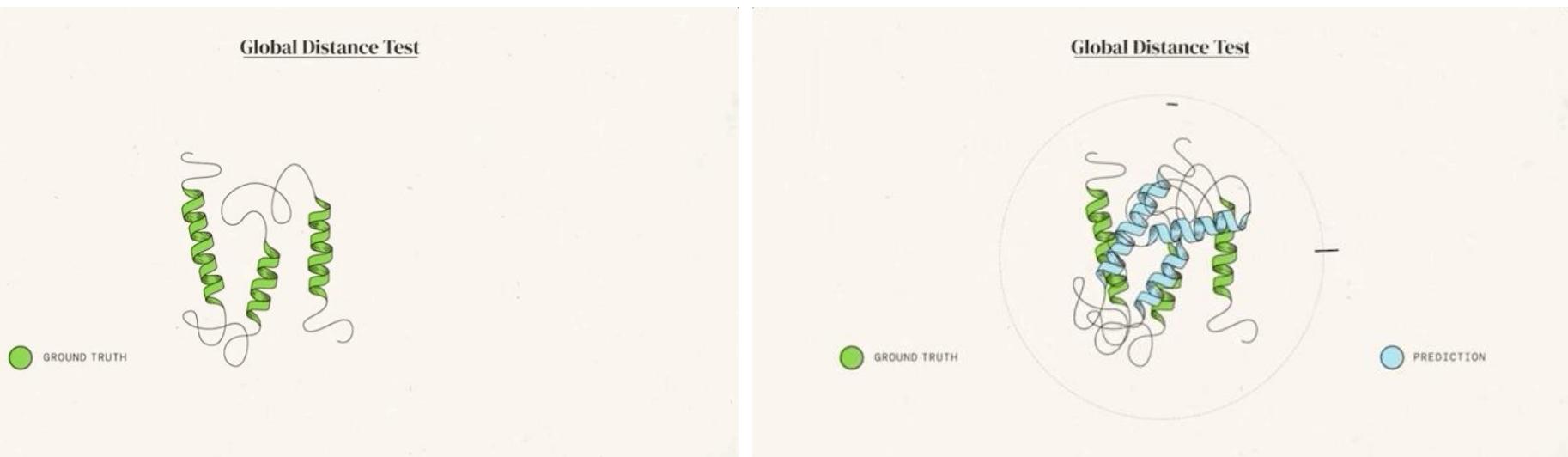
CASP

(Critical Assessment of Techniques for Protein Structure Prediction)



CASP

(Critical Assessment of Techniques for Protein Structure Prediction)



CASP

(Critical Assessment of Techniques for Protein Structure Prediction)



I-TASSER
Protein Structure & Function Predictions

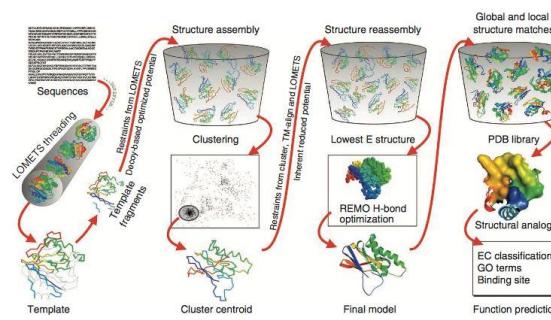
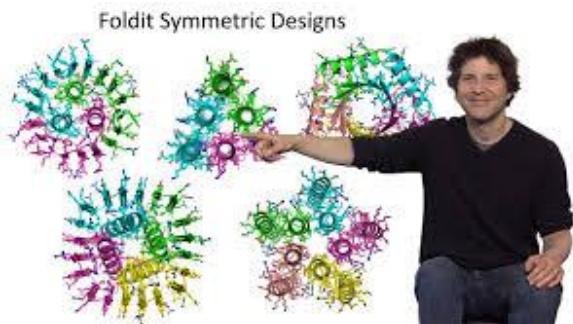


Figure 1 | A schematic representation of the I-TASSER protocol for protein structure and function predictions. The protein chains are colored from blue at the N-terminus to red at the C-terminus. 駿波



Protein 3D structure

1972年，克里斯蒂安·安芬森（Christian Anfinsen）在诺贝尔化学奖的获奖感言中，提出了一个著名的假设：

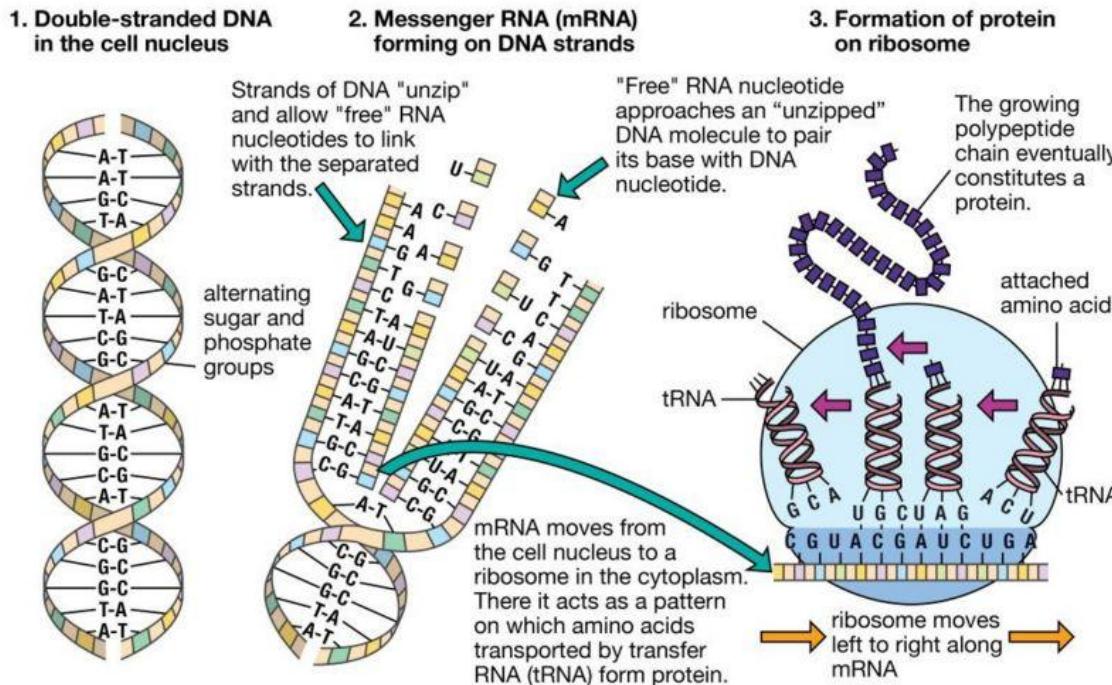
“理论上来说，蛋白质的氨基酸序列应该完全决定其结构。”



Protein 3D structure

这一假设引发了长达五十年的探索，即仅仅基于蛋白质的一维氨基酸序列计算出其三维结构。

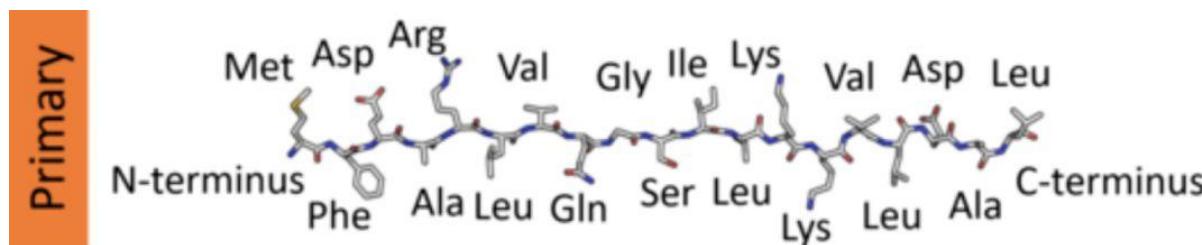
How DNA directs protein synthesis



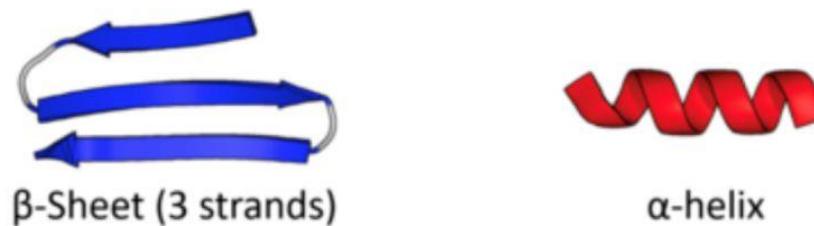
Levinthal 悖论：一种蛋白质大约存在 10^{300} 种可能构象。但在自然界中，蛋白质会自发折叠，有些只需几毫秒。

Protein 3D structure

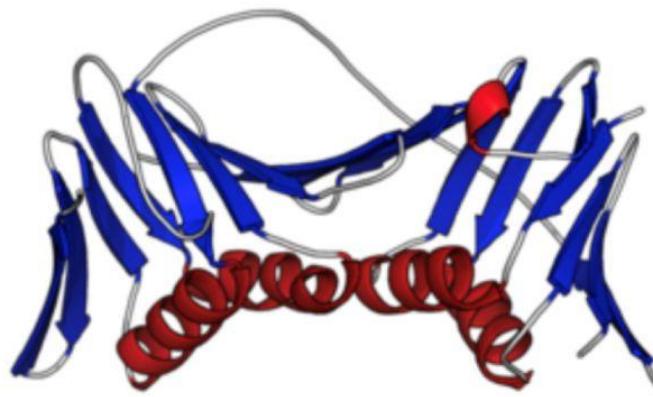
基本原理



Secondary



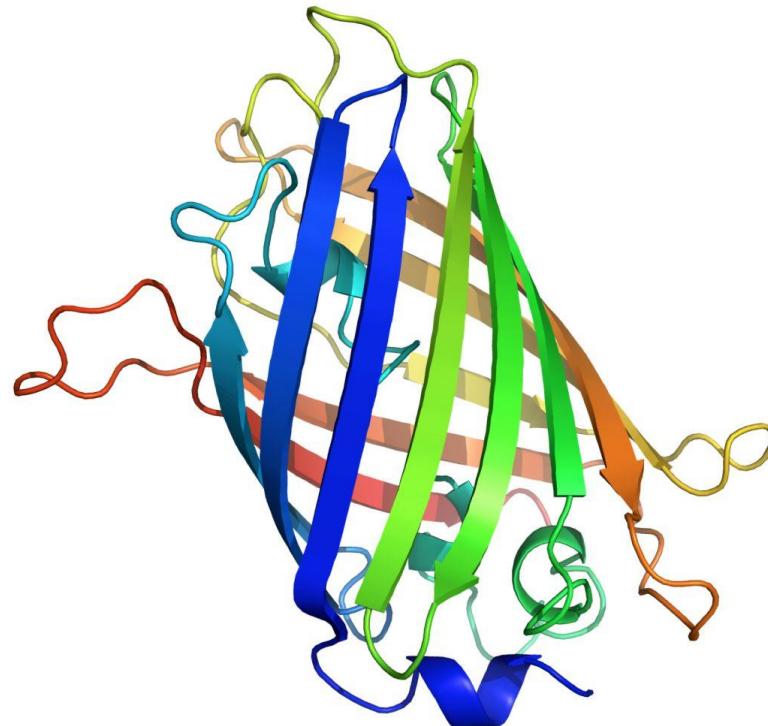
Tertiary



Protein 3D structure

结构和序列

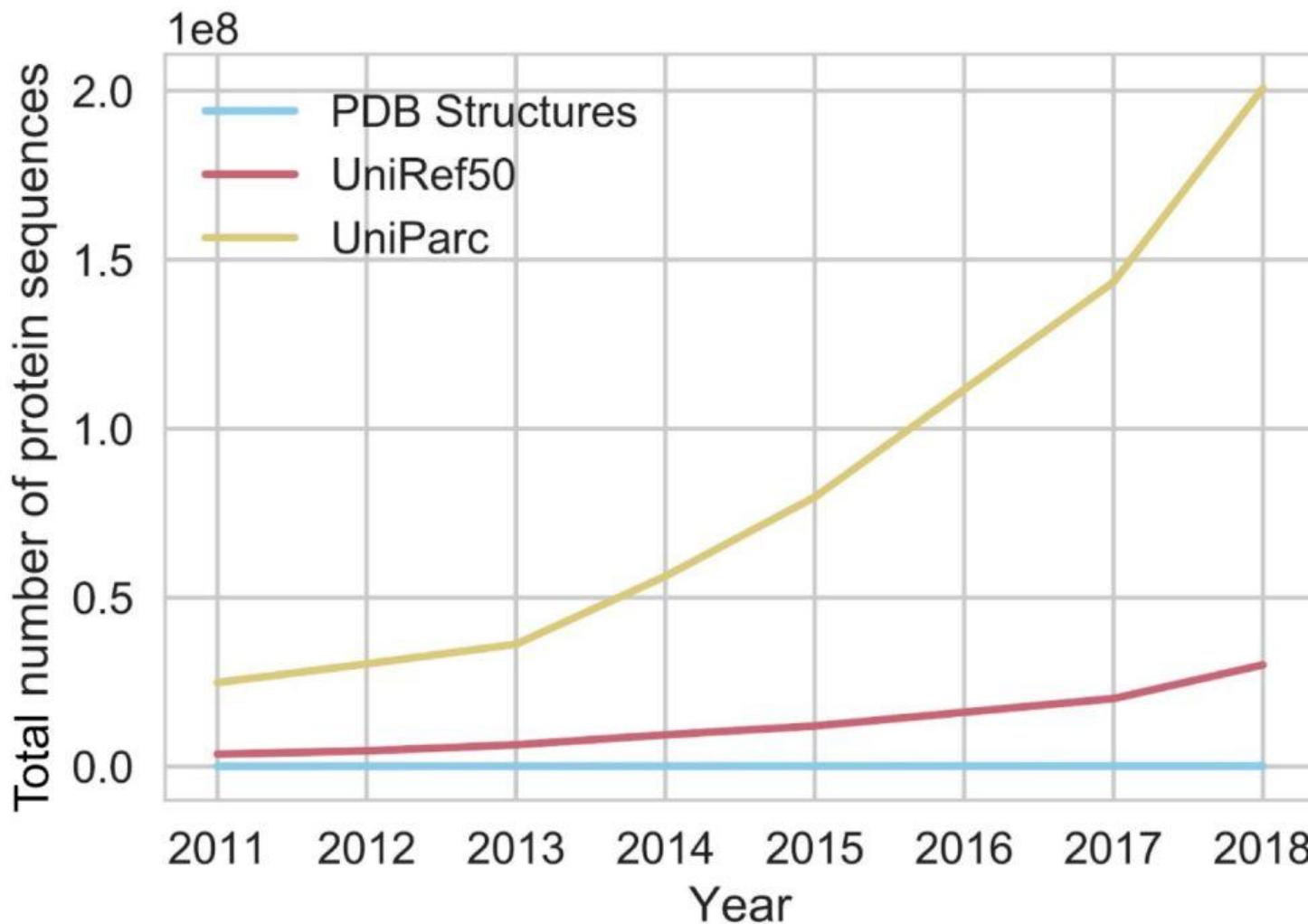
其中颜色渐变表示序列中从头到尾的索引



ELFTGVVPILVELDDGVNGHKFSVSGEGERGATYGKLTLLKFICTTGK-LPVWPWPTLVTTFGYGLQCFARYPD
SLSKDAMLHFKMEGSVNGHCFEIQGVGEGERGKAFDGEHWSKLCVVKGKHLPPFDILMPSMSYGTQFAKYPA
msvptn-----LDLHIYGSINGMEFDMVGGGSGNPNDGSLSVNKSTKGA-LRVSPPLLGVPHLGYGHYQYLPFPD
MFYGSKAFAKYPD
MKLHFKELEGSVNGHCFEIQGEGERGKPFEGEQWAHKCVVKGKHLPPFLDDIMPNI-TFAKYPD
athe-----IHLHGSVNGHEFDLVGSKGDPKAGSLVTEVKSTMGP-LKFSPSPHLMIPHLGYGYQYLPYPD
ELFTGVVPILVELDDGVNGHKFSVSGEGERGATYGKDCLLFICTTGK-LPVWPWPTLVTTFGYGLMCFARYPD
ptthe-----LHIFGSFNGVEFDMVGRGIGNPNDGYEELNLKSTKGA-LKFSPSPWILVLPQIGYGFHQYLPYPD
plptthe-----LHIFGSFNGVEFDLVGRGEGRNPKDGSQNHLKSTKGA-LQFSPSPWMLVPHIGYGFYQYLPYPD
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pkthe-----LHIFGSFNGVEFDMVGRGIGNPNDGYEELNLKSTKGA-LKFSPSPWILVPHLGYAYQYLPFPD
athd-----IHLHGSVNGHEFDMVGGGKGDPNAGSLVTTAKSTKGA-LKFSPSPYILVPHLGYGYQYLPFPD
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pkthe-----LHIFGSFNGVKFDMVGEGTGNPNEGSEELKLKSTNGP-LKFSPSPYILVPHLGYAFNQYLPFPD
tahd-----LHIFGSVNGAEFDLVGGGKGPNPNDGTLETSVKSTRGA-LPCSPPLIGPNLGYGFYQYLPFPD
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tthd-----LHIFGSVNGAEFDLVGGGKGPNPNDGTLETSVKSTRGA-LPCSPPLIGPNLGYGFYQYLPFPD
npy-----
q-----ELFTGVVPILVELDDGVNGHKFSVSGEGERGATYGKLTLLKFICTTGK-LPVWPWPTLVTTFGYGLQCFARYPD
m-----
ahdc-----HMFGSINGHEFDLVGGGNGNPNDGTLETKVRSTKGA-LPFSPSPVILAPNLGYGYHQYLPFPD
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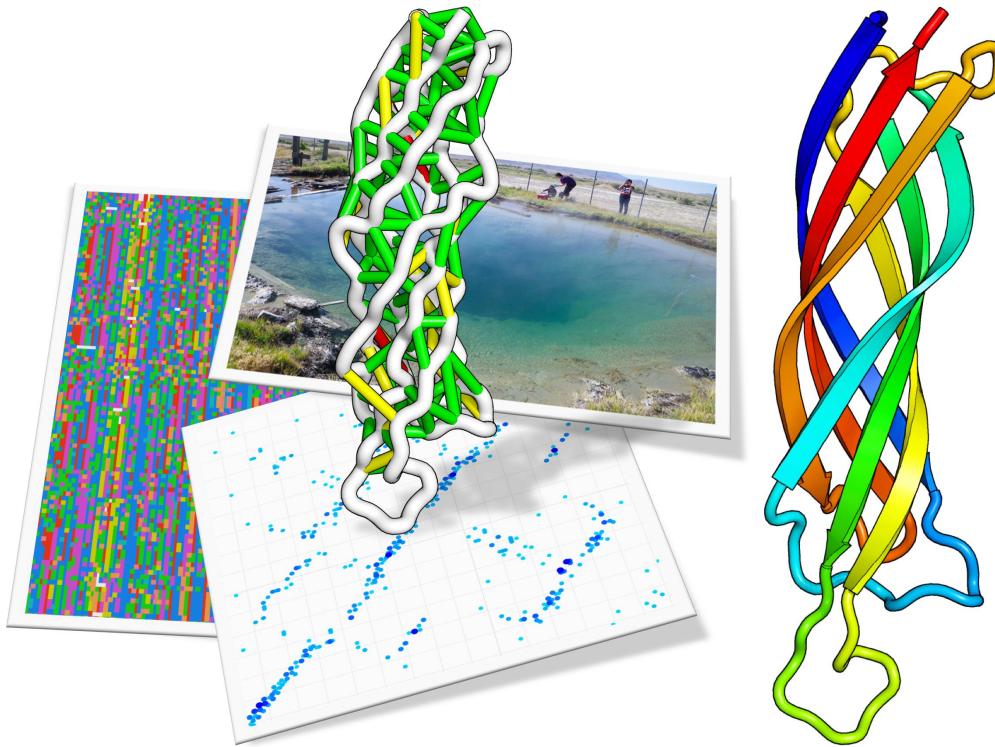
Protein 3D structure

大数据问题





The hub for Rosetta modeling software



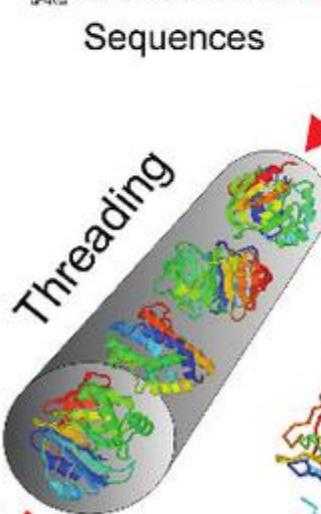
Top: Researchers gathering samples from Great Boiling Spring in Nevada. Left: a snapshot of aligned metagenomic sequences. Each row is a different sequence (the different colors are the different amino acid groups). Each position (or column) is compared to all other positions to detect patterns of co-evolution. Bottom: the strength of the top co-evolving residues is shown as blue dots, these are also shown as colored lines on the structure above. The goal is to make a structure that makes as many of these contacts as possible. Right: a cartoon of the protein structure predicted. The protein domain shown is from Pfam DUF3794, this domain is part of a Spore coat assembly protein SafA. (Image of Great Boiling Spring by Brian Hedlund, UNLV. Protein structure and composite image by Sergey Ovchinnikov, UW)



I-TASSER

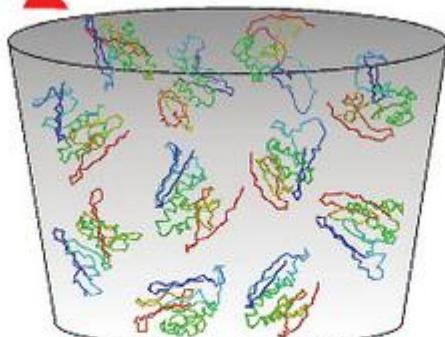
Protein Structure & Function Predictions

Sequences
Template
Structural
alignments
Multiple
alignments
Sequence
conservation
scores
Secondary
structure
constraints
Contact
optimization
scores

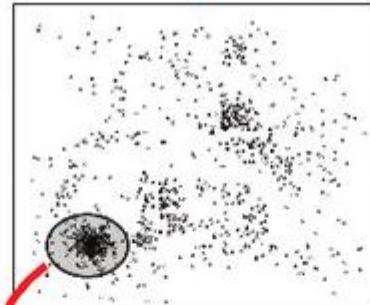


Predicted contact restraints
Decoy-based optimized potential

Structure assembly



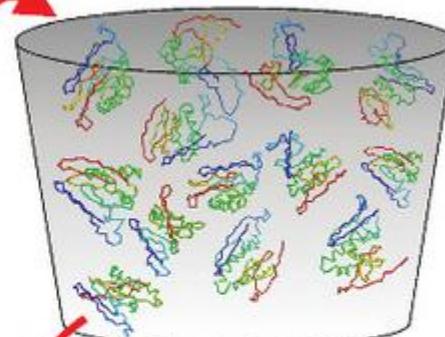
Clustering



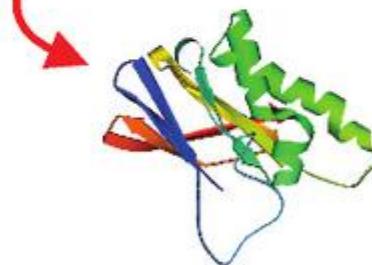
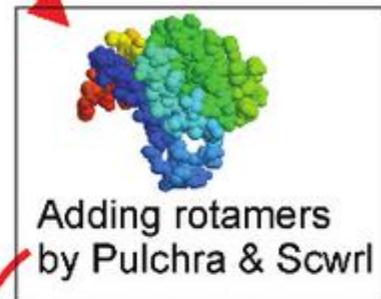
Cluster Centroid

Restraints from cluster centroid
Decoy-based optimized potential

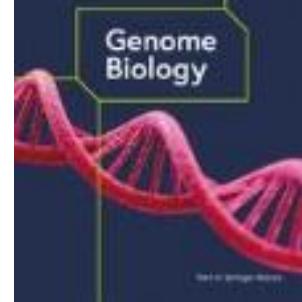
Structure re-assembly



Lowest E structure



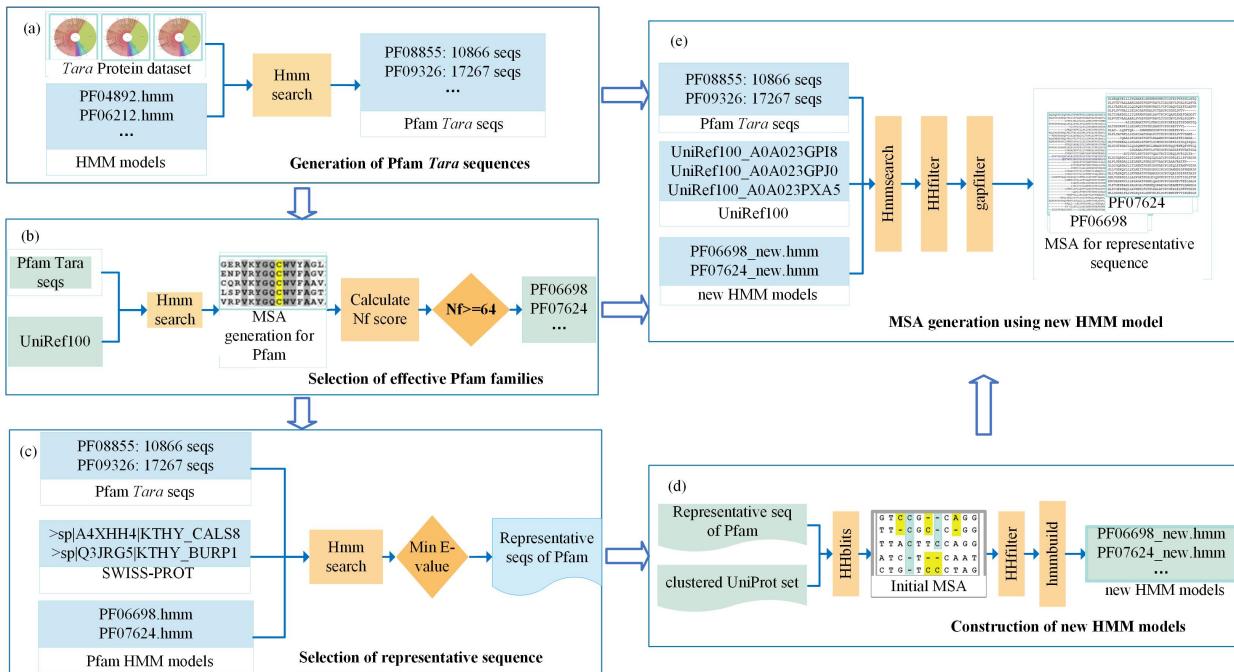
Final model

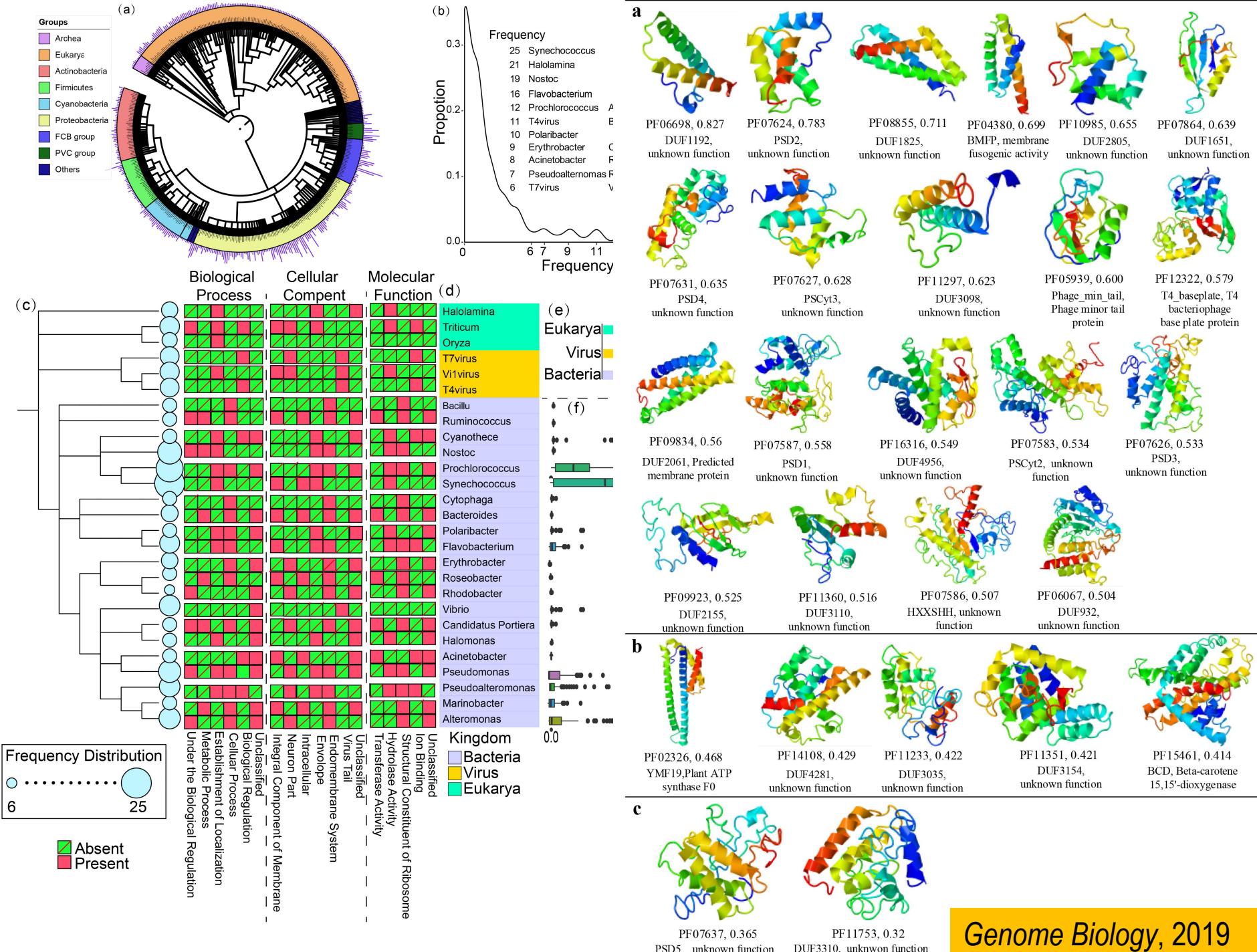


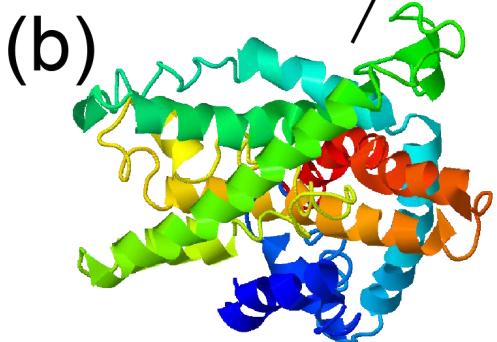
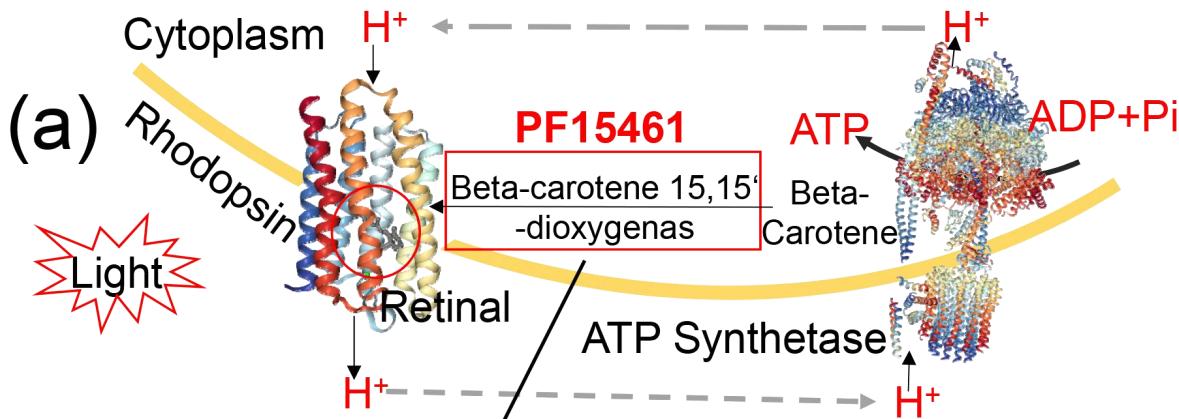
微生物组大数据 + 蛋白质3D结构

基于大数据挖掘的蛋白质结构预测和功能解析

- 2TB的海洋微生物组大数据—>鉴定出了超过9千万的非冗余基因和超过3万个微生物物种
- 预测出了之前没有任何结构信息的27个蛋白质结构
- 利用人工神经网络挖掘蛋白结构和生境的关系



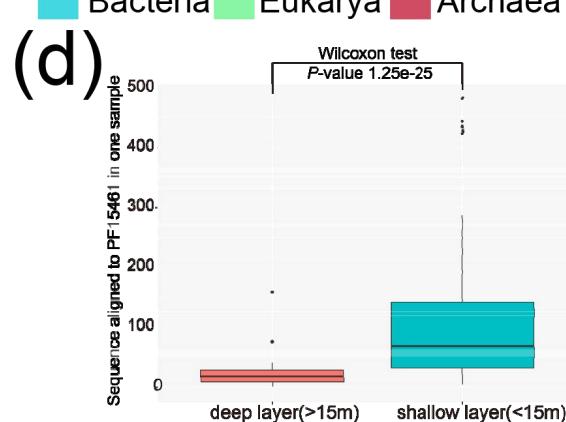




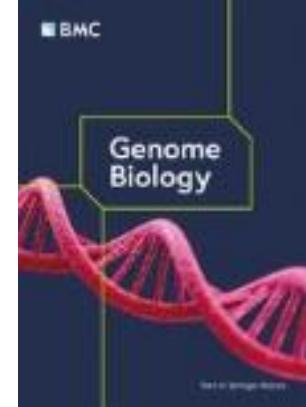
Predicted structure of PF15461

318 Amino Acid
Beta-carotene 15,15'-dioxygenase
369 sequence → 14,353 sequence

Predicted Function:
Cellular Component: Respiratory Chain
Biological Process:
Single-organism Metabolic Process
Molecular Function: Oxidoreductase Activity



微生物组大数据 + 蛋白质3D结构



潜在应用途径

- 非定向/定向方法可以发掘大量未知功能基因
- 为合成生物学提供功能模块
- 药物发掘和药物设计
 - 环境菌群功能基因
 - 环境菌群代谢物

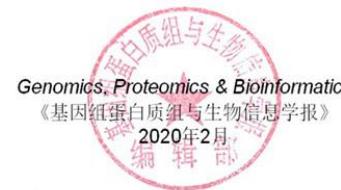
2019年度中国在生物信息学十大应用

榮譽證書

Fueling *ab initio* folding with marine metagenomics enables structure and function predictions of new protein families
(*Genome Biology* 2019;20:229)

入选

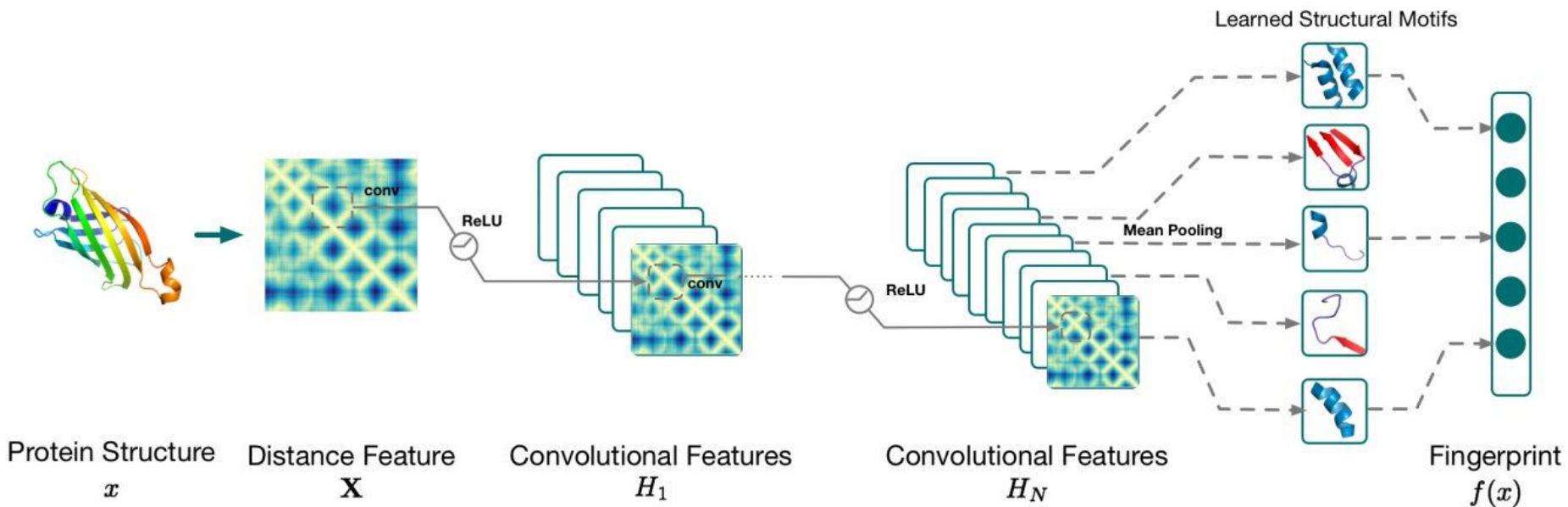
2019年度中国生物信息学十大应用



CASP13

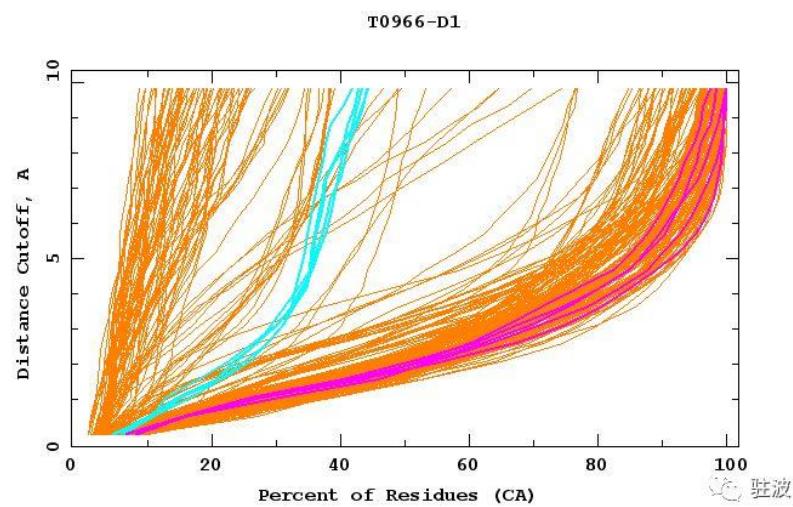
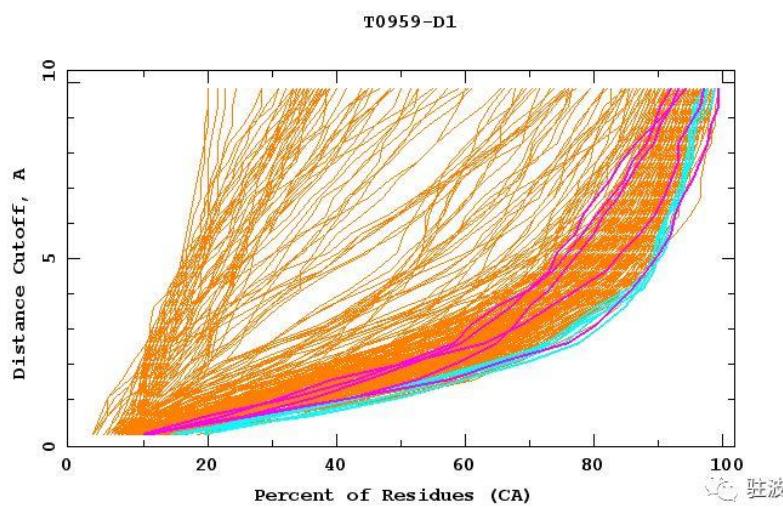
(Critical Assessment of Techniques for Protein Structure Prediction)

DeepFold



CASP13

(Critical Assessment of Techniques for Protein Structure Prediction)



NEWS • 30 NOVEMBER 2020

'It will change everything': DeepMind's AI makes gigantic leap in solving protein structures

Google's deep-learning program for determining the 3D shapes of proteins stands to transform biology, say scientists.

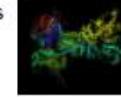
Ewen Callaway



A protein's function is determined by its 3D shape. Credit: DeepMind

RELATED ARTICLES

AI protein-folding algorithms solve structures faster than ever



The revolution will not be crystallized: a new method sweeps through structural biology



The computational protein designers



Revolutionary microscopy technique sees individual atoms for first time



SUBJECTS

CASP14

(Critical Assessment of Techniques for Protein Structure Prediction)

**AlphaFold: a solution to
a 50-year-old grand
challenge in biology**

DeepMind宣布，其新一代AlphaFold人工智能系统，在国际蛋白质结构预测竞赛（CASP）上击败了其余的参会选手，能够精确地基于氨基酸序列，预测蛋白质的3D结构。其准确性可以与使用冷冻电子显微镜（CryoEM）、核磁共振或X射线晶体学等实验技术解析的3D结构相媲美。

CASP14

(Critical Assessment of Techniques for Protein Structure Prediction)



Sundar Pichai ✅ @sundarpichai · 10h

@DeepMind's incredible AI-powered protein folding breakthrough will help us better understand one of life's fundamental building blocks + enable researchers to tackle new and hard problems, from fighting diseases to environmental sustainability.

...



AlphaFold: a solution to a 50-year-old grand challenge in biology

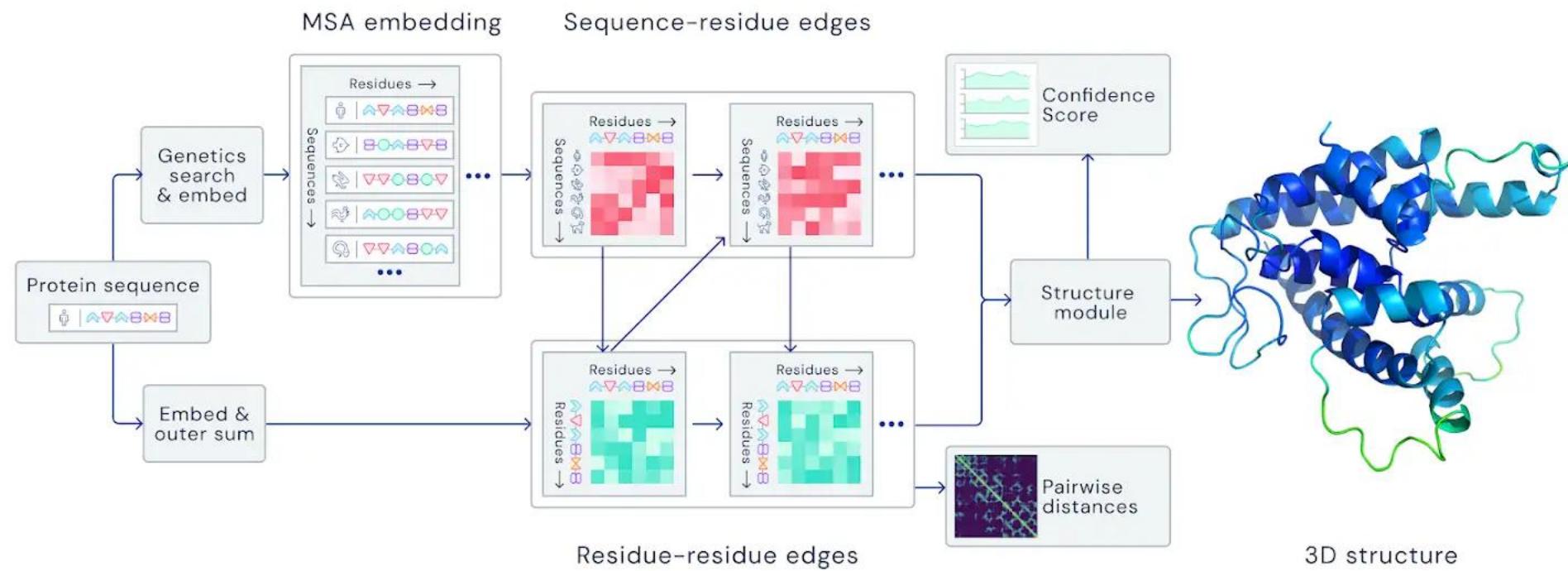
In a major scientific advance, the latest version of our AI system AlphaFold has been recognised as a solution to this grand challenge ...

deepmind.com

CASP14

(Critical Assessment of Techniques for Protein Structure Prediction)

AlphaFold2

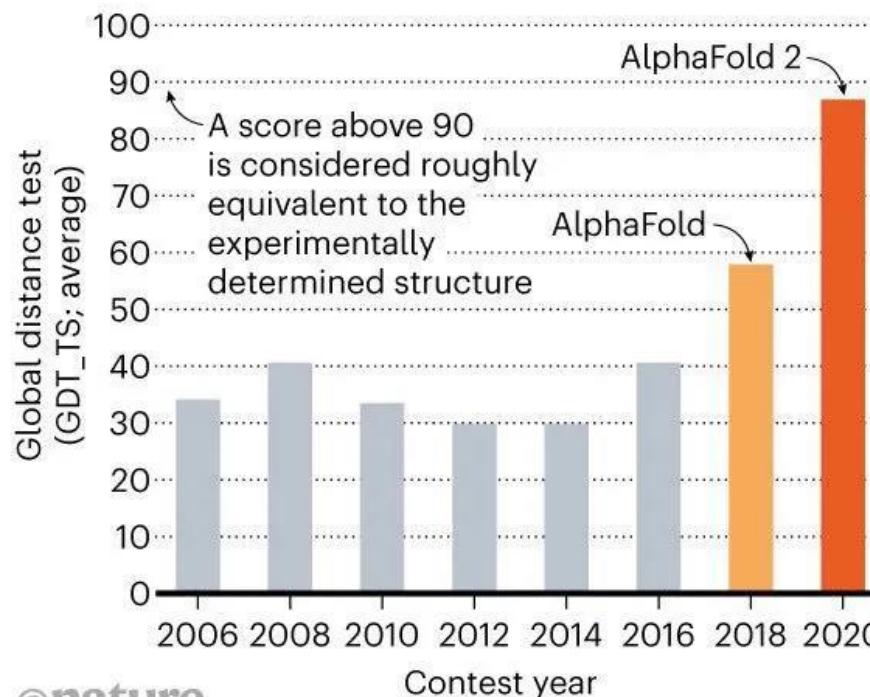


CASP14

(Critical Assessment of Techniques for Protein Structure Prediction)

STRUCTURE SOLVER

DeepMind's AlphaFold 2 algorithm significantly outperformed other teams at the CASP14 protein-folding contest — and its previous version's performance at the last CASP.

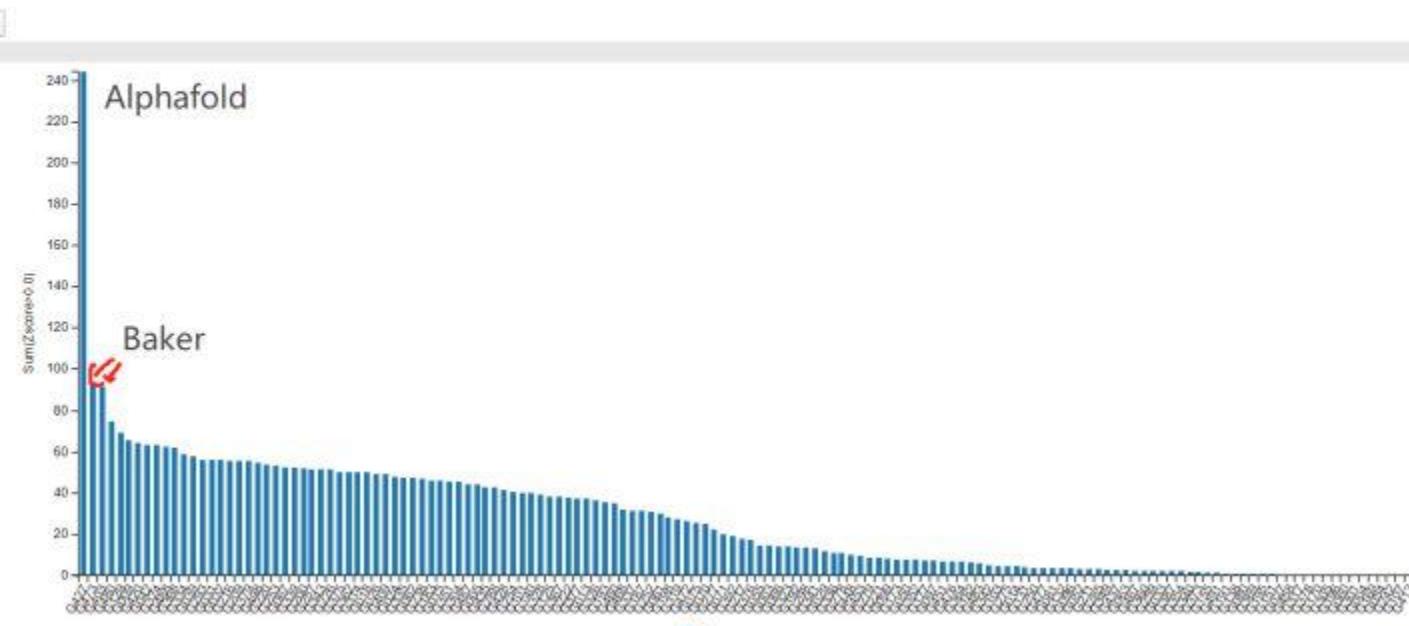


CASP14

(Critical Assessment of Techniques for Protein
Structure Prediction)

The ranking of the groups is based on the analysis of zscores for GDT_TS

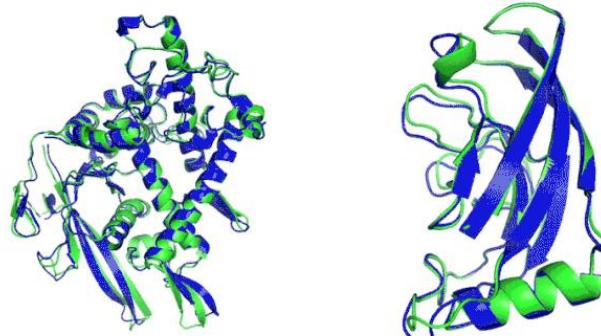
- o TBM-easy
 - o TBM-hard
 - o TBM/FM
 - o FM
 - o Multidom



https://predictioncenter.org/casp14/zscores_final.cgi

CASP14

(Critical Assessment of Techniques for Protein Structure Prediction)



T1037 / 6vr4
90.7 GDT
(RNA polymerase domain)

T1049 / 6y4f
93.3 GDT
(adhesin tip)

- Experimental result
- Computational prediction

在2020的CASP中，AlphaFold系统对所有蛋白靶点3D结构预测的中位GDT评分为92.4分。即便是针对最难解析的蛋白靶点，AlphaFold的中位GDT评分也达到了87.0分。在接受检验的近100个蛋白靶点中，AlphaFold对三分之二的蛋白靶点给出的预测结构与实验手段获得的结构相差无几。CASP创始人Moult教授表示，在有些情况下，已经无法区分两者之间的区别是由于AlphaFold的预测出现错误，还是实验手段产生的假象。

CASP14

(Critical Assessment of Techniques for Protein Structure Prediction)

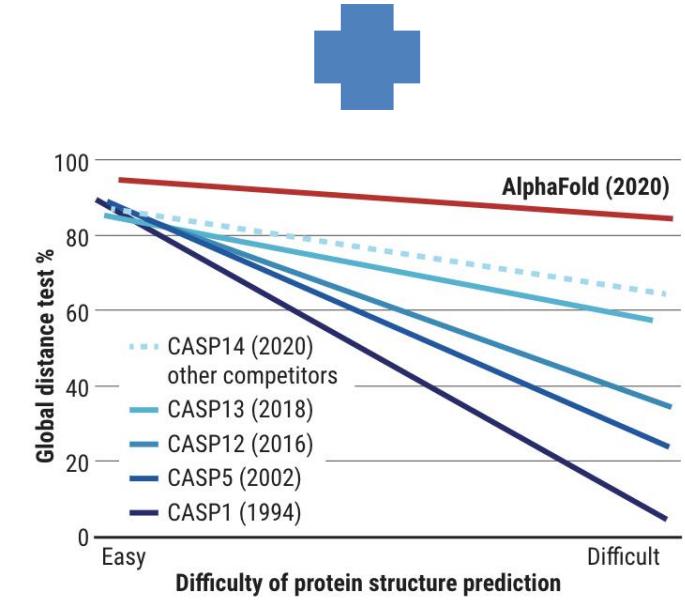
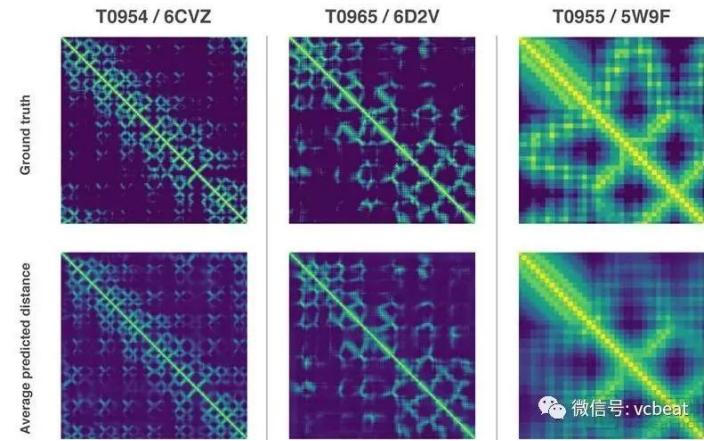
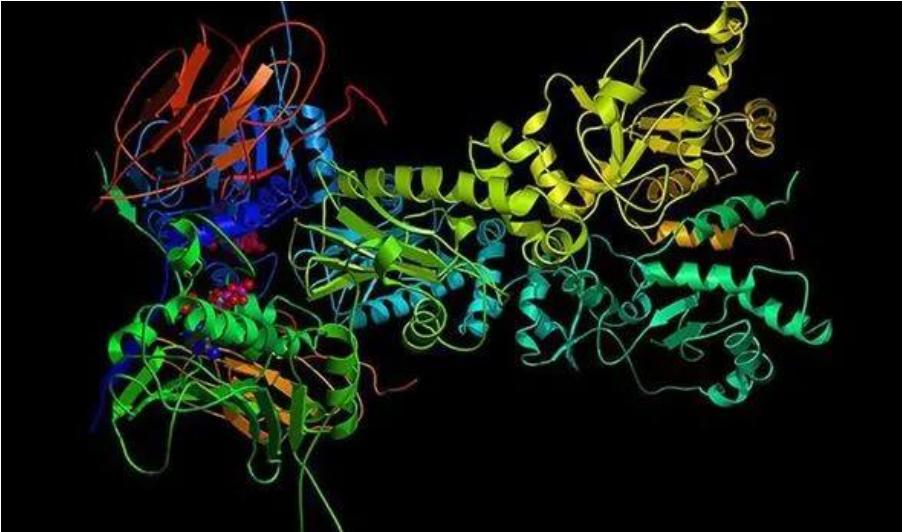
- 我们可以把蛋白质折叠看作一个「空间图」，节点表示残基（residue），边则将残基紧密连接起来。这个空间图对于理解蛋白质内部的物理交互及其演化史至关重要。对于在 CASP14 比赛中使用的最新版 AlphaFold，DeepMind 团队创建了一个基于注意力的神经网络系统，并用端到端的方式进行训练，以理解图结构，同时基于其构建的隐式图执行推理。该方法使用进化相关序列、多序列比对（MSA）和氨基酸残基对的表示来细化该图。
- DeepMind 团队在公开数据上训练这一系统，这些数据来自蛋白质结构数据库（PDB）和包含未知结构蛋白质序列的大型数据库，共包括约 170,000 个蛋白质结构。该系统使用约 128 个 TPUv3 内核（相当于 100-200 个 GPU）运行数周，与现今机器学习领域出现的大型 SOTA 模型相比，该系统所用算力相对较少。
- AlphaFold 还具备很多令人兴奋的技术潜力：探索数亿个目前还没有模型的数亿蛋白质，以及未知生物的广阔领域。由于 DNA 指定了构成蛋白质结构的氨基酸序列，基因组学革命使大规模阅读自然界的蛋白质序列成为可能——在通用蛋白质数据库（UniProt）中有 1.8 亿个蛋白质序列。相比之下，考虑到从序列到结构所需的实验工作，蛋白质数据库（PDB）中只有大约 170000 个蛋白质结构。在未确定的蛋白质中可能有一些新的和未确定的功能——就像望远镜帮助人类更深入的观察未知宇宙一样，像 AlphaFold 这样的技术可以帮助找到未确定的蛋白质结构。

CASP14

(Critical Assessment of Techniques for Protein Structure Prediction)

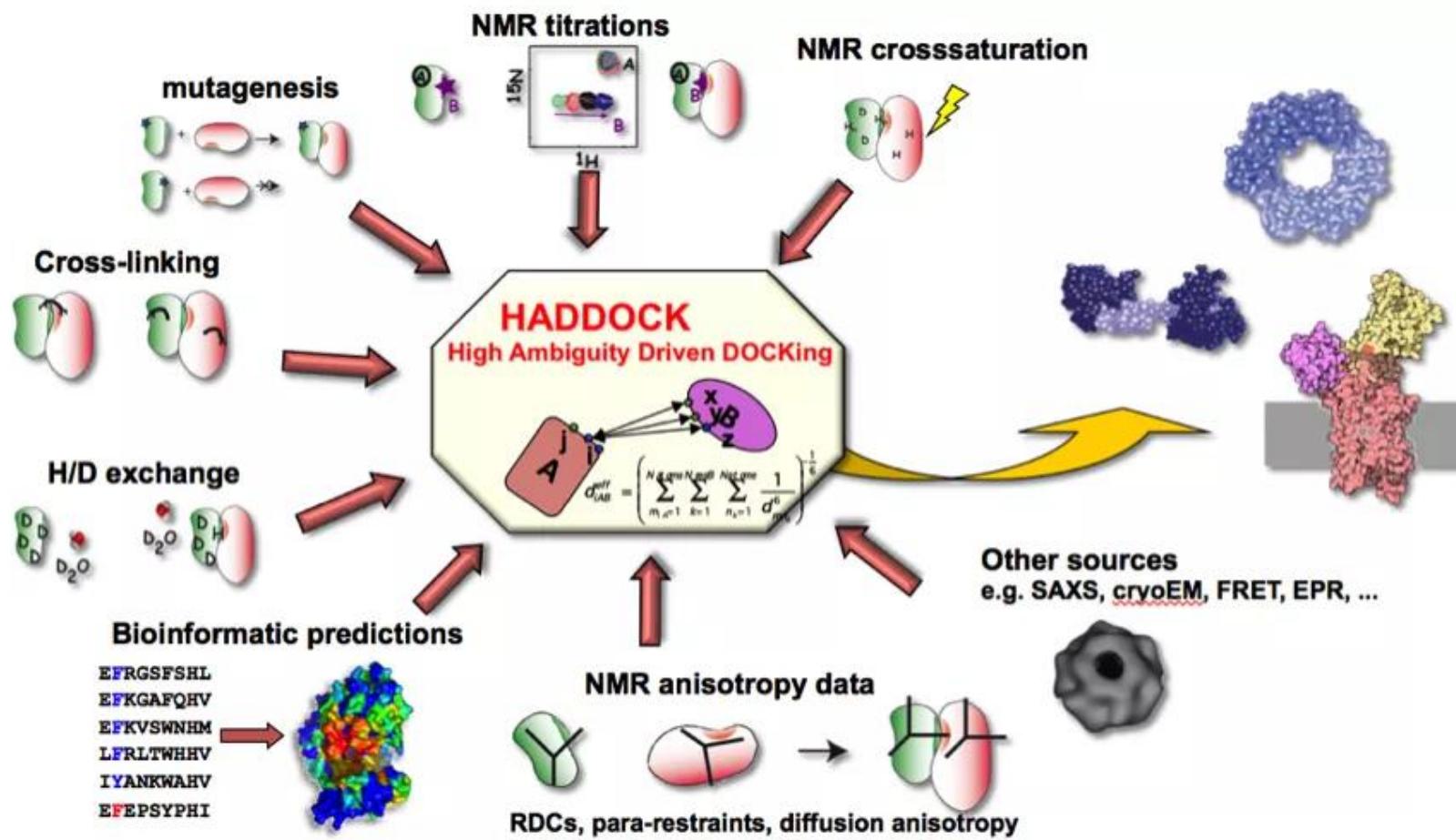
- 在今年早些时候，DeepMind已经利用这一系统预测了多种新冠病毒蛋白的结构。后续的实验显示，AlphaFold预测的新冠病毒Orf3a蛋白结构与冷冻电镜解析的结构非常相似。
- 虽然，AlphaFold不见得会取代冷冻电子显微镜等其它实验手段，但是DeepMind的研究人员表示，这一令人兴奋的结果表明，生物学家们可以使用计算结构预测作为科学研究的核心工具之一。这一手段对于特定类型的蛋白来说可能尤为便利，例如膜蛋白一直非常难于结晶，因此很难用实验手段获得它们的结构。
- 而对于从事计算和机器学习研究的DeepMind团队来说，AlphaFold的表现证明了AI在辅助基础科学发现方面惊人的潜力。该团队在公司发布的博文中表示，他们相信，AI将成为人类拓展科学知识前沿最有力的工具之一！

AI + 蛋白质3D结构

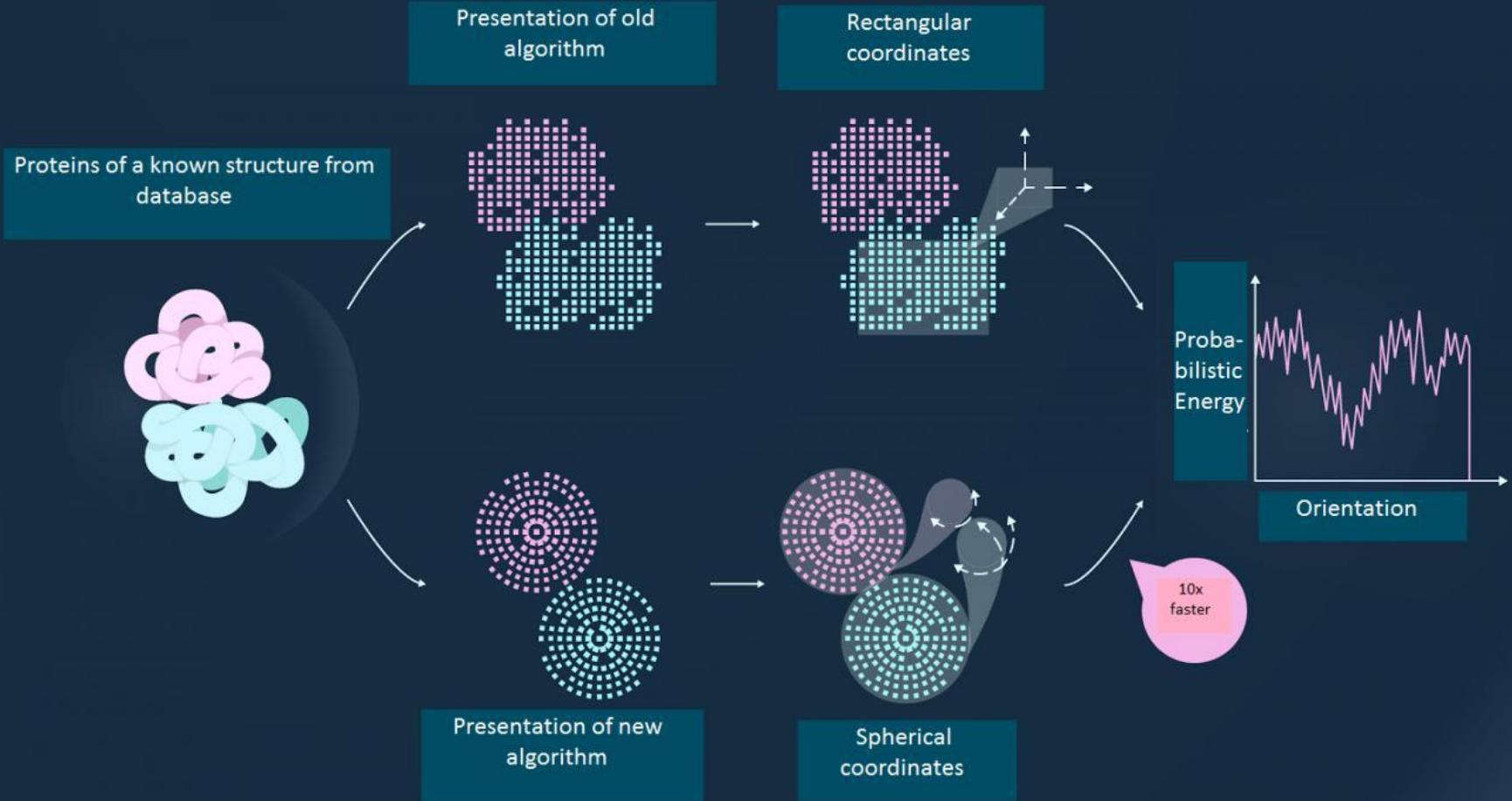


CAPRI

(Critical Assessment of PRediction of Interactions)



CAPRI

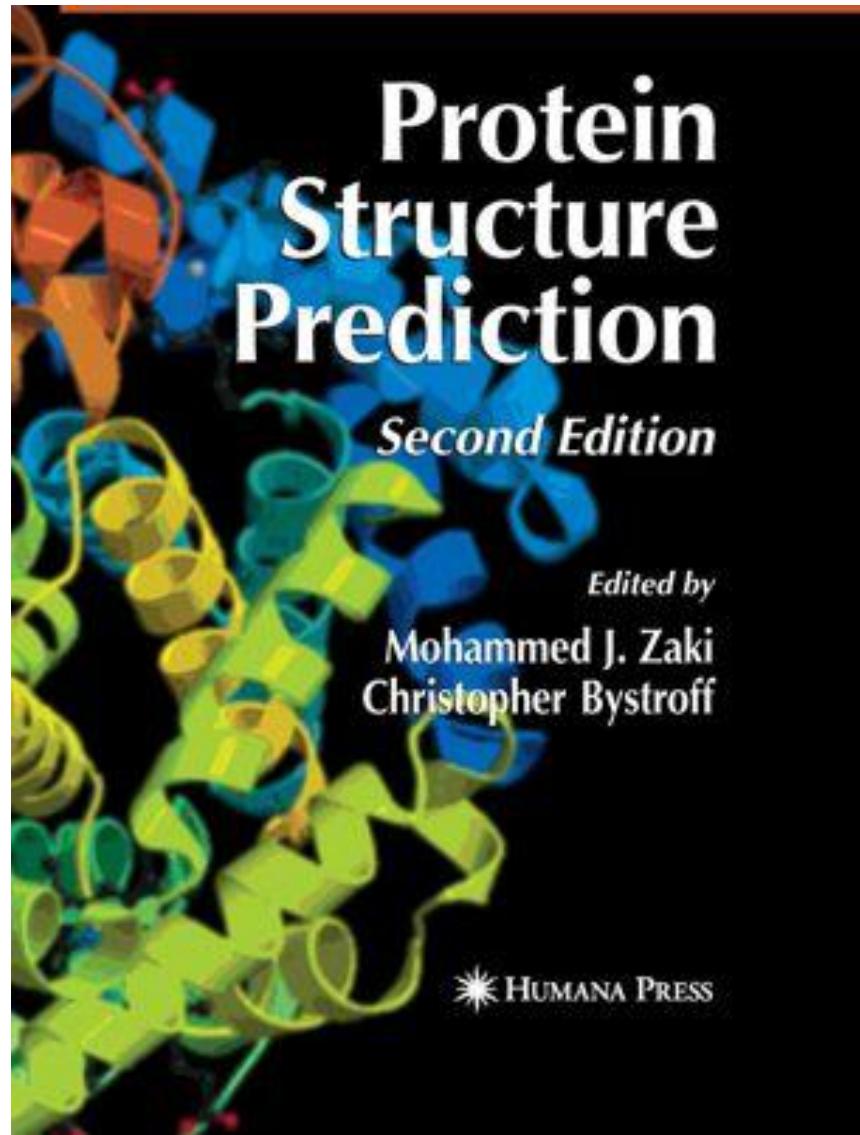


Protein 3D structure

小教程101

基于蛋白质序列的功能推断和结构解析

References



Slides credits

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- 生物统计学: 卜东波@中国科学院计算技术研究所, 邓明华@北京大学
- 神经网络与深度学习: 邱锡鹏@复旦大学
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