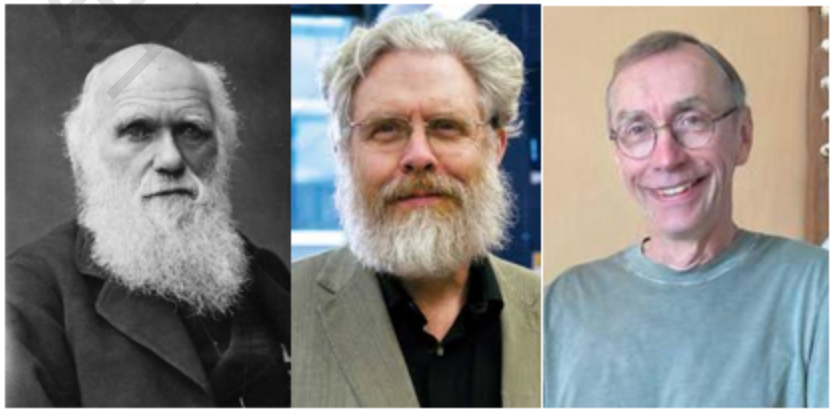
生物统计学：
生物信息中的概率统计模型

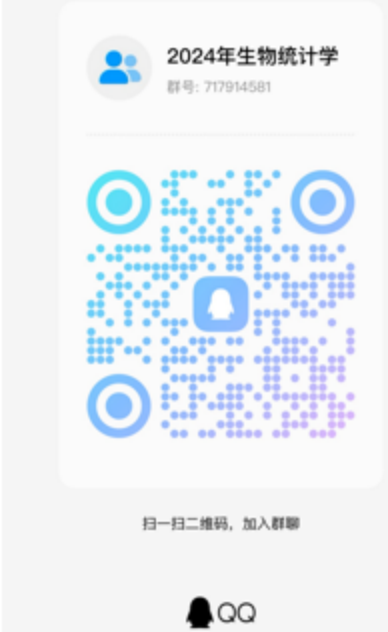
2024年秋



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606室
  - Phone: 18627968927

- 课程网页
  - http://www.microbioinformatics.org/Biostatistics.html
  - QQ群：717914581



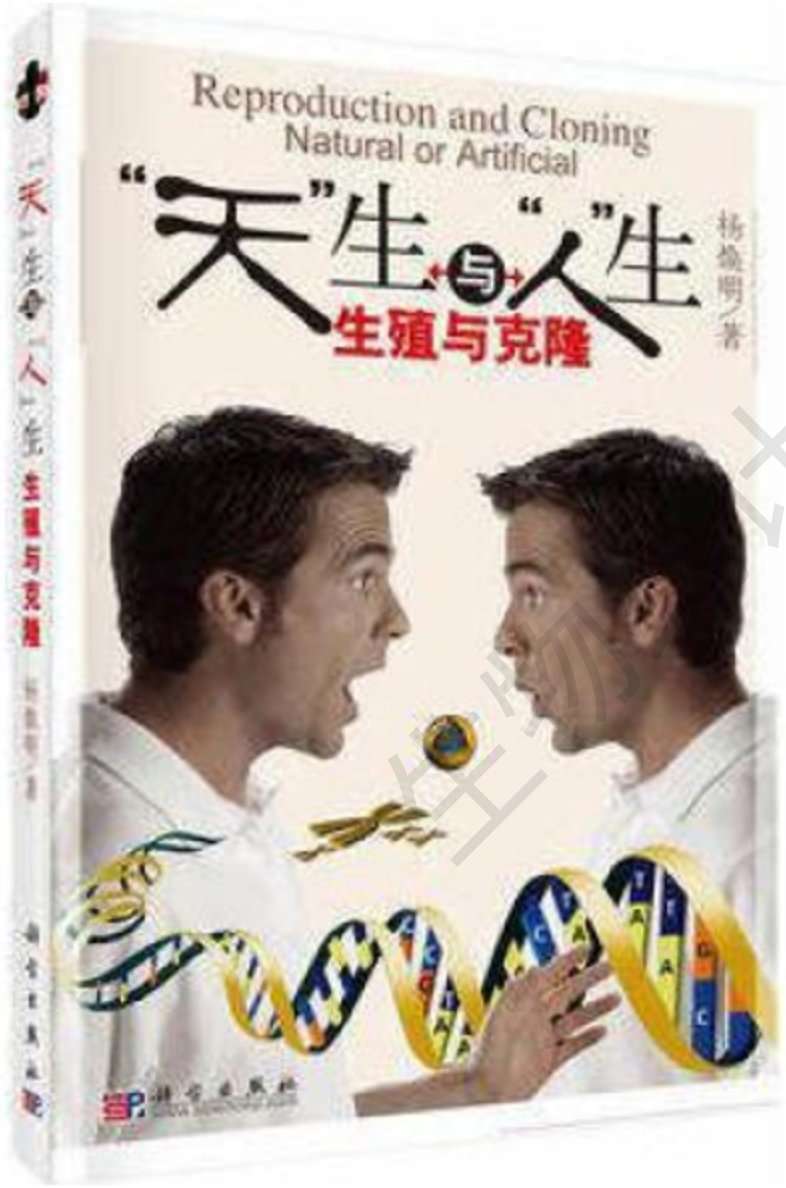
课程安排

- 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
...

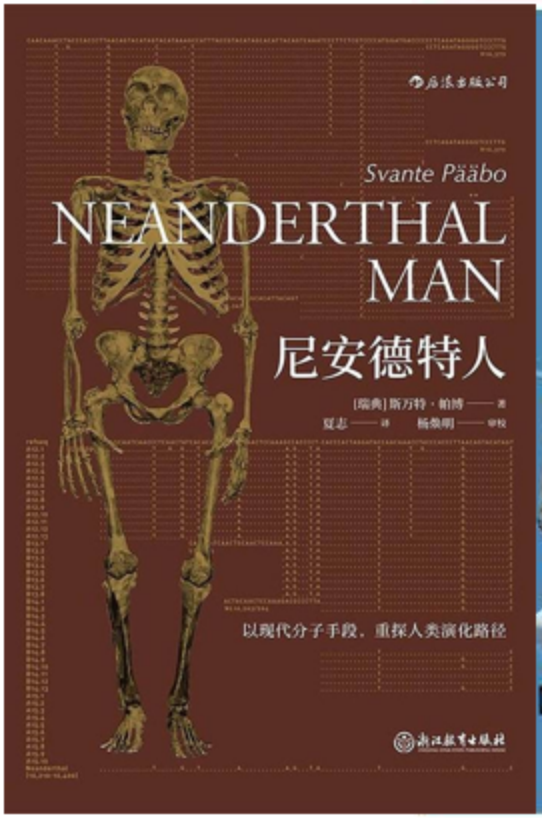
方法:
生物计算与生物统计

读物推荐


Reproduction and Cloning
Natural or Artificial
“天”生与“人”生
生殖与克隆
杨焕明 著

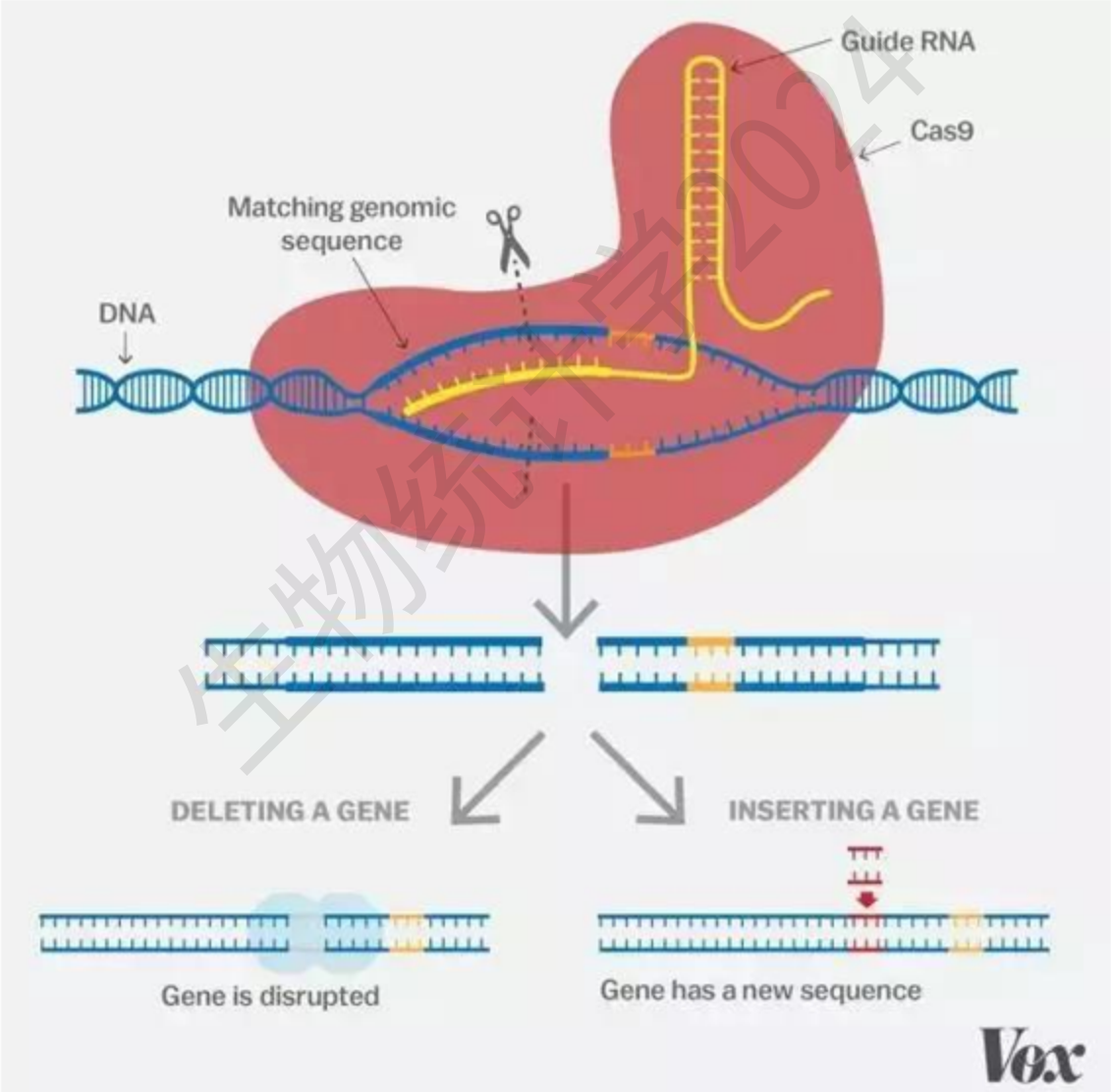

How Synthetic Biology Will Reinvent Nature and Ourselves
Regenesis
[美] 乔治·丘奇（George Church） [美] 艾德·里吉西（Ed Regis） 著
再创世纪
合成生物学将如何重新
创造自然和我们人类
周东 译

人类的进化

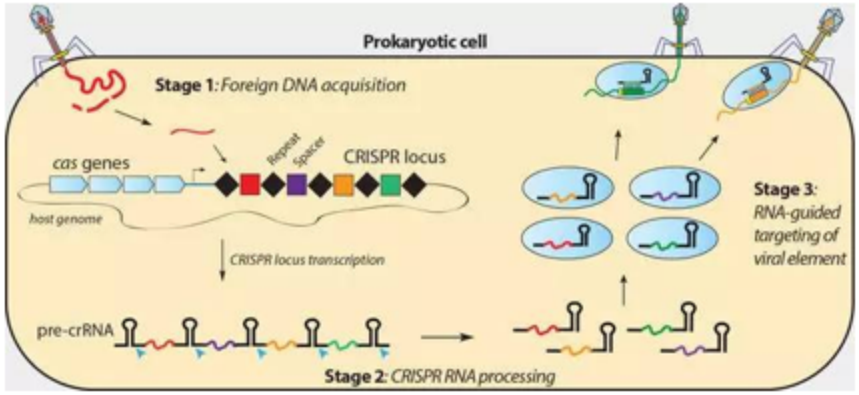


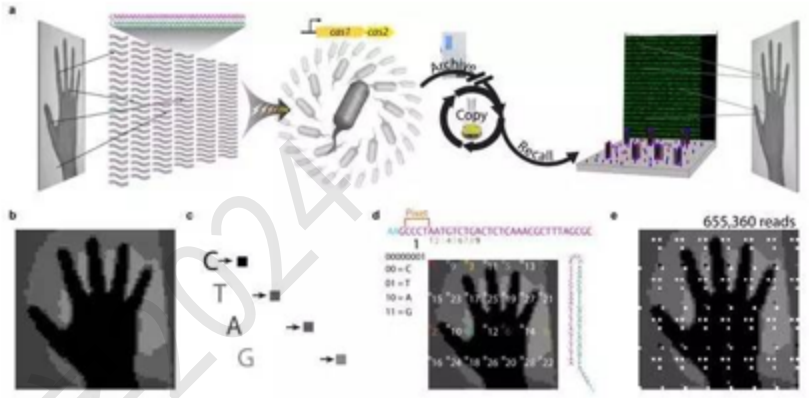
人类的进化

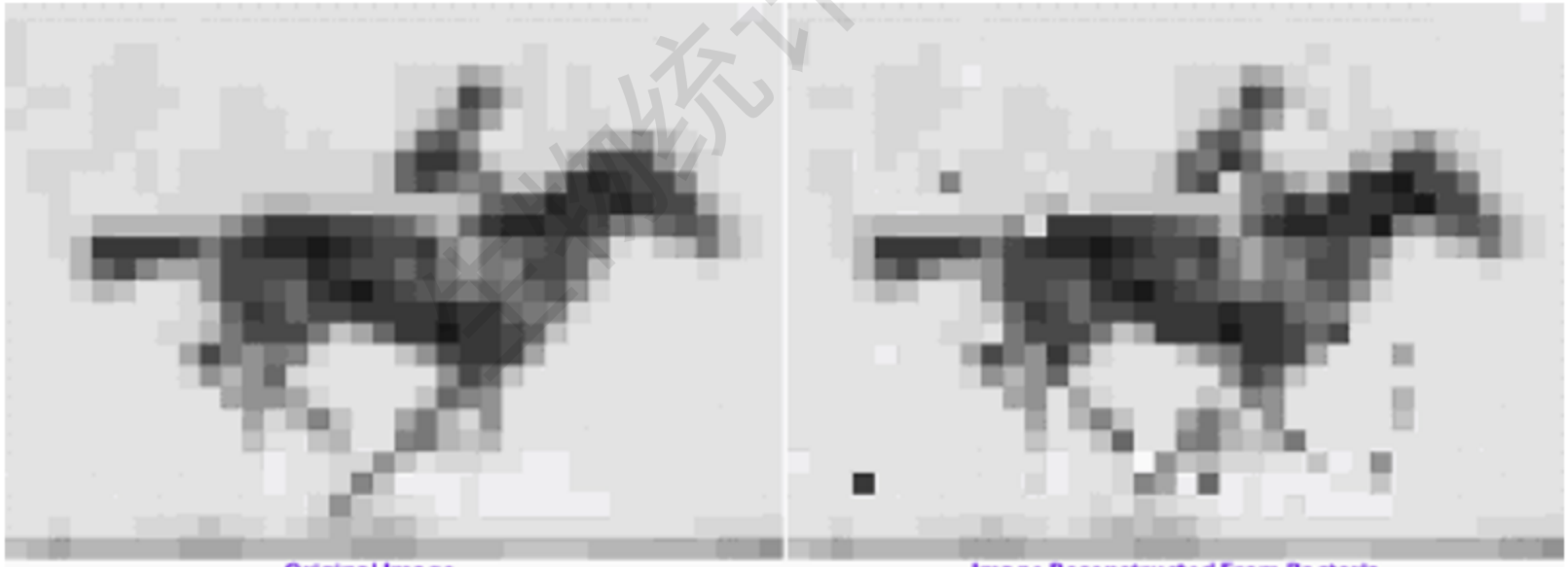
CRISPR和基因编辑技术



Understand it, create it!





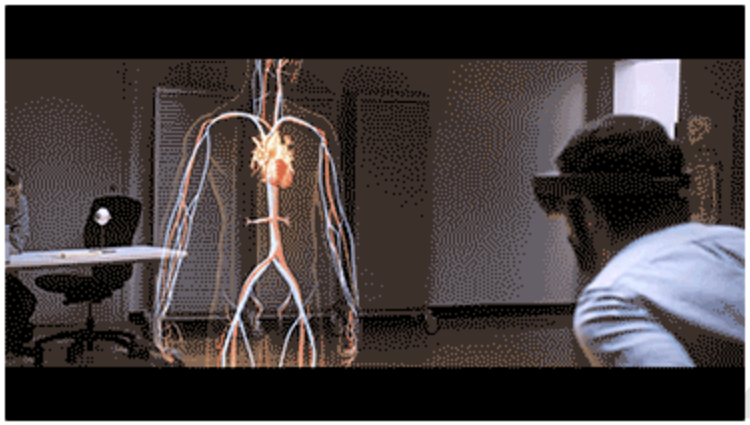


Original Image

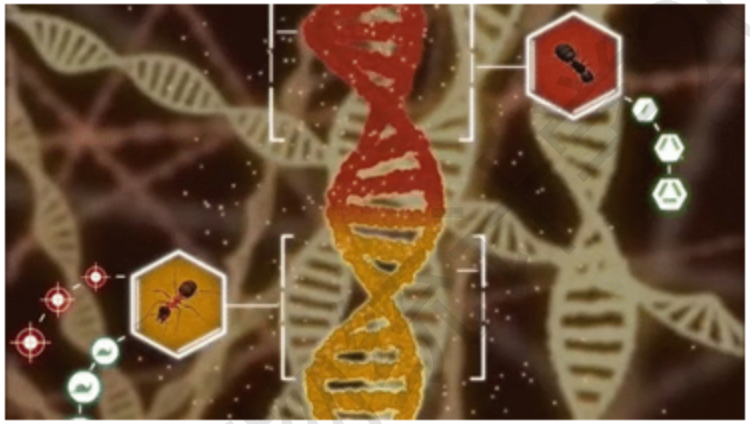
原始图像

Image Reconstructed From Bacteria

从细菌DNA还原的图像



See it!

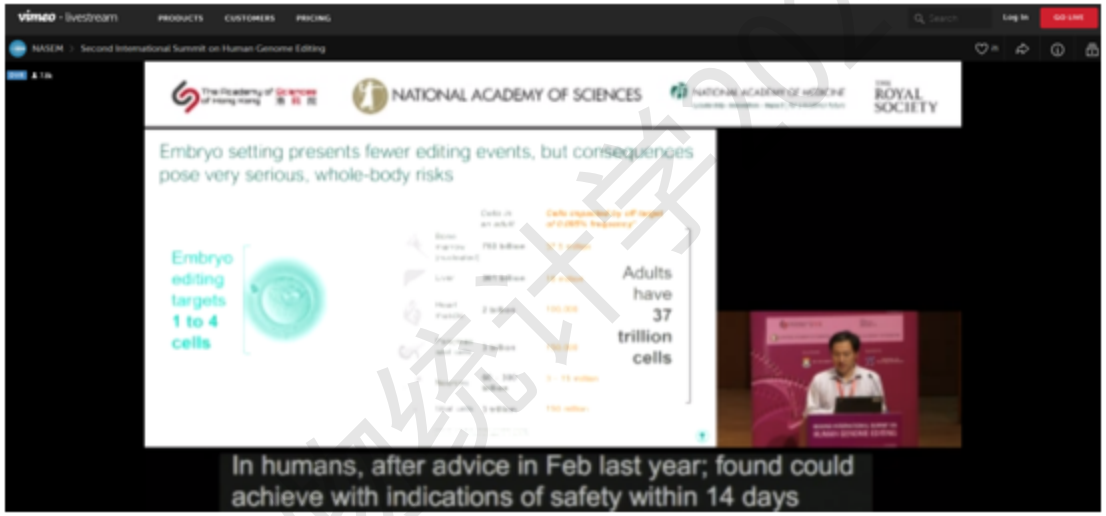


Understand it!

Create it!

CRISPR和基因编辑技术

要清楚什么可以做，什么不可以做！

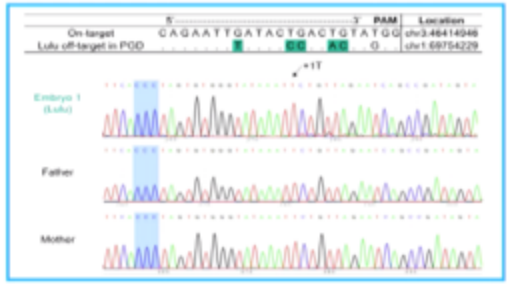


PGD identified one potential intergenic off-target

WGS Analysis

Analysis	PGD	
	Lulu	Nana
Total variants	3,380,550	3,581,757
Candidate off-targets	1	0
Validated off-targets	1	-
Large deletion	0	0

Sanger Sequencing Validation

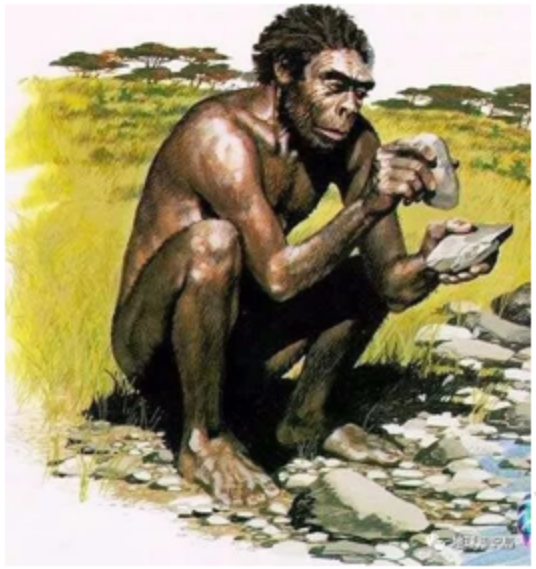


Not expected to impact any biological function.

- 279 kb away from any known gene
- Not near any known non-coding RNA or transcription factor binding site

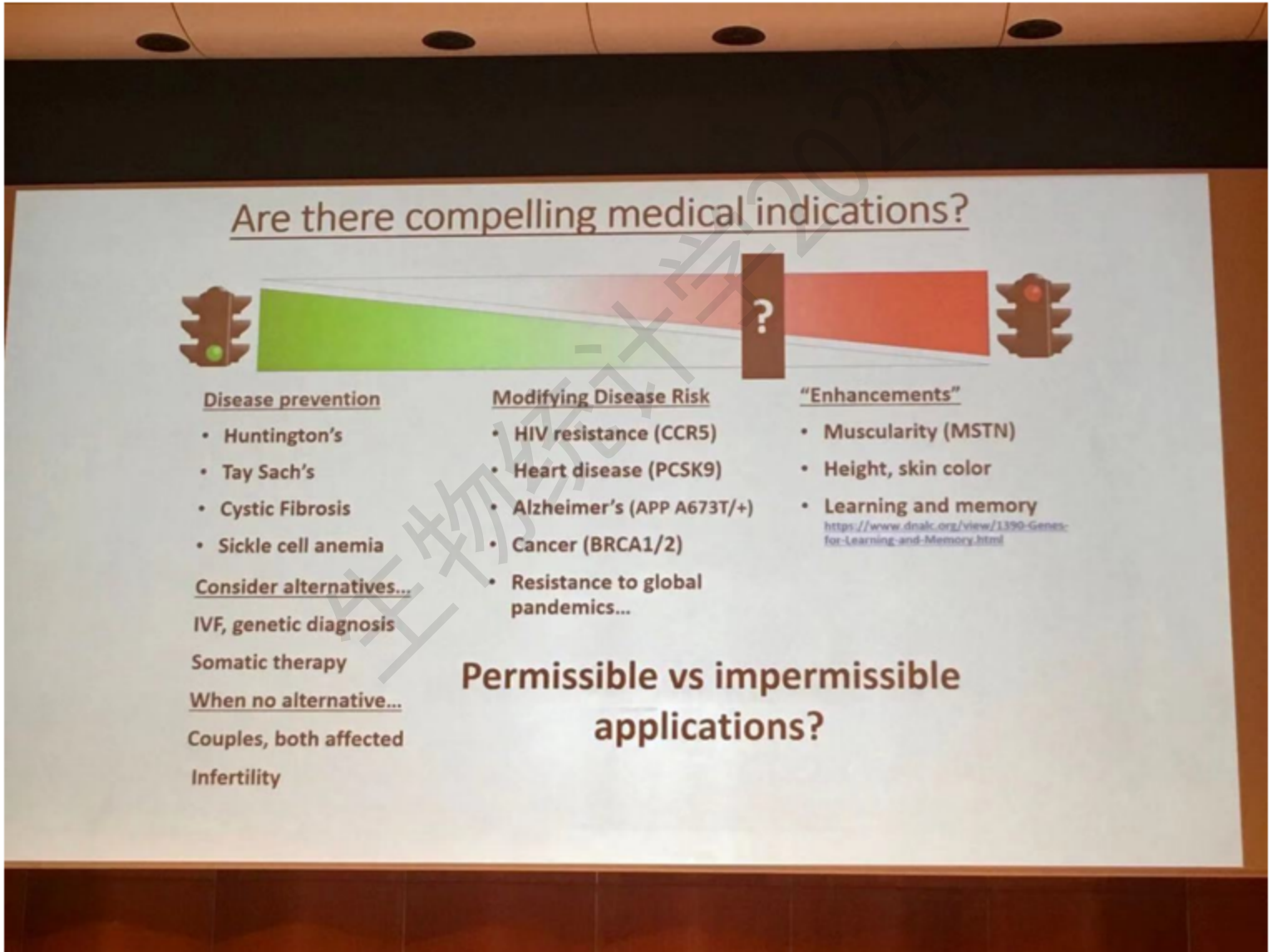
Volunteers were

CRISPR和基因编辑技术



OR

CRISPR和基因编辑技术

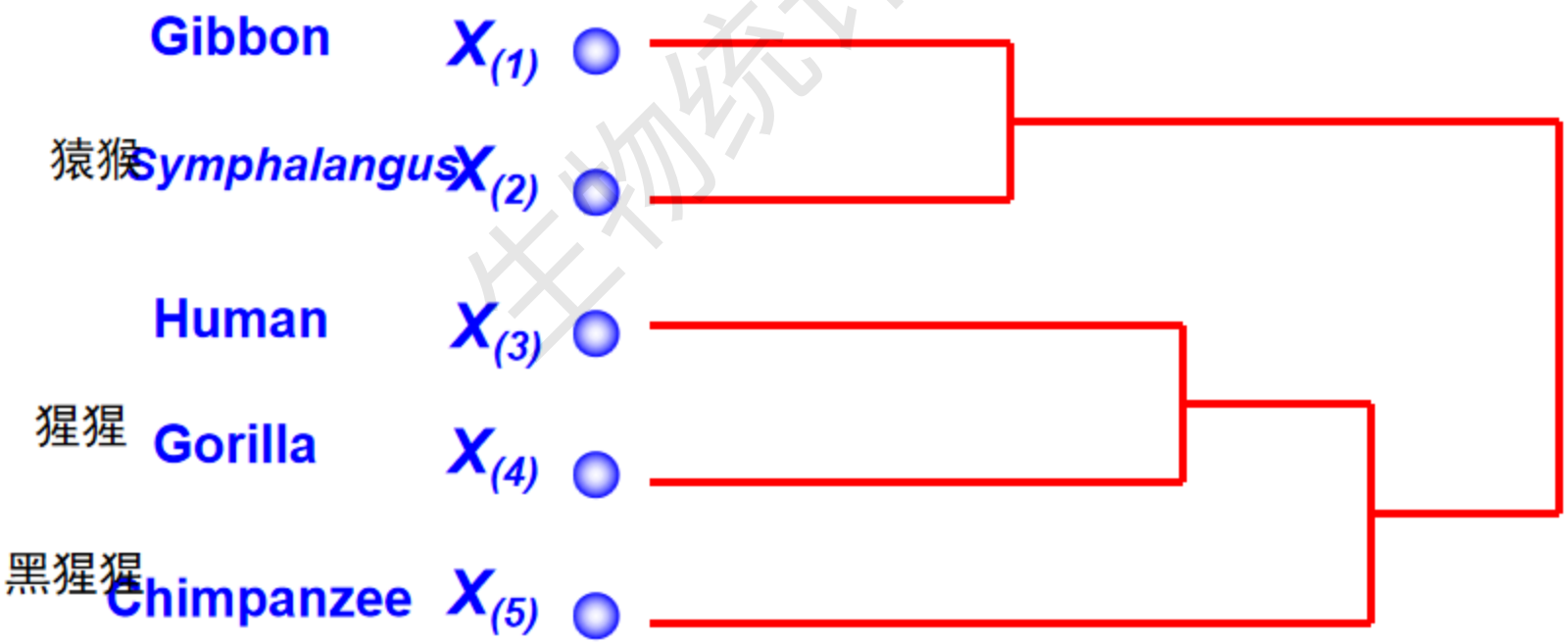


第4章：进化树构建的概率方法

- 问题介绍
- 进化树构建方法的概率方法

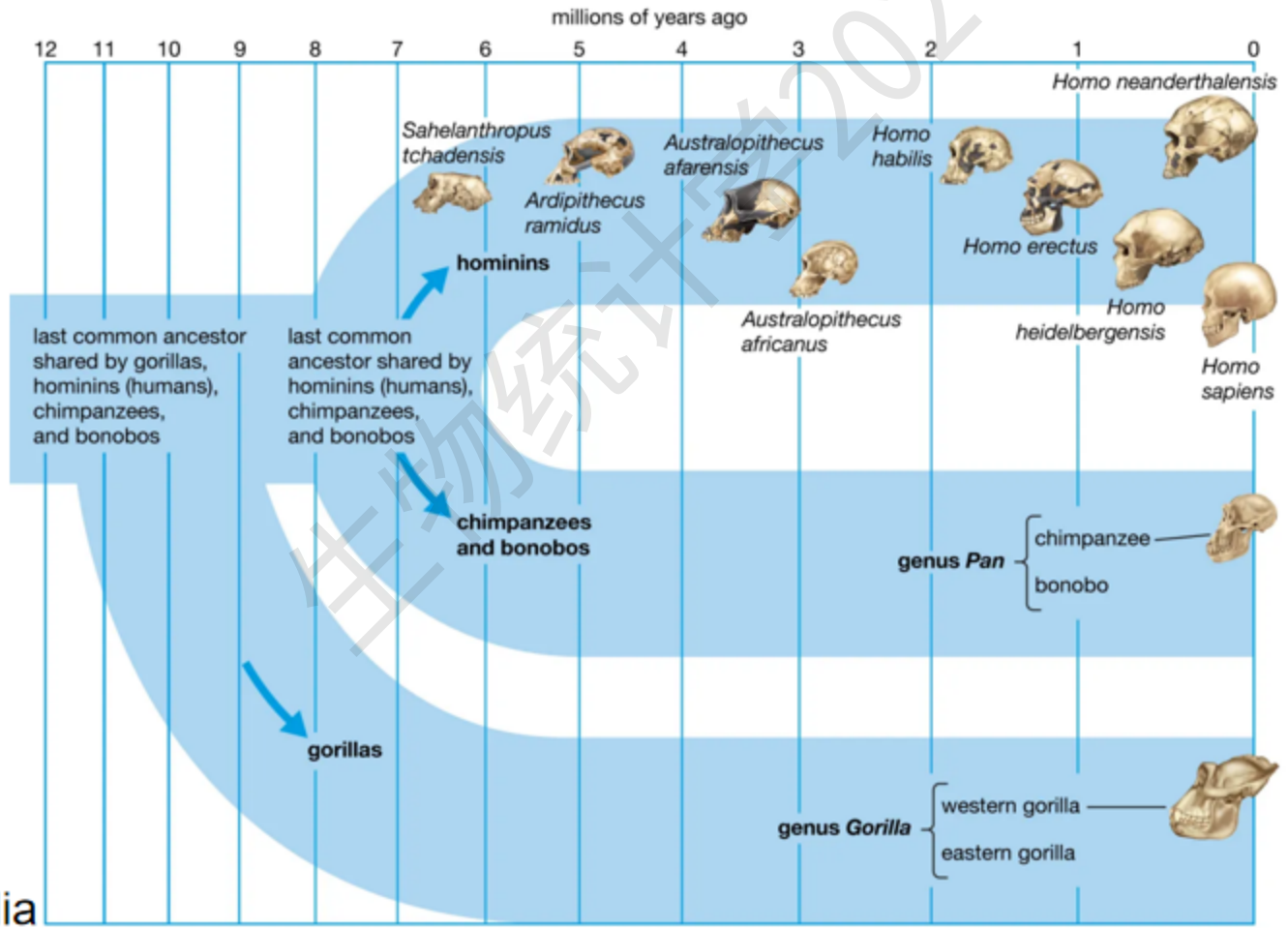
Phylogenetic Tree

A toy example:primates



Phylogenetic Tree

The evolution of primates as of 2020

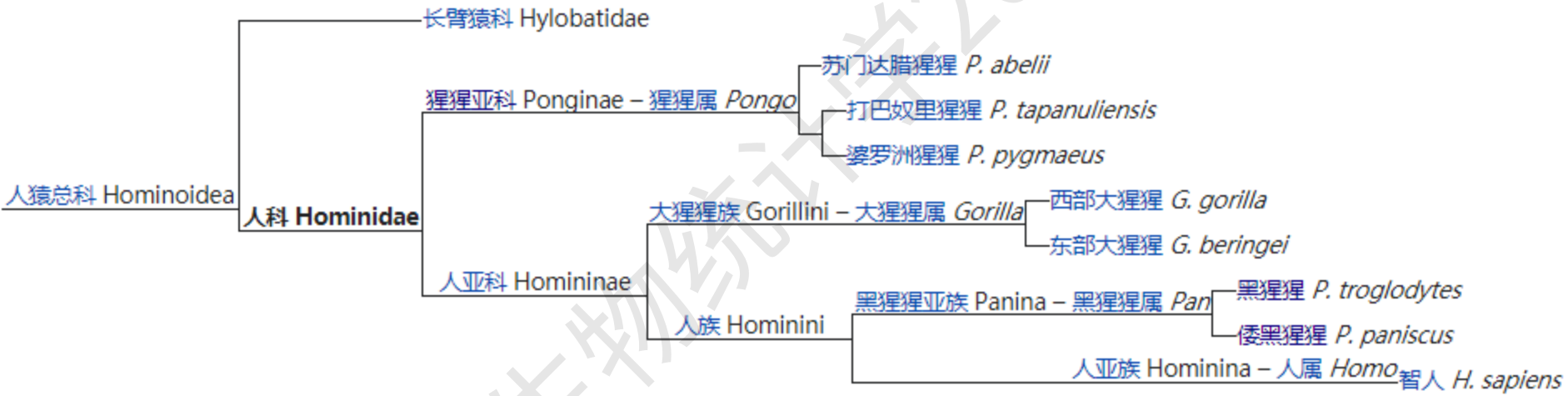


Encyclopedia Britannica

Phylogenetic Tree

The evolution of primates as of 2020

现存人科动物的分化关系：



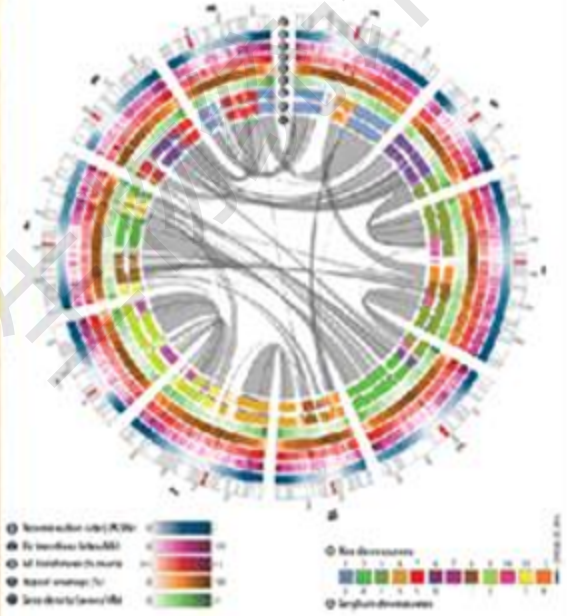
３１００万年前，人猿类跟猴猱类分离；
２０４０万年前，长臂猿跟“红＋大＋黑＋人”分离；
１５７０万年前，红猩猩跟“大＋黑＋人”分离；
８８０万年前，大猩猩跟“黑＋人”分离；
６３０万年前，黑猩猩跟人类分离……

Wikipedia

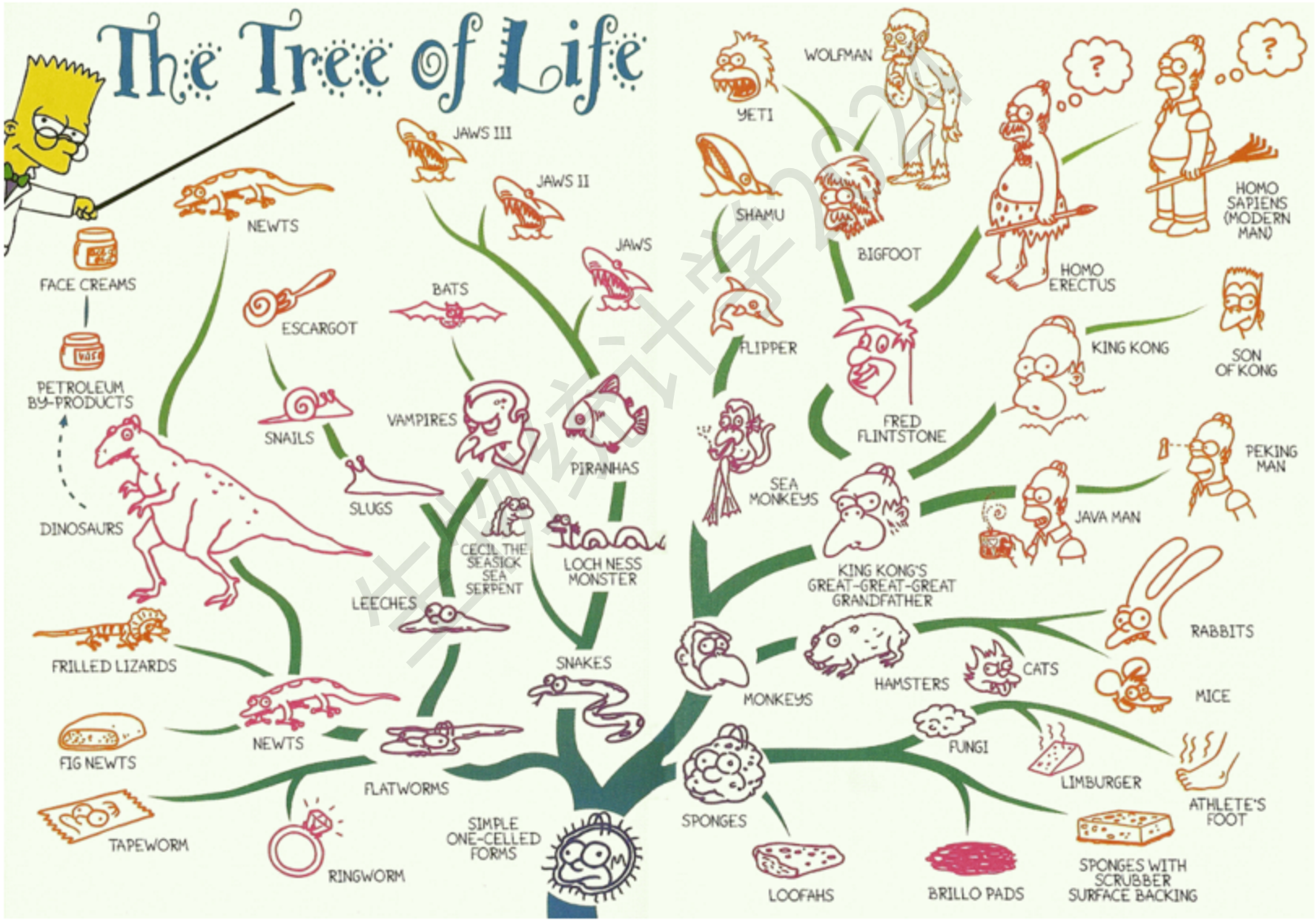
视频资料：
https://b23.tv/ep12091

Phylogenetic Tree

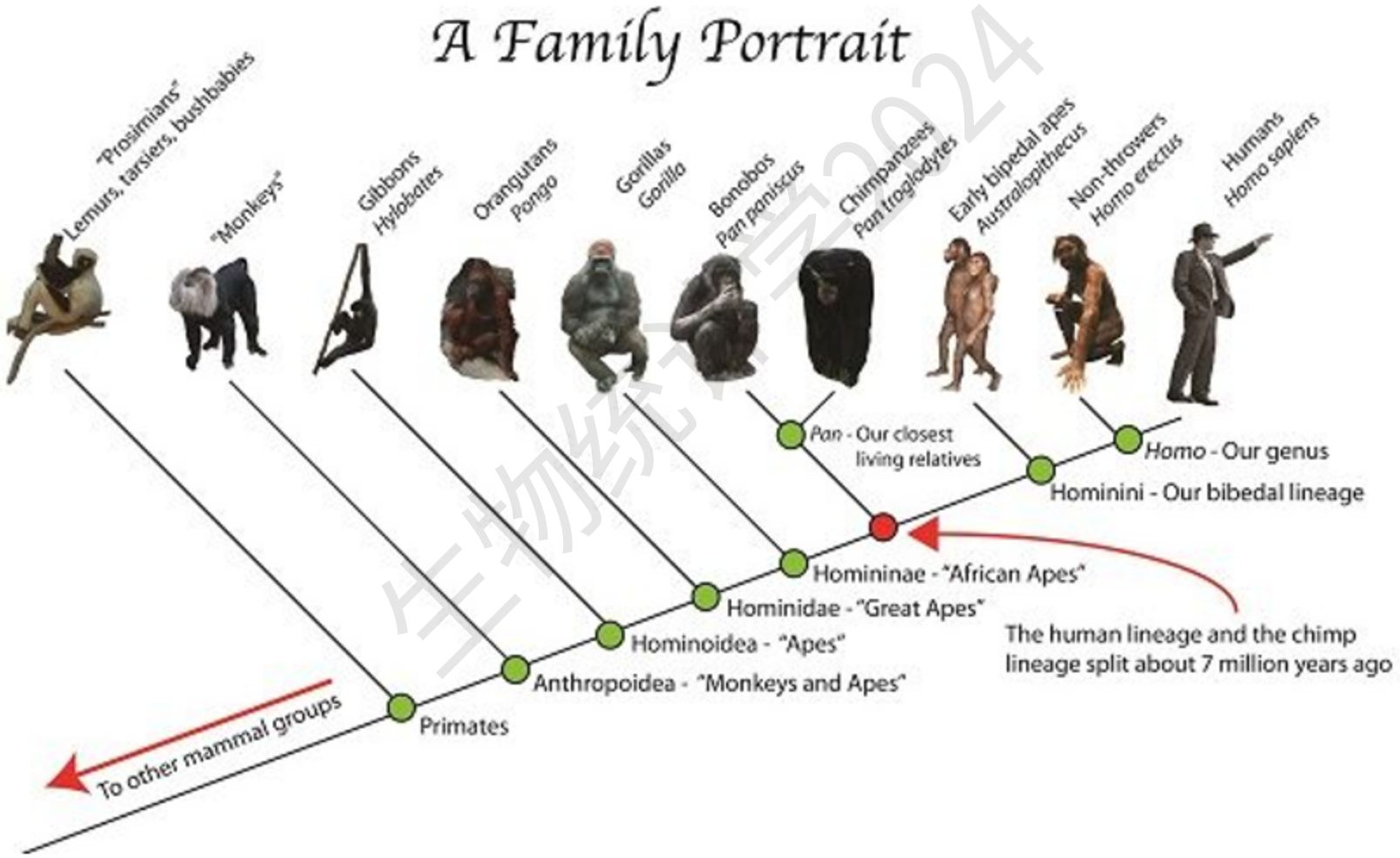
Everyone what to know how this tree look like...



Phylogenetic Tree

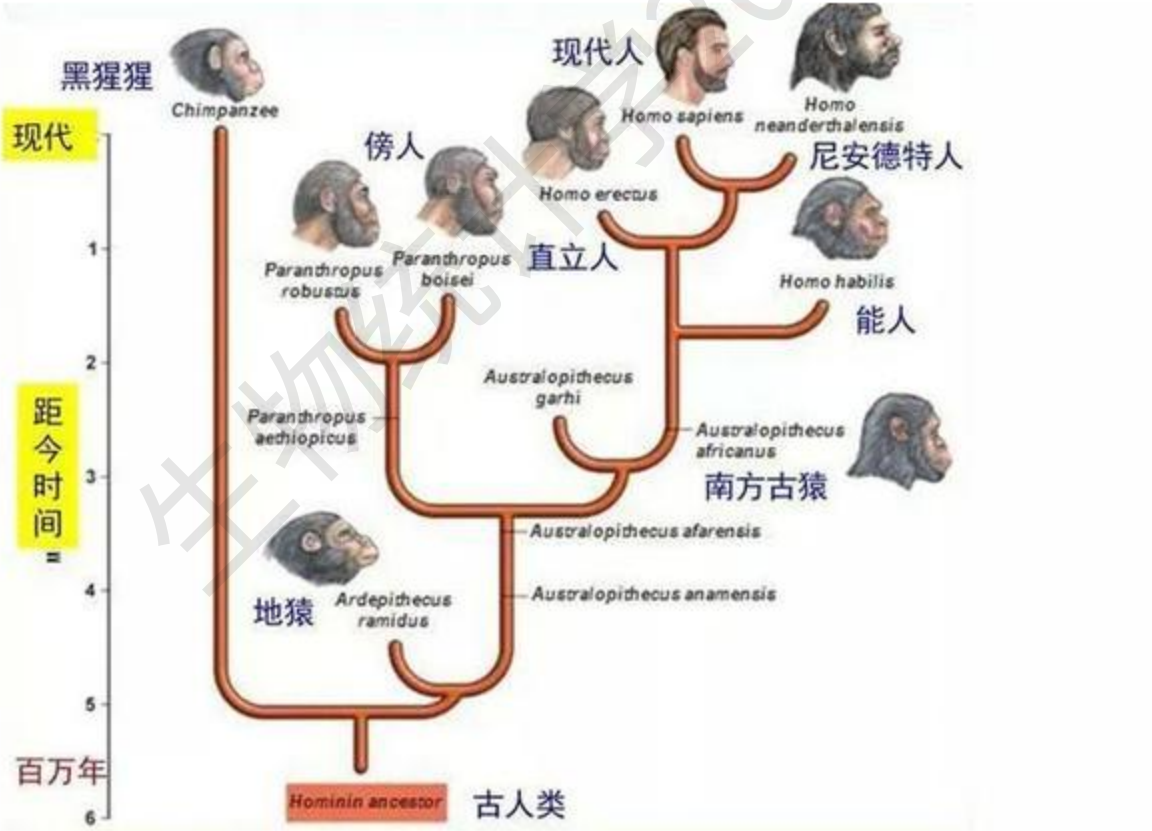


Evolution everywhere



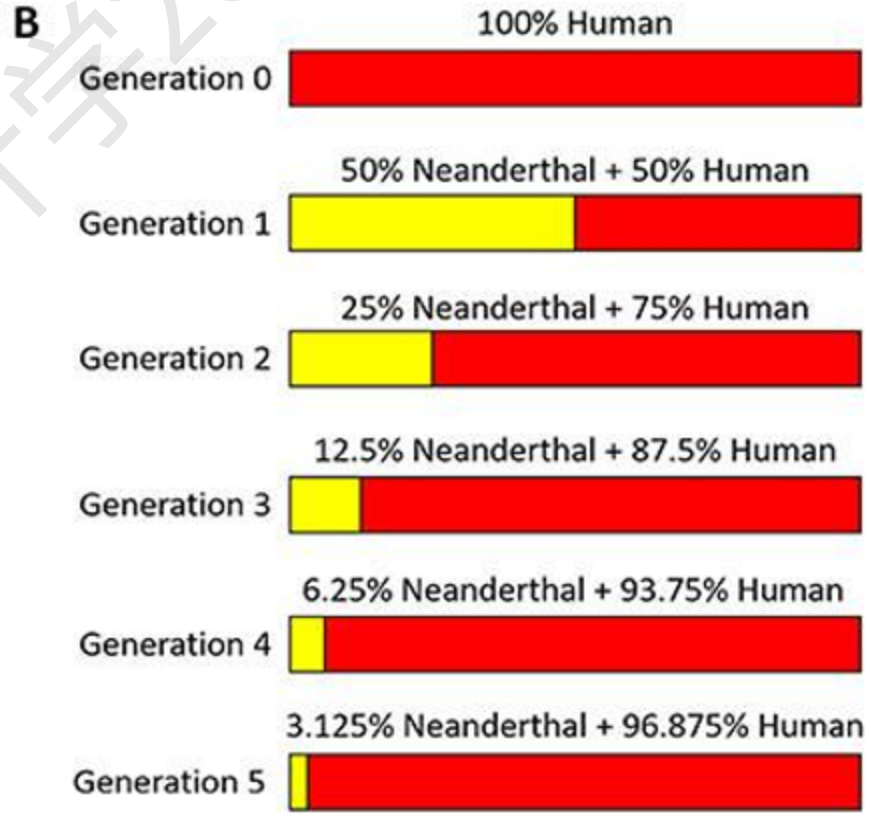
Evolution everywhere

Human evolution



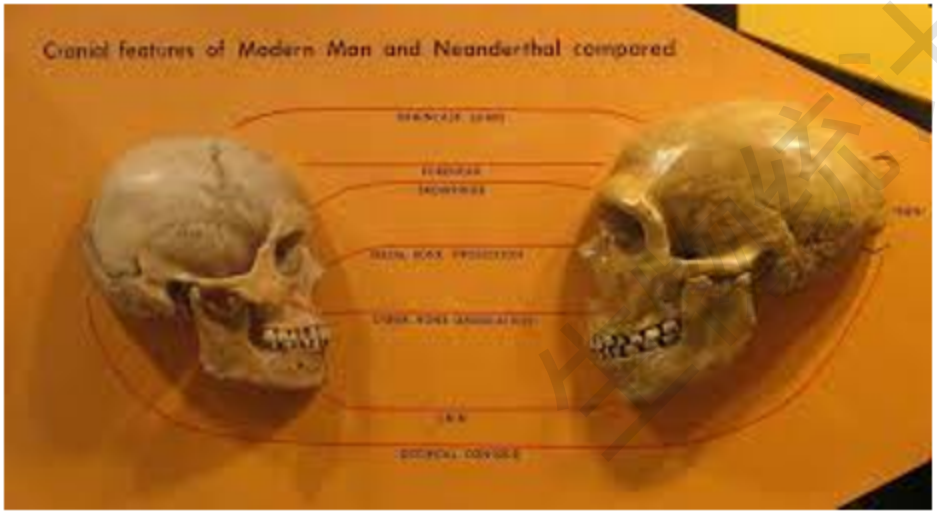
Evolution everywhere

Human evolution



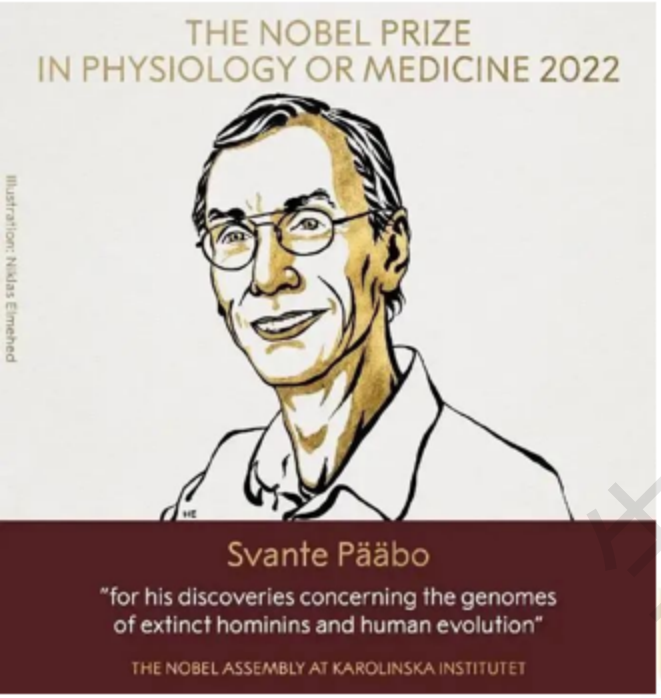
Evolution everywhere

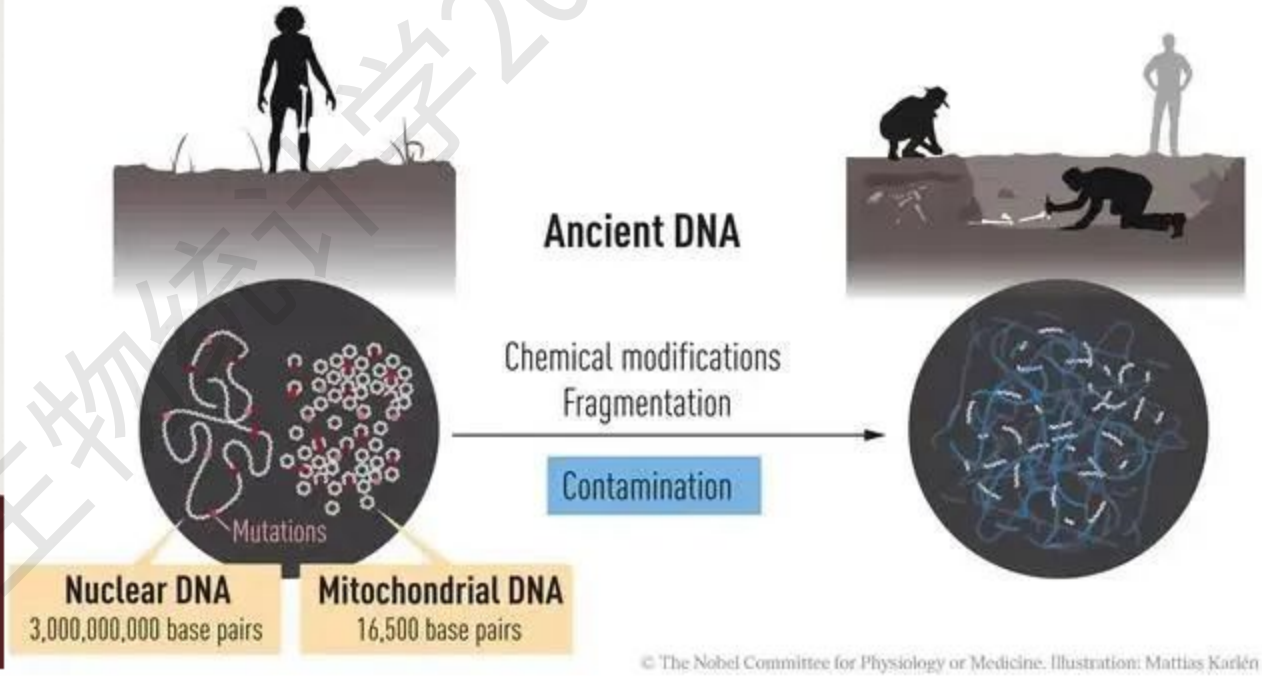
Human evolution



Evolution everywhere

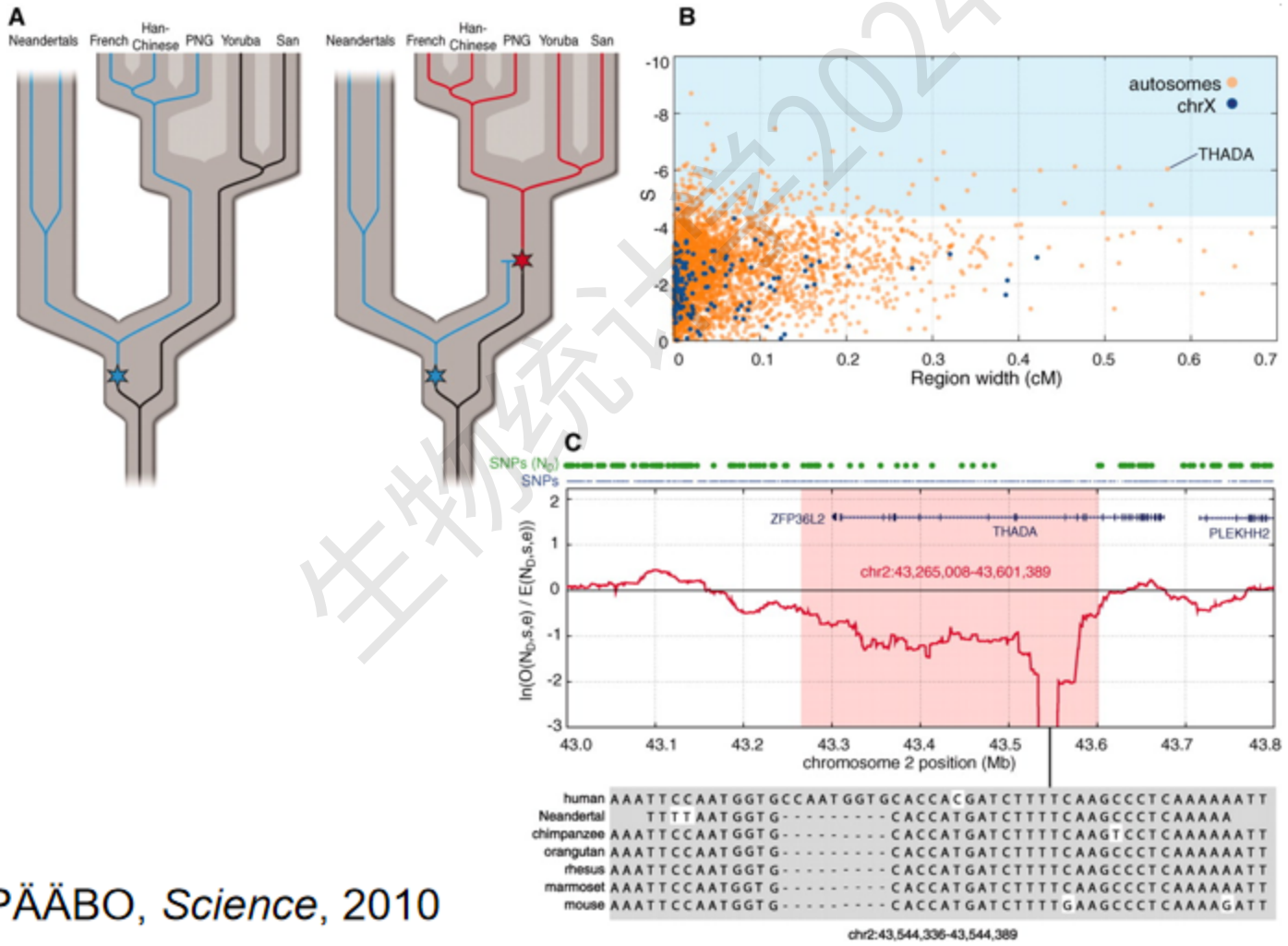
Human evolution





Evolution everywhere

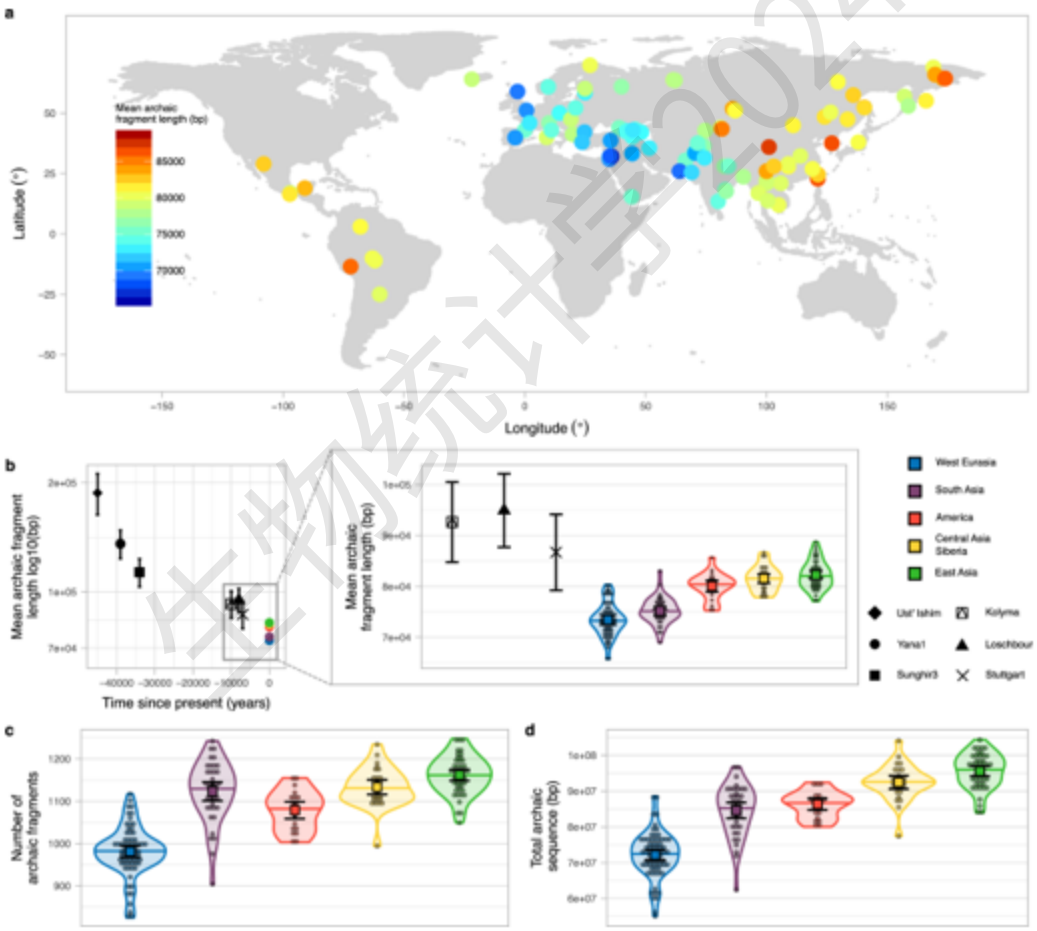
Human evolution



SVANTE PÄÄBO, *Science*, 2010

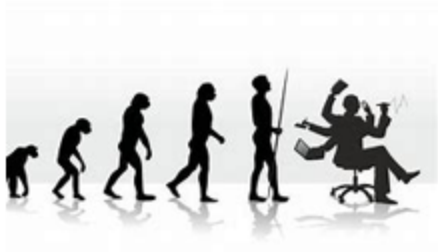
Evolution everywhere

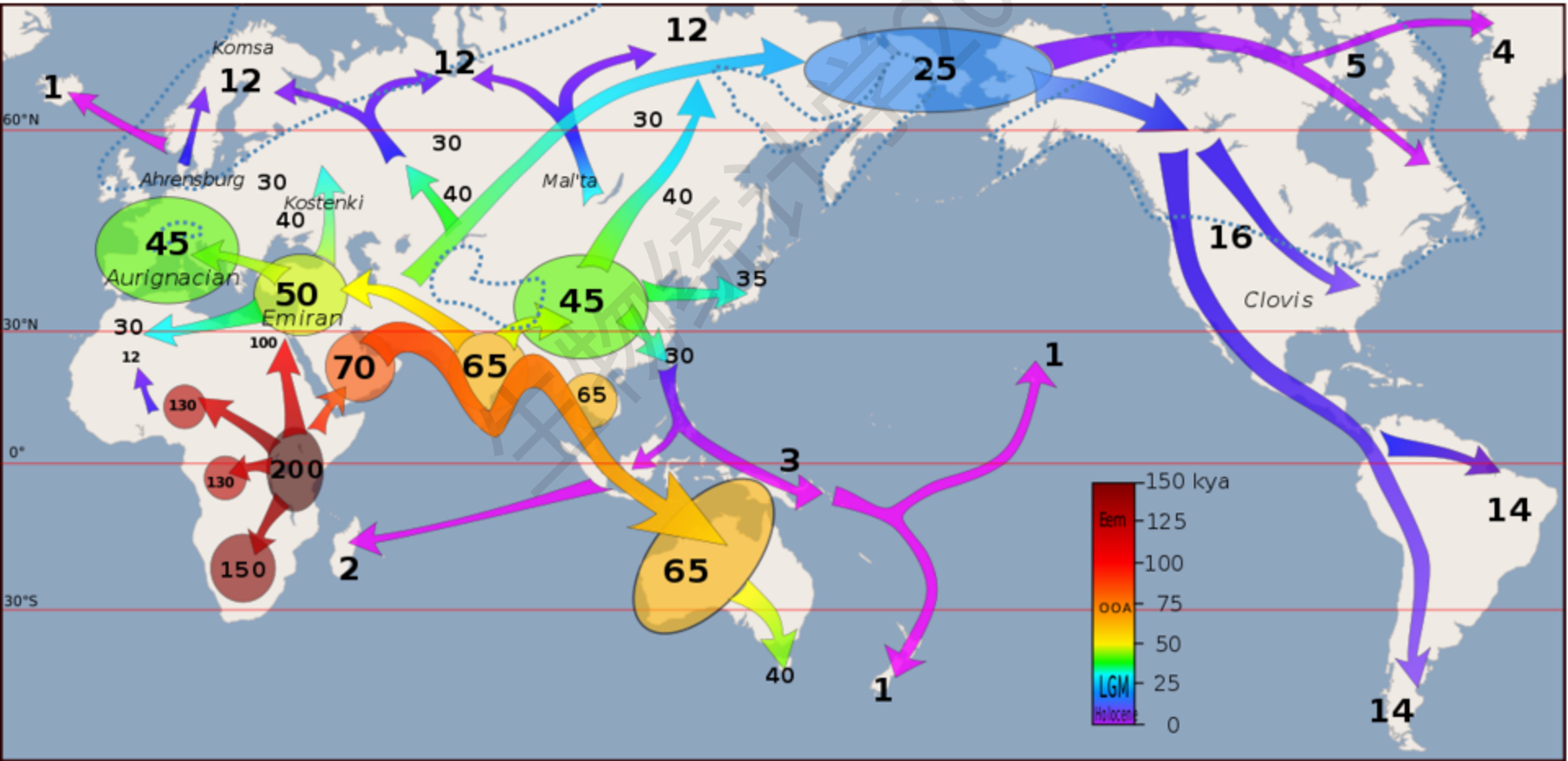
Human evolution



Mikkel Heide Schierup, *Nature*, 2021

Evolution everywhere

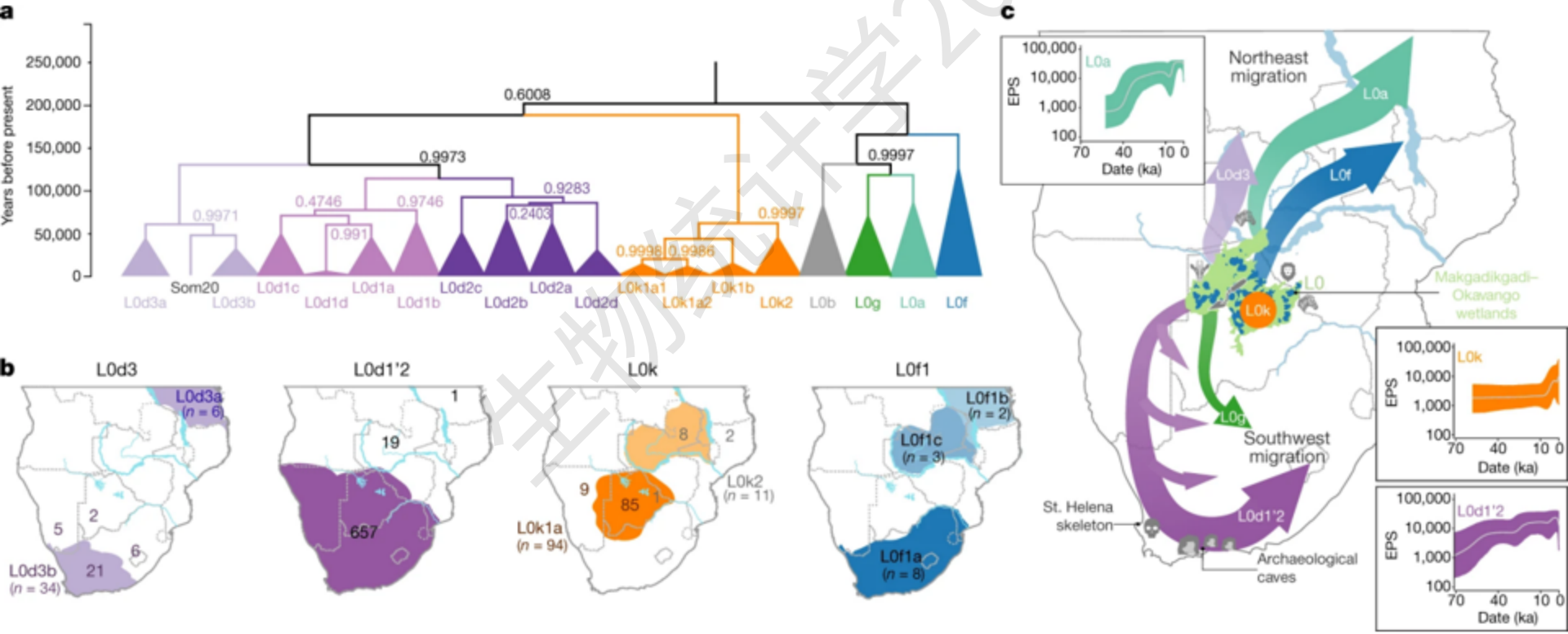




Evolution everywhere

Evolution everywhere

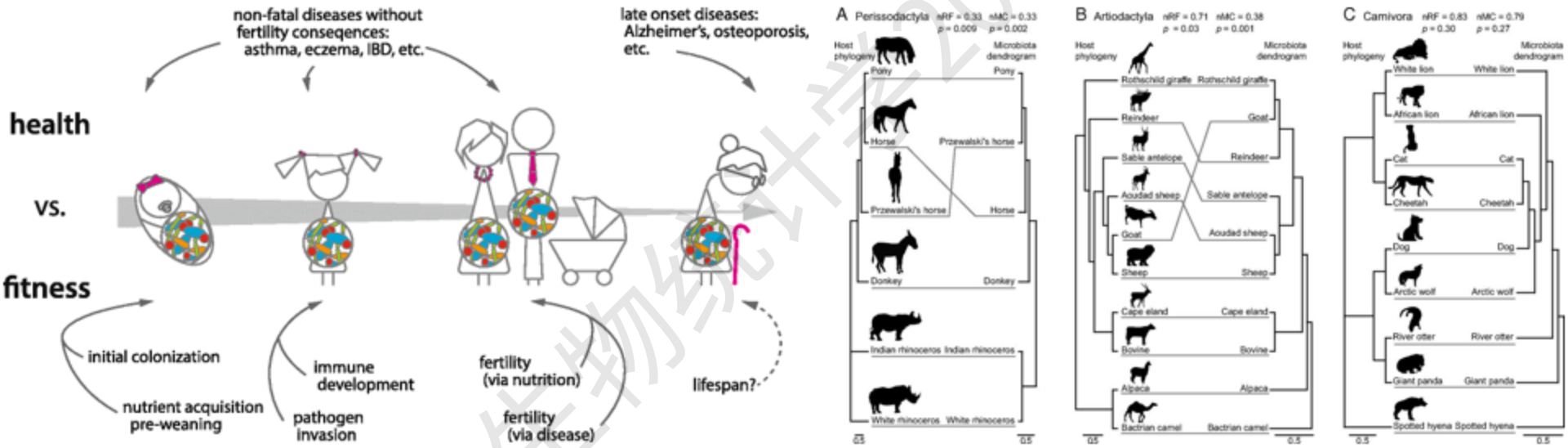
Out of “homeland”?



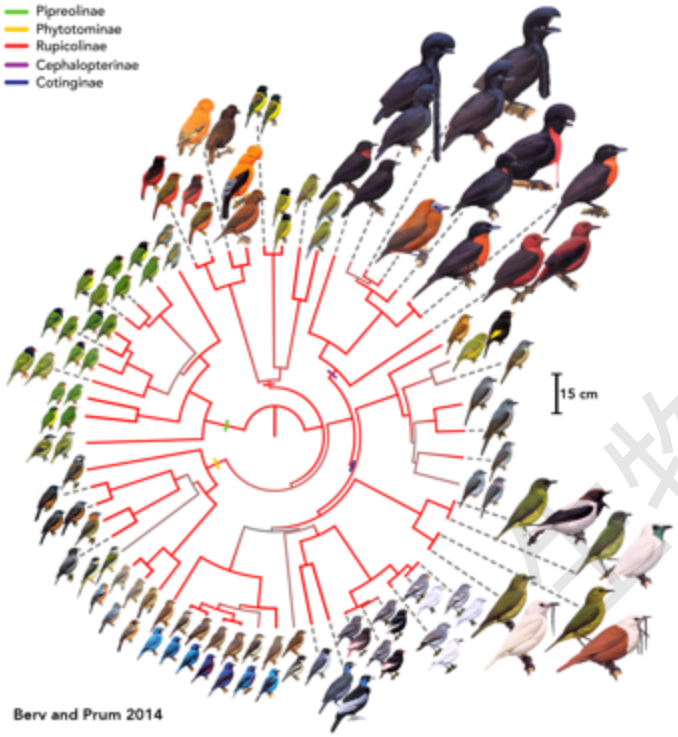
Eva K. F. Chan et al., *Nature*, 2019

Evolution everywhere

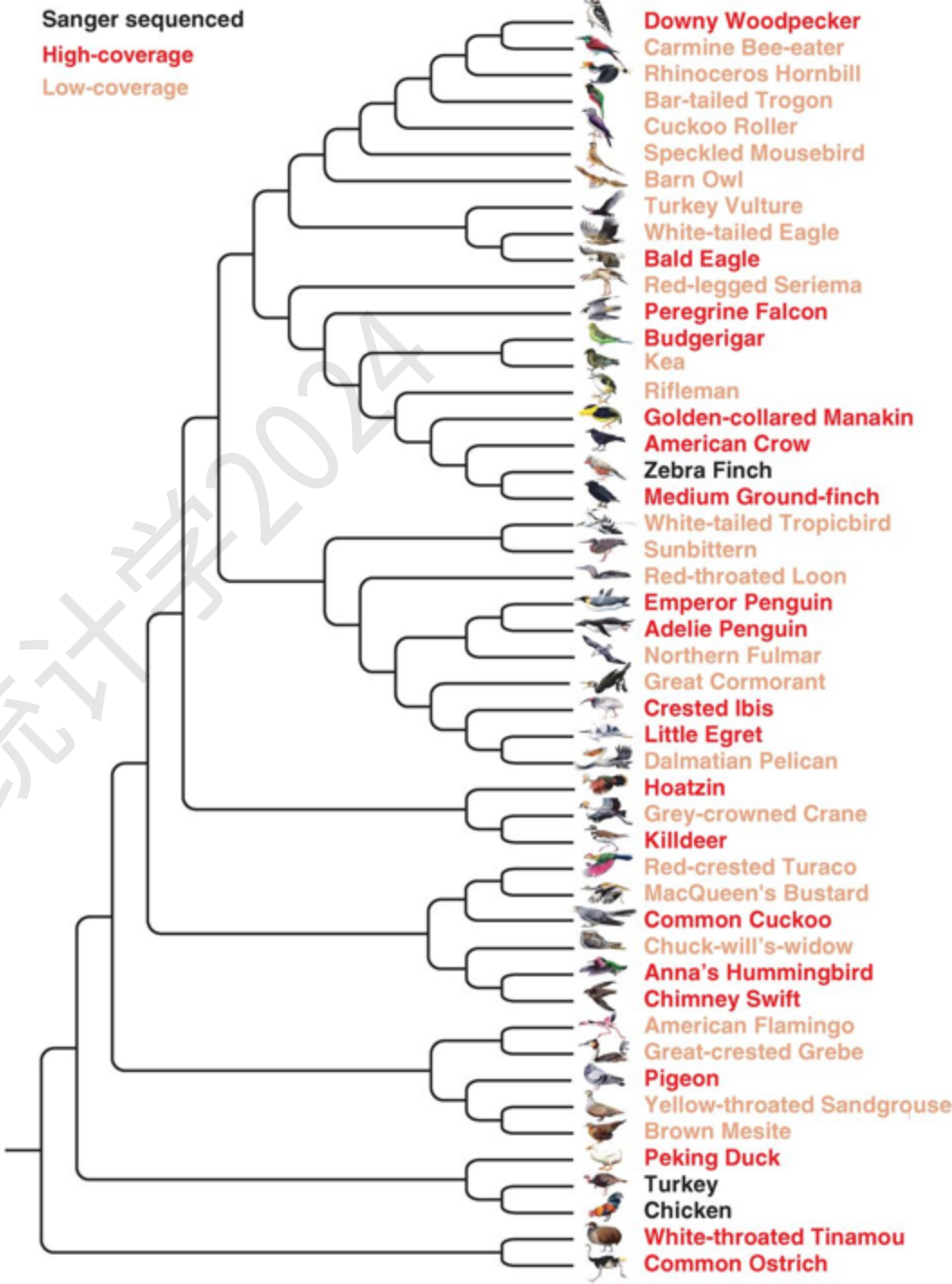
Microbiome evolution also exists



Phylogenetic Tree



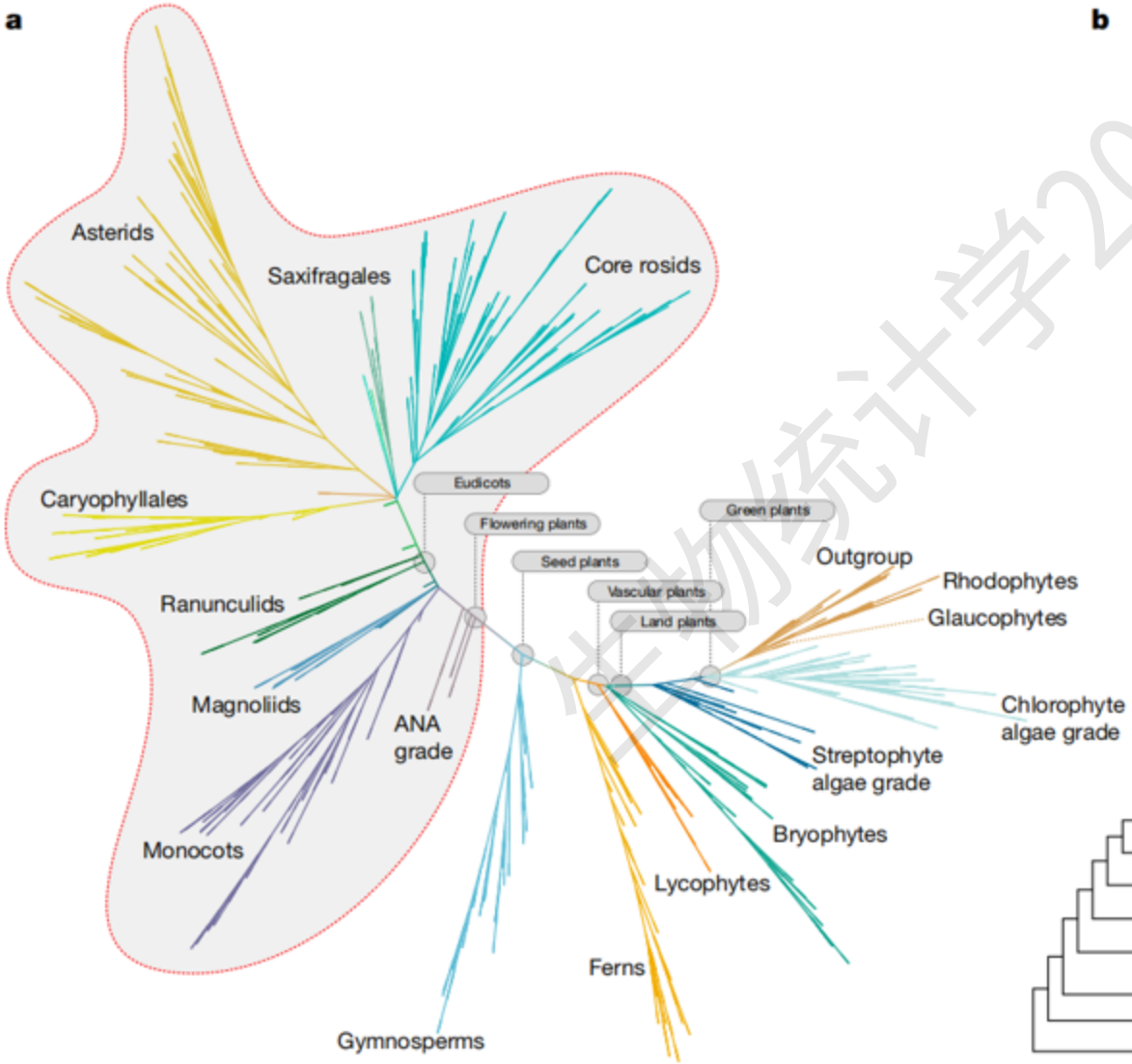
Reference:
https://b10k.genomics.cn/

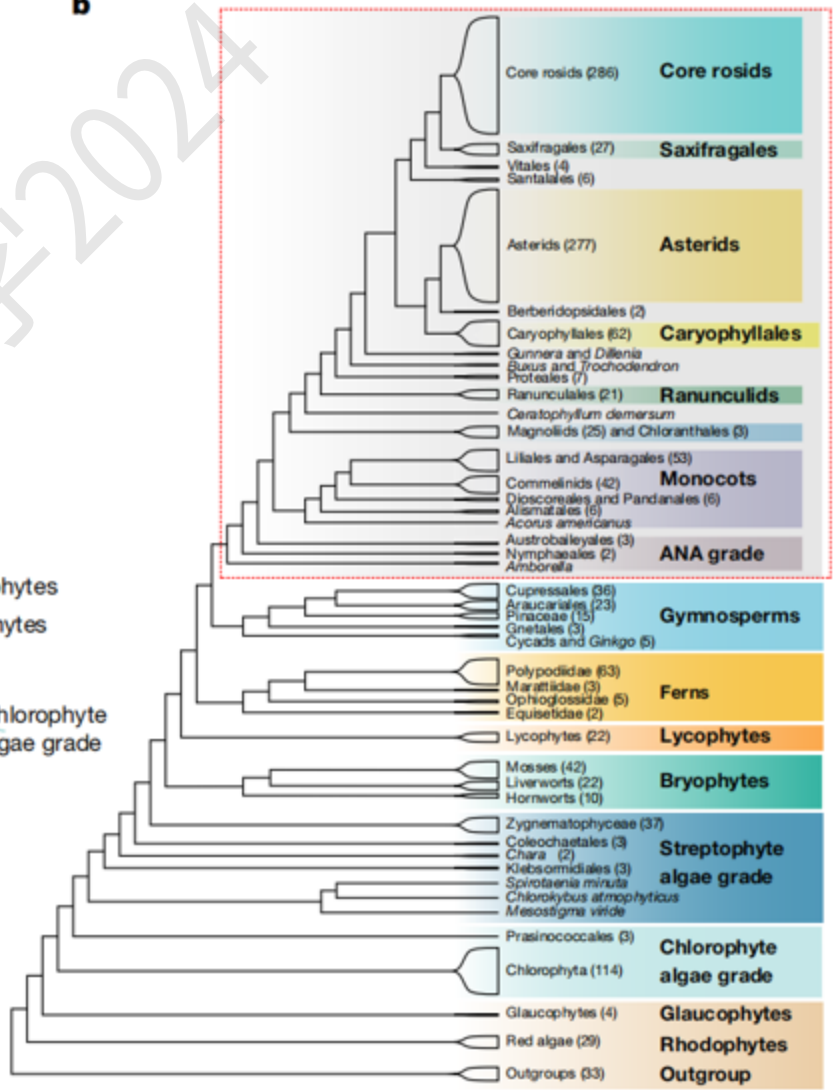


Phylogenetic Tree

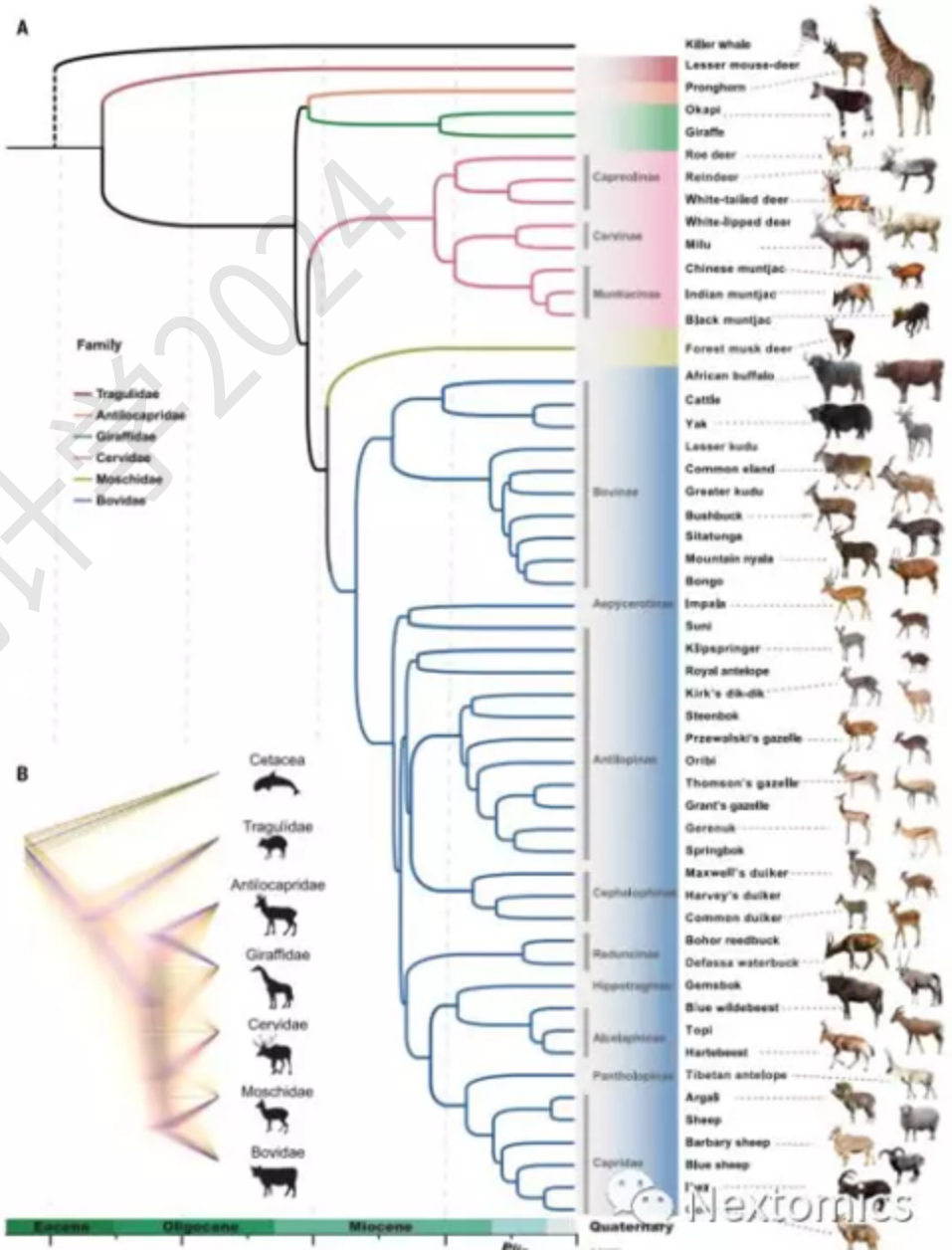
Reference:

One thousand plant transcriptomes and the phylogenomics of green plants, *Nature*, 2019

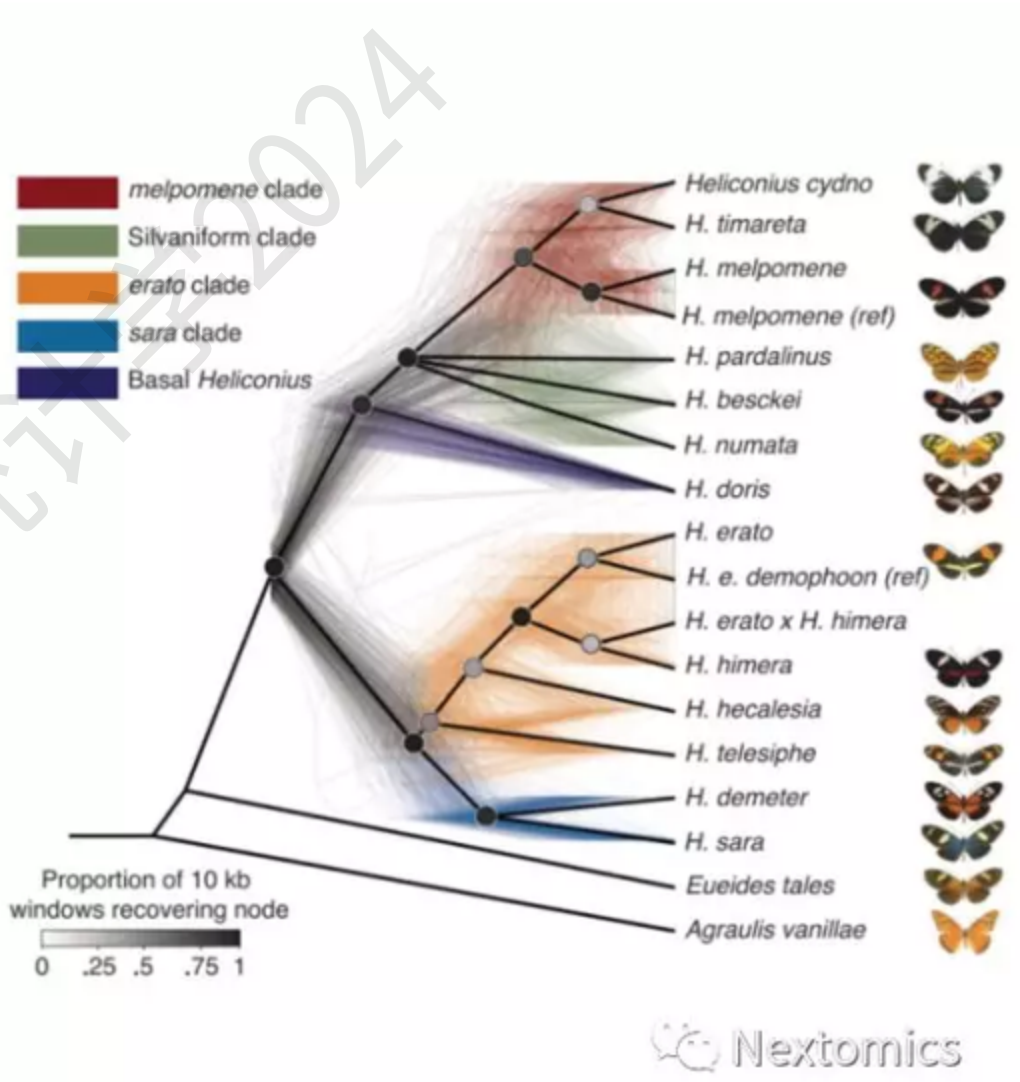




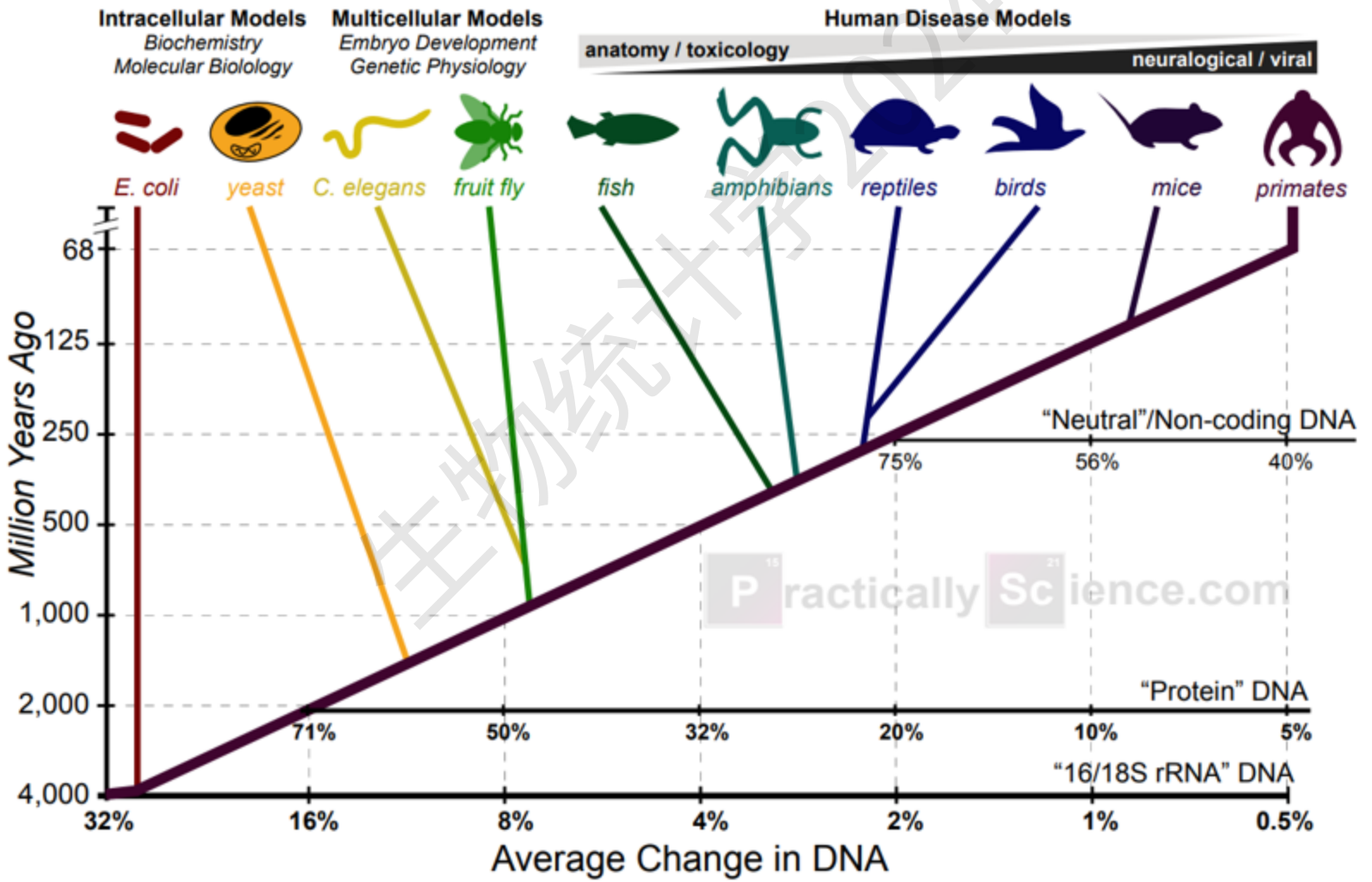
Phylogenetic Tree



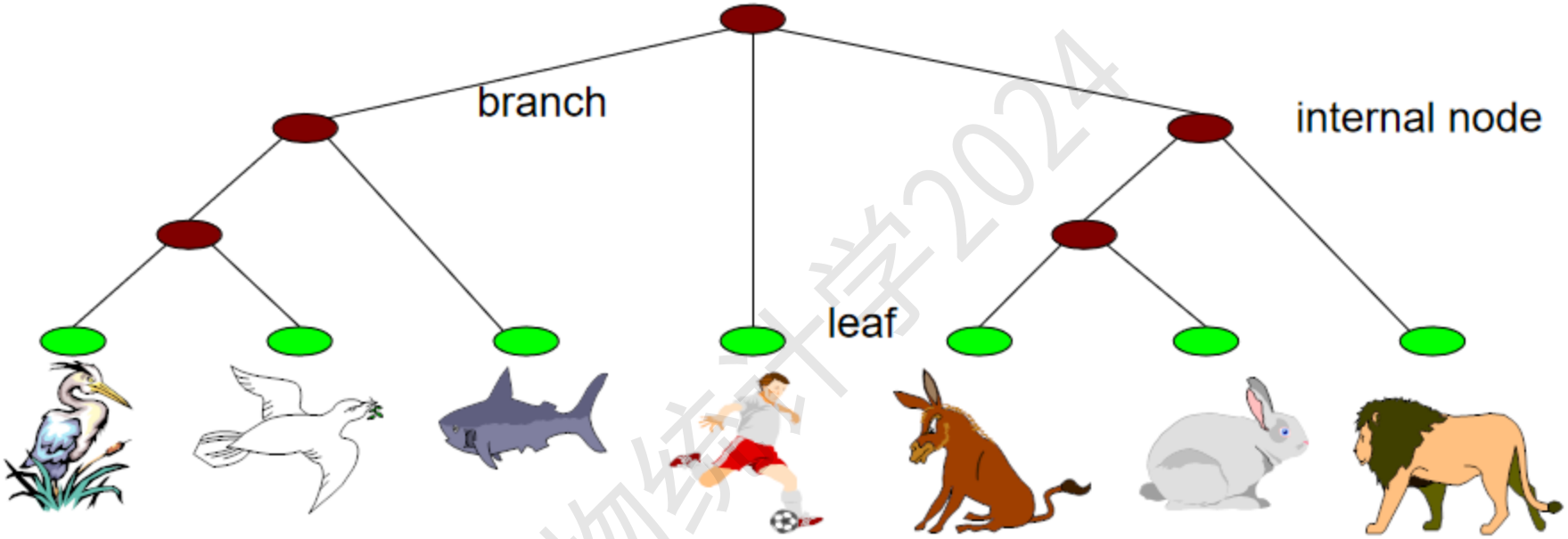
Phylogenetic Tree



Phylogenetic Tree



Phylogenetic Tree



- Topology: bifurcating
  - Leaves - *1…N*
  - Internal nodes *N+1…2N-2*
- Branch length

Reference:
https://itol.embl.de/

构建进化树算法

- 基于距离的构建方法：
  - UPGMA（Unweighted pair group method with arithmetic mean，平均连接聚类法）
  - ME（Minimum Evolution，最小进化法）
  - NJ（Neighbor-Joining，邻接法）

- 基于特征的构建方法：
  - 最大简约法（MP法）
  - 最大似然法（ML法）
  - 进化简约法（EP法）
  - 相容性方法

基于距离的构建方法

- UPGMA

①以已求得的距离系数,所有比较的分类单元的成对距离构成一个t×t方阵,即建立一个距离矩阵M。

②对于一个给定的距离矩阵,寻求最小距离值Dpq。

③定义类群p和q之间的分支深度Lpq=Dpq/2。

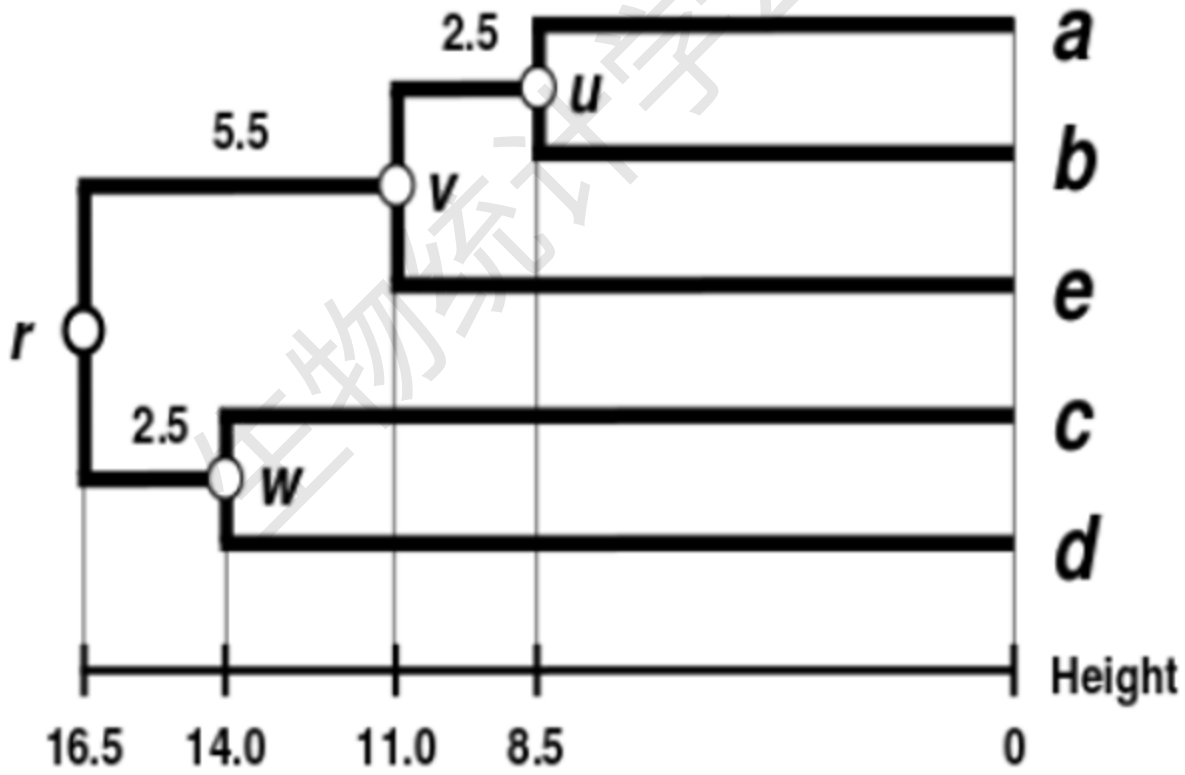
④若p和q是最后一个类群,侧聚类过程完成,否侧合并p和q成一个新类群r。

⑤定义并计算新类群r到其他各类群i(i≠p和q)的距离Dir=(Dpi+Dqi)/2。

⑥回到第一步,在矩阵中消除p和q,加入新类群r,矩阵减少一阶,重复进行直至达到最后归群。

基于距离的构建方法

- UPGMA



基于距离的构建方法

- Neighbor-Joining

① 对于给定距离矩阵中的每一端结i,用下式计算与其它分类单元之间的净趋异量(Ri) (t:矩阵中的分类单元数)

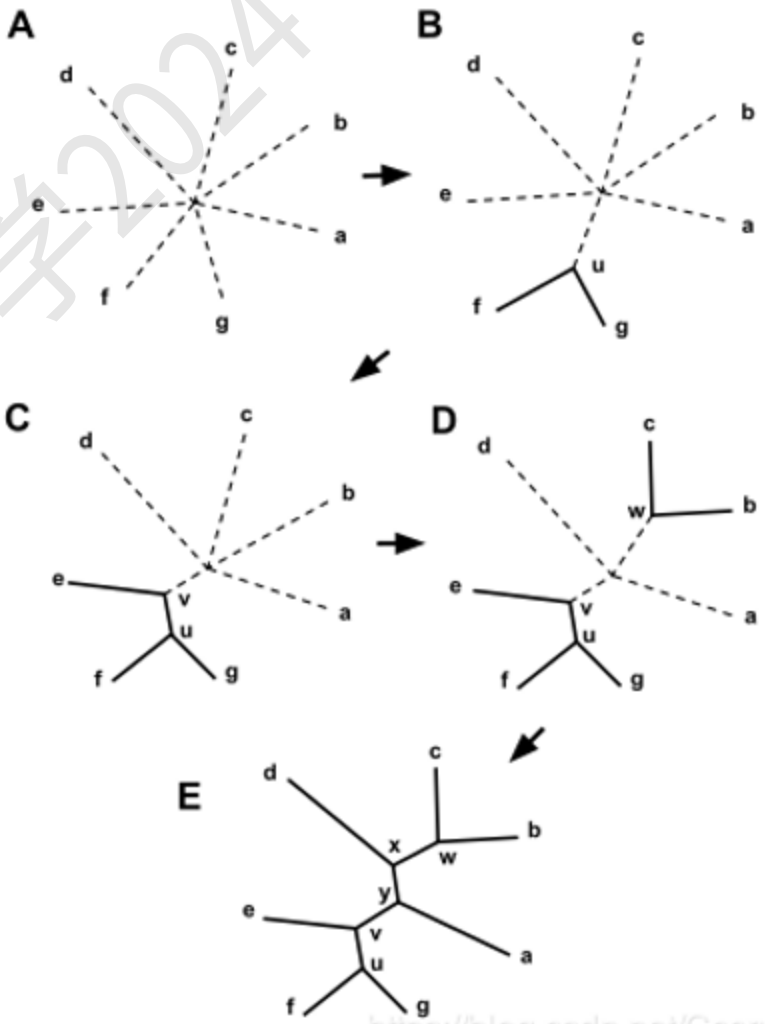
② 建立一个速率校正距离矩阵M,其元素由下式确定:

③ 定义一个新节点u,u的三个分支分别与节点i,j和树的其余部分相连,并且Dij为矩阵中距离最小者,u到节点i和j的分支长度定义为

④ 定义u到树的其它节点k(k≠i和j外的所有节点)的距离:

⑤ 从距离矩阵中删除i和j的距离,矩阵减少一阶。

⑥ 如果矩阵仍然多于两个的节点,重复第①-⑤步,否测除最外两个节点的分支长度来确定外,树上其余节点都确定,最后是剩余的2个的分支长度Sy=Dij



基于距离的构建方法

- Neighbor-Joining

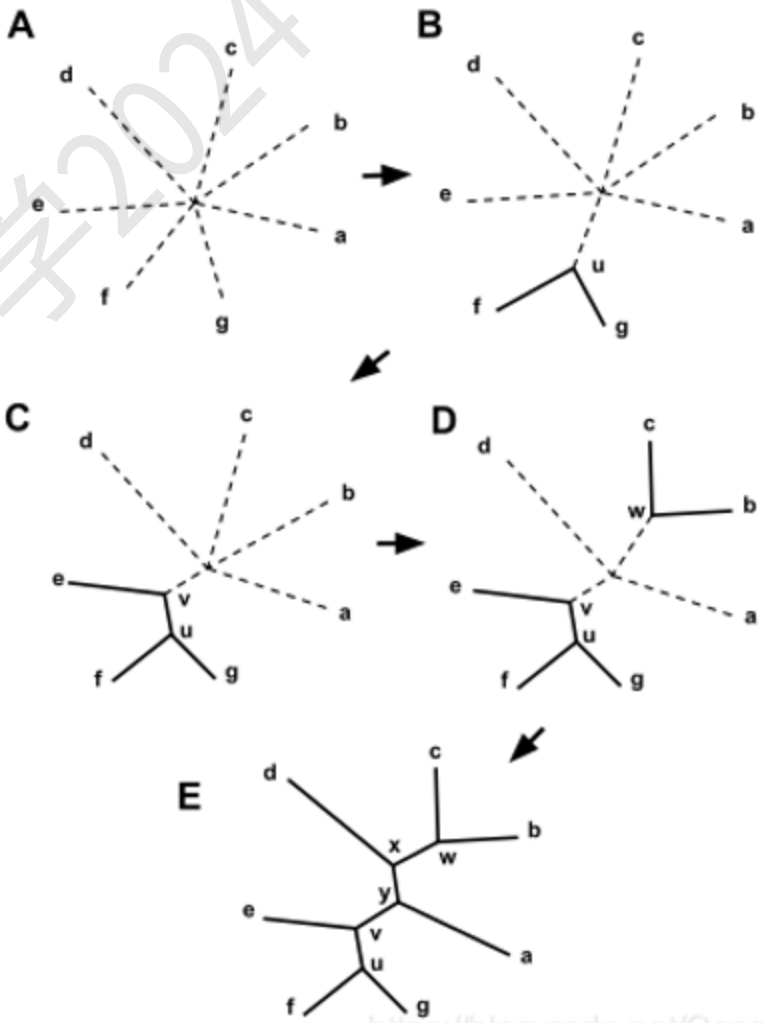
在概念上与UPGMA法相同,但是有四点区别

a. NJ法不要求距离符合超度量特性,但要求数据应非常接近或符合叠加性条件,即该方法要求对距离进行校正。

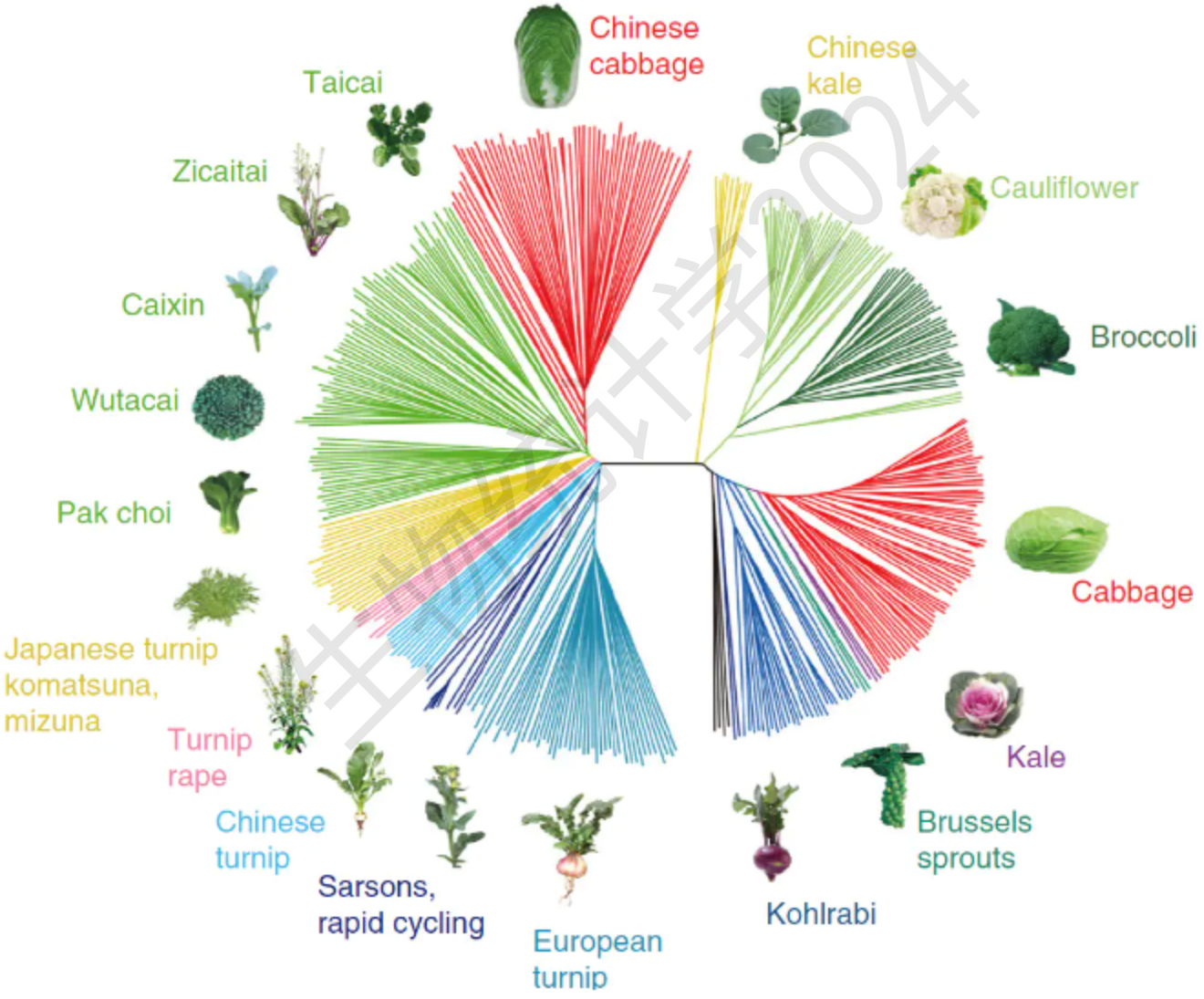
b. 邻接法在成聚过程中连接的是分类单元之间的节点(node),而不是分类单元本身。

c. NJ法中原始距离数据用于估算系统树上所有端结分类单元之间的距离矩阵,校正后的距离用于确定节点之间的连接顺序。

d. 在重建系统发育树时,NJ法取消了UPGMA法所做的假定,认为在此进化分支上,发生趋异的次数可以不同。



基于距离的构建方法



无根树

构建进化树算法

- 基于距离的构建方法：
  - UPGMA（Unweighted pair group method with arithmetic mean，平均连接聚类法）
  - ME（Minimum Evolution，最小进化法）
  - NJ（Neighbor-Joining，邻接法）

- 基于特征的构建方法：
  - 最大简约法（MP法）
  - 最大似然法（ML法）
  - 进化简约法（EP法）
  - 相容性方法

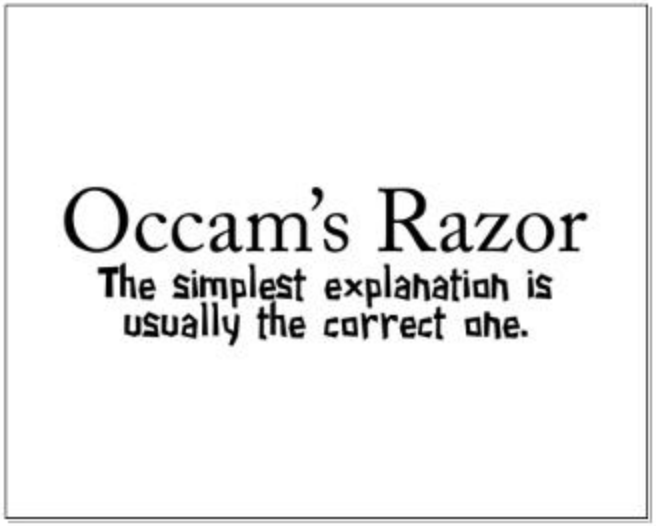
最大简约法（Maximum Parsimony）

最大简约法的理论基础是奥卡姆（Ockham）哲学原则，这个原则认为：解释一个过程的最好理论是所需假设数目最少的那一个。

方法：

计算所有可能的拓扑结构；

计算出所需替代数最小的那个拓扑结构，作为最优树。



occam's razor method

The Role of Ockham's Razor: To Screen for Plurality at the Beginning of the Scientific Method

1. OBSERVATION
2. NECESSITY
3. INTELLIGENCE/AGGREGATION OF DATA (The Three Key Questions)
4. CONSTRUCT FORMULATION
5. SPONSORSHIP/PEER INPUT (Ockham's Razor)
6. HYPOTHESIS DEVELOPMENT
7. PREDICTIVE TESTING
8. COMPETITIVE HYPOTHESES FRAMING (ASKING THE RIGHT QUESTION)
9. FALSIFICATION TESTING
10. HYPOTHESIS MODIFICATION
11. FALSIFICATION TESTING/REPEATABILITY
12. THEORY FORMULATION/REFINEMENT
13. PEER REVIEW (Community Vetting)
14. PUBLISH
15. ACCEPTANCE

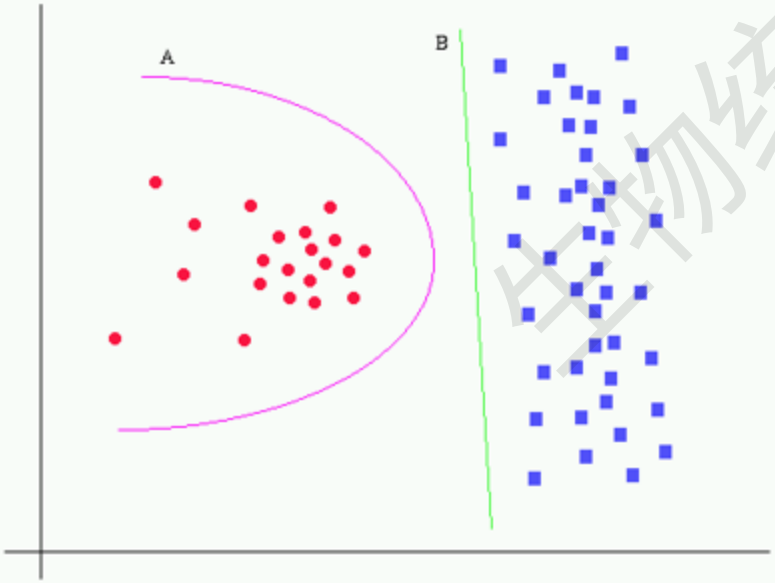
Ockham's Razor

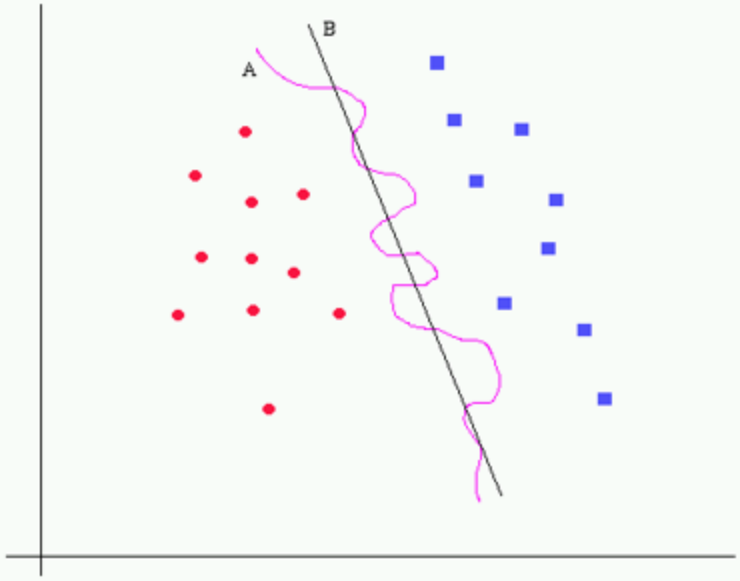
False SSkeptics seek to block this step at all costs.

Plurality

Proof

occam's razor method





最大简约法（Maximum Parsimony）

依据 基于奥卡姆（Ockham）哲学原则，这个原则认为：解释一个过程的最好理论是所需假设数目最少的那一个。

方法 计算所有可能的拓扑结构，计算出所需替代数最小的那个拓扑结构，作为最优树。

特点 用于分析如插入、缺失等序列。在分析序列上存在较多的回复突变或平行突变，而被检验的序列位点数又比较少的时候，最大简约法可能会给出一个不合理的或者错误的进化树推导结果。

最大似然法（Maximum Likelyhood）

ML法对所有可能的系统发育树都计算似然函数，似然函数值最大的那棵树即为最可能的系统发育树。

利用最大似然法来推断一组序列的系统发生树，需首先确定序列进化的模型，如Jukes—Cantor模型、Kimura二参数模型及一般二参数模型等。在进化模型选择合理的情况下，ML法是与进化事实吻合最好的建树算法。其缺点是计算强度非常大，极为耗时。

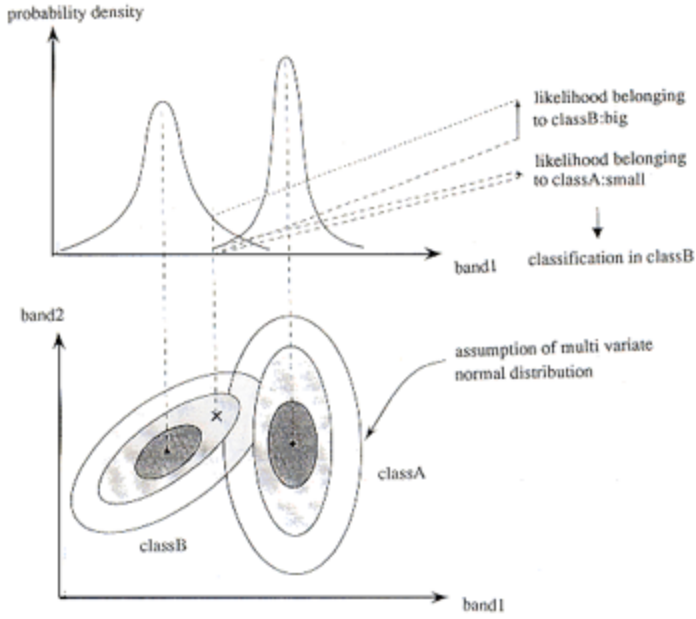
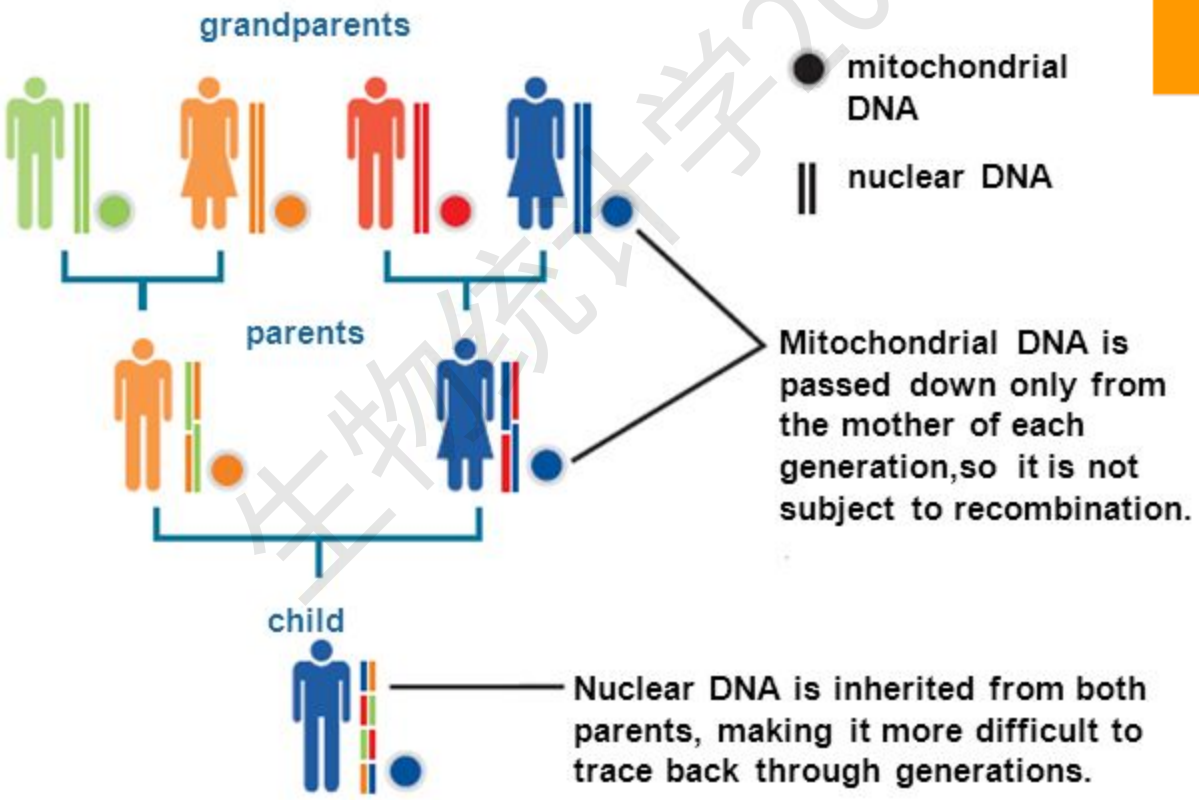


Figure 11.7.1 Concept of Maximum Likelihood Method

Molecular Clock Hypothesi

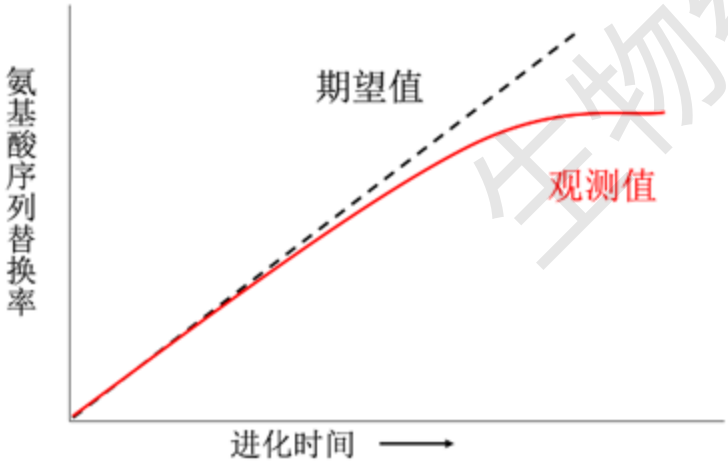
- Amount of genetic difference between sequences is a function of time since separation.
- Rate of molecular change is constant (enough) to predict times of divergence

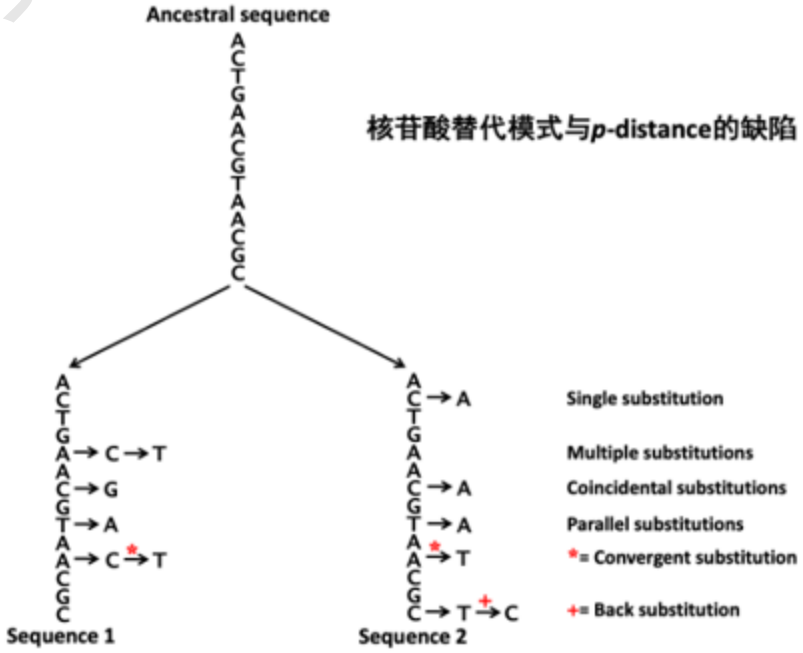
Molecular Clock Hypothesis



Molecular Clock Hypothesis

实际情况：DNA受到自然选择的压力，各个位点的碱基出现频率并不相等。





Likelihood of a Tree

- Given:
  - n aligned sequences M= $X_1,\ldots,X_n$
  - A tree T, leaves labeled with $X_1,\ldots,X_n$
- Reconstruction t*:
  - Labeling of internal nodes
  - Branch lengths

Goal: Find optimal reconstruction t* : One maximizing the likelihood P(M|T, t*)

Probabilistic Methods

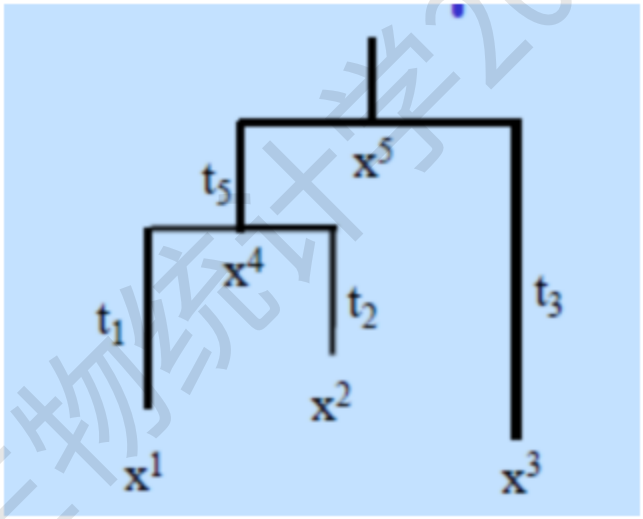
- The phylogenetic tree represents a generative probabilistic model (like HMMs) for the observed sequences.
- Background probabilities: q(a)
- Mutation probabilities: P(a|b, t)
- Models for evolutionary mutations
  - Jukes Cantor
  - Kimura 2-parameter model
- Such models are used to derive the probabilities

Probabilistic Model

- Assumptions:
  - Each character is independent
  - The branching is a Markov process: The probability that a node x has a specific label is only a function of the parent node y and the branch length t between them
  - The probabilities P(x|y,t) are known

Example

- Given the tree



$$P(x_1, x_2, x_3, x_4, x_5 | T, t^*)$$
$$= P(x_1|x_4, t_1)P(x_2|x_4, t_2)P(x_3|x_5, t_3)P(x_4|x_5, t_5)$$

Molecular Evolution

Q: How can we model evolution on nucleotide level? (ignore gaps, focus on substitutions)

A: Consider what happens at a specific position for small time interval Δt

- $P(t)$ = vector of probabilities of {A,C,G,T} at time t
- μ_{AC} = rate of transition from A to C per unit time
- $\mu_A = \mu_{AC} + \mu_{AG} + \mu_{AT}$ rate of transition out of A
- $p_A(t+\Delta t) = p_A(t) - p_A(t)\,\mu_A\,\Delta t + p_C(t)\,\mu_{CA}\,\Delta t + \ldots$

Molecular Evolution

In matrix/vector notation, we get

$$P(t + \Delta t) = P(t) + QP(t)\Delta t$$

where Q is the substitution rate matrix

$$Q = \begin{pmatrix} -\mu_A & \mu_{AG} & \mu_{AC} & \mu_{AT} \\ \mu_{GA} & -\mu_G & \mu_{GC} & \mu_{GT} \\ \mu_{CA} & \mu_{CG} & -\mu_C & \mu_{CT} \\ \mu_{TA} & \mu_{TG} & \mu_{TC} & -\mu_T \end{pmatrix}$$

Molecular Evolution

- This is a differential equation:

$$P'(t) = Q\,P(t)$$

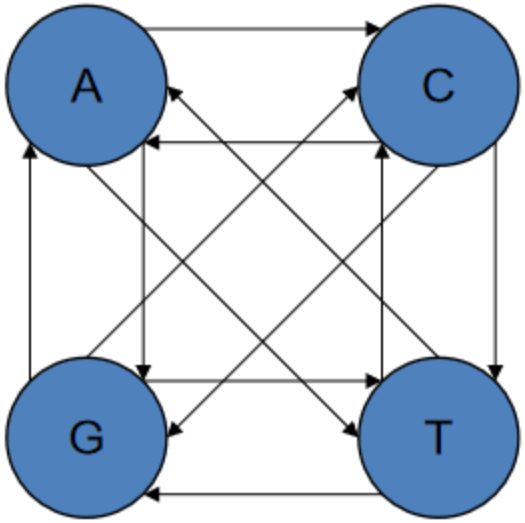
- A substitution rate matrix Q implies a probability distribution over {A,C,G,T} at each position, including stationary (equilibrium) frequencies π_A, π_C, π_G, π_T
- Each Q is an evolutionary model (some work better than others)

Mutation Probabilities

P(t) satisfy the following two property:

- **Lack of memory**:
  - $P_{a\to c}(t+t') = \sum_b P_{a\to b}(t) P_{b\to c}(t')$
- **Reversibility**:
  - Exist stationary probabilities $\{P_a\}$ s.t.

$$P_a P_{a\to b}(t) = P_b P_{b\to a}(t)$$



PAM矩阵

- Point accepted mutation (Dayhoff et al 1978)
- Given an tree of protein family, the frequence matrix A_{ab} counting the occurrence of an “a” in the ancestral sequence was replaced by a “b” in the descendant.
- Estimate the conditional probability p(b|a)

$$P(b|a) = B_{a,b} = \frac{A_{ab}}{\sum_c A_{ac}}$$

PAM矩阵

- Scaling B

$$C_{ab} = \sigma B_{ab}, C_{aa} = \sigma B_{aa} + (1 - \sigma)$$

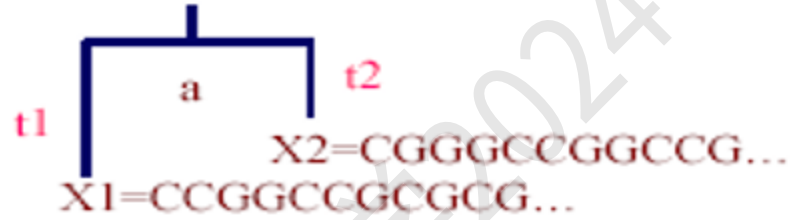
- Such that the expected number of substitution is 1%, i.e.

$$\sum_{ab} q_a q_b C_{ab} = 0.01$$

- Then the PAM(1) matrix is given by

$$S(1) = (C_{ab})$$

Calculating the Likelihood for Ungapped Alignments



$$P\left(x^1, x^2 \mid T, t_1, t_2\right) = \prod_{u=1}^{N} P\left(x_u^1, x_u^2 \mid T, t_1, t_2\right)$$

$$P\left(x_u^1, x_u^2 \mid T, t_1, t_2\right) = \sum_a q_a P\left(x_u^1 \mid a, t_1\right) P\left(x_u^2 \mid a, t_2\right)$$

Assuming Jukes-Cantor model & $q_C = q_G = q_A = q_T = \frac{1}{4}$:

$$P\left(C, C \mid T, t_1, t_2\right) = q_C r_{t_1} r_{t_2} + q_G s_{t_1} s_{t_2} + q_A s_{t_1} s_{t_2} + q_T s_{t_1} s_{t_2} = \tfrac{1}{4}\left(r_{t_1} r_{t_2} + 3 s_{t_1} s_{t_2}\right)$$

$$P(C, G \mid T, t) = P(G, C \mid T, t) = \tfrac{1}{4}\left(r_{t_1} s_{t_2} + s_{t_1} r_{t_2} + 2 s_{t_1} s_{t_2}\right)$$

$$\Rightarrow P\left(x^1, x^2 \mid T, t_1, t_2\right) = 16^{-(n1+n2)}\left(1 + 3e^{-4\alpha(t_1+t_2)}\right)^{n1}\left(1 - e^{-4\alpha(t_1+t_2)}\right)^{n2}$$

where $n1$=matches,n2=mismatches

Calculating the Likelihood for Ungapped Alignments

- n sequences of length N, site u=1...N
- Given a rooted tree contains *2n - 1* nodes, *1... n* being the leaf nodes, n+1 ... 2n-1 non-leaf, tree lengths t1, …, t_{2n-1}.
- Let a(i) denote the ancestor of node a^i

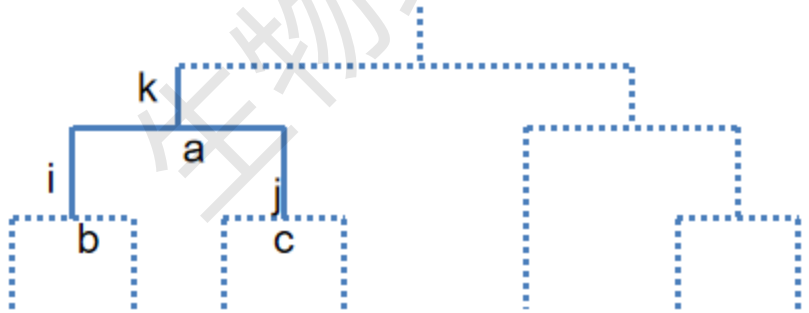
$$P(x^1, \cdots, x^n | T, t) = \prod_{u=1}^{N} P(x_u^1, \cdots, x_u^n | T, t)$$

$$P(x_u^1, \cdots, x_u^n | T, t) = \sum_{a^{n+1}, \cdots, a^{2n-1}} q_{a^{2n-1}} \prod_{i=n+1}^{2n-2} P(a^i | a^{\alpha(i)}, t_i)$$

$$\times \prod_{i=1}^{n} P(x_u^i | a^{\alpha(i)}, t_i)$$

Felsenstein's Recursive Algorithm

- Let $P(L_k|a)$ denote the probability of all the leafs below node k given that the residue at k is a.
- Then we compute $P(L_k|a)$ from the probabilities $P(L_i \mid b)$ and $P(L_j \mid c)$ for all b and c, where i and j are the daughter nodes of k.



Felsenstein's Recursive Algorithm

- Initialization: set k=2n-1
- Recursion: Compute $P(L_k \mid a)$ for all a as follows:
  - If k is leaf node: $P(L_k|a)=1$ only $a = x_u^k$.
  - If k is not a leaf node:
    - Compute $P(L_i|a)$, $P(L_j|a)$ for all a at the daughter nodes i,j , and set $P(L_k|a) = \sum_{bc} P(b|a,t_i)P(L_i|b)P(c|a,t_j)P(L_j|c)$
- Temination: Likelihood at site u,

$$P(x_u|T,t) = \sum_a P(L_{2n-1}|a)q_a$$

Reversibility & Independence of Root Position

- The score of the optimal tree is independent of the root position if and only if:
  - the substitution matrix is **multiplicative**
  - the substitution matrix is **reversible**
- A substititution matrix is reversible if for all a,b and t:

$$P(b|a,t)q_a = P(a|b,t)q_b$$

Maximum Likelihood (ML)

- Score each tree by
  - Assumption of independent positions “m”
- Branch lengths *t* can be optimized
  - Gradient Ascent
  - EM
- We look for the highest scoring tree
  - Exhaustive
  - Sampling methods (Metropolis)

Computational Problem

- Such procedures are computationally expensive!
- Computation of optimal parameters, per candidate, requires non-trivial optimization step.
- Spend non-negligible computation on a candidate, even if it is a low scoring one.
- In practice, such learning procedures can only consider small sets of candidate structures

最大似然法（Maximum Likelyhood）

基本思想 当从模型总体随机抽取n组样本观测值后，最合理的参数估计量应该使得从模型中抽取该n组样本观测值的概率最大。

方法 选取一个特定的替代模型来分析给定的一组序列数据，使得获得的每一个拓扑结构的似然率都为最大值，然后再挑出其中似然率最大的拓扑结构作为最优树（所以分析时间比较长）

特点 最大似然法具有很好的统计学理论基础，是一个比较成熟的统计学方法。选择合理的模型后，最大似然法可以推导出一个效果很好的进化树结果。

构建进化树算法

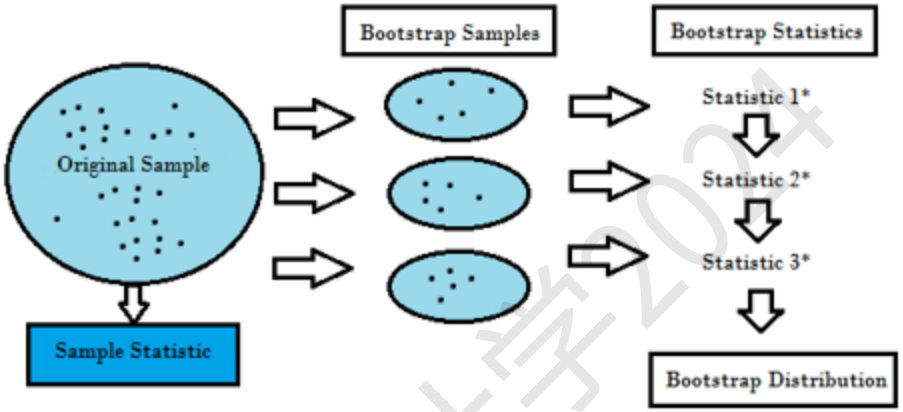
- 如果序列的相似性较高，各种方法都会得到不错的结果，模型间的差别也不大.
- 若有合适的分子进化模型可供选择，用最大似然法构树获得的结果较好.
- 对于近缘物种序列，通常情况下使用最大简约法.
- 而对于远缘物种序列，一般使用邻接法或最大似然法.
- 对于相似度很低的序列，邻接法往往出现长枝吸引(branch attraction)现象，有时严重干扰进化树的构建.

邻接法和最大似然法是需要选择模型的:

蛋白质序列的构树模型一般选择Poisson correction(泊松修正).

核酸序列的构树模型一般选择Kimura 2-parameter (Kimura-2参数).

进化树检验：Bootstrap



在重建进化树过程中，均需选择bootstrap进行树的检验：

- 一般bootstrap的值>70，则认为重建的进化树较为可靠。
- 如果bootstrap的值太低，则有可能进化树的拓扑结构有错误，进化树是不可靠的。
- 一般推荐用两种以上不同的方法构建进化树，如果所得到的进化树类似，且bootstrap值总体较高，则得到的结果较为可靠。
- 通常情况下，只要选择了合适的方法和模型，构出的树均是有意义的，研究者可根据自己研究的需要选择最佳的树进行分析。

进化树检验： Bootstrap

原始序列

S1 AACAAC
S2 AACCCC
S3 ACCAAC
S4 CCACCA
S5 CCAAAC

Bootstrap1

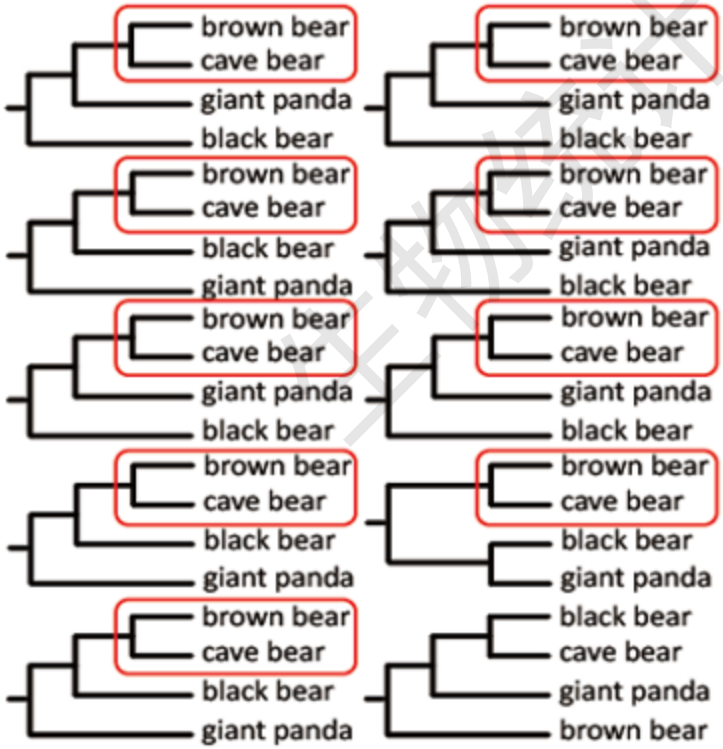
S1 ACAAAC
S2 ACCCCC
S3 ACAAAC
S4 CACCCA
S5 CAAAAC

Bootstrap2

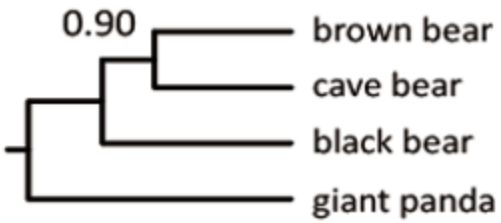
S1 AAAACC
S2 AACCCC
S3 CCAACC
S4 CCCCAA
S5 CCAACC

Bootstrap3

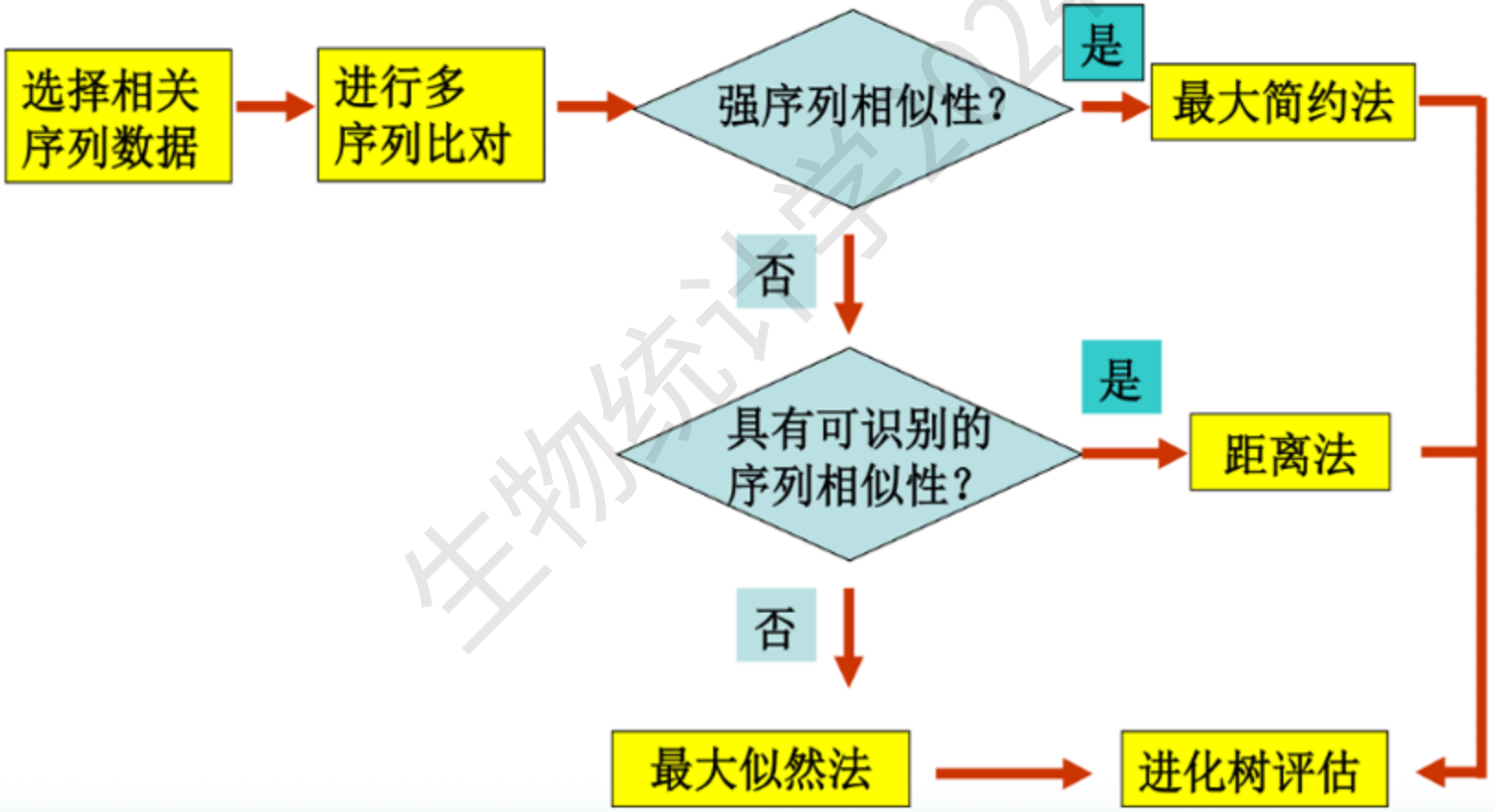
S1 ACAAAC
S2 ACCCCC
S3 CCAAAC
S4 CACCCA
S5 CAAAAC



ML tree

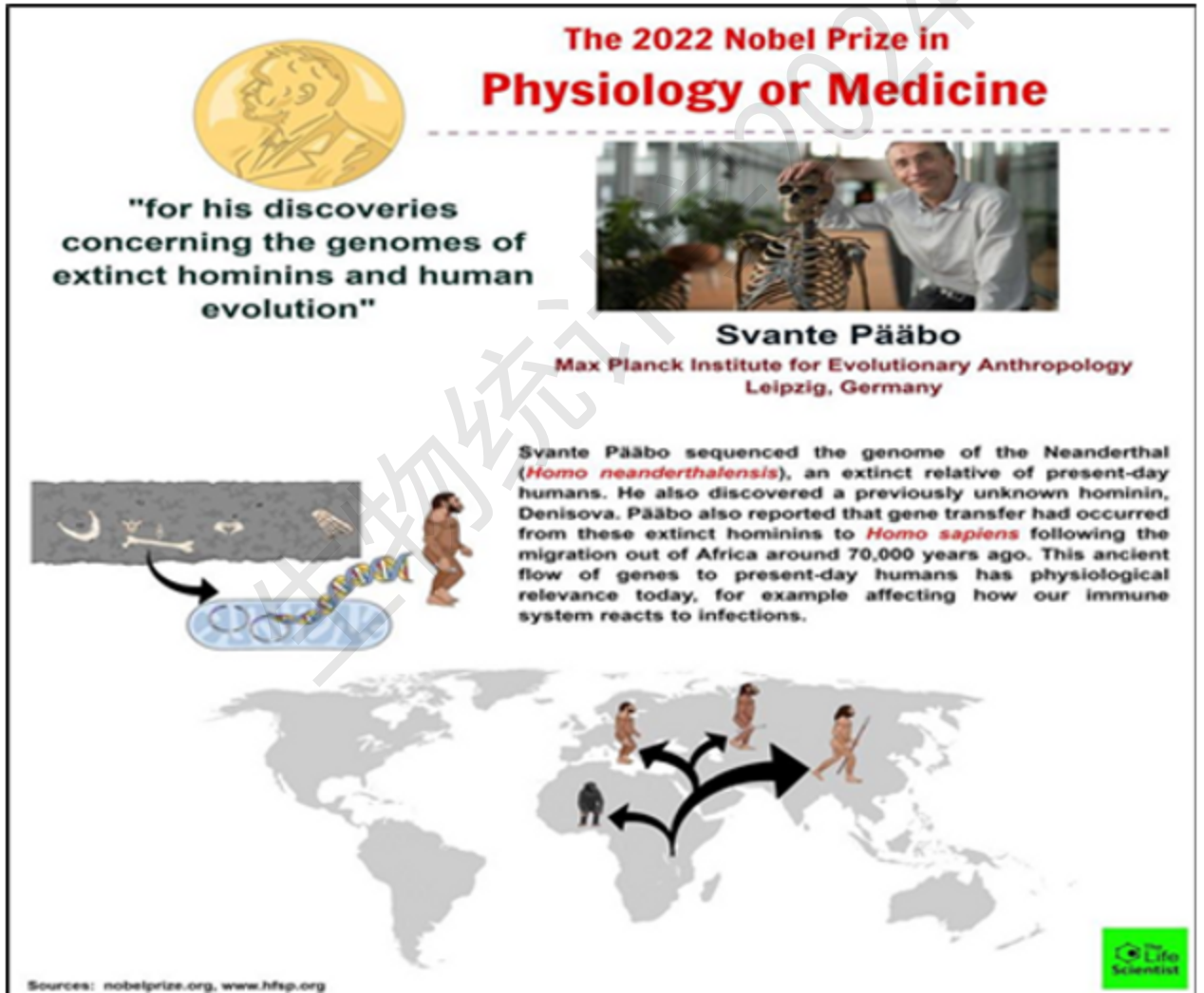


进化树构建方法的选择



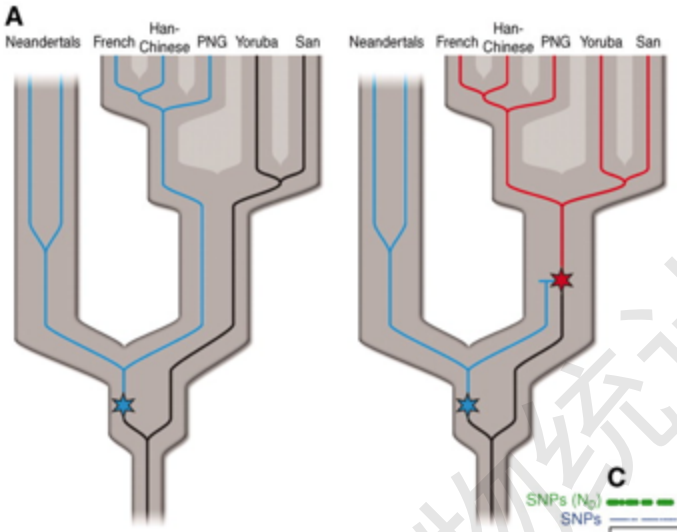
进化树构建的经典案例

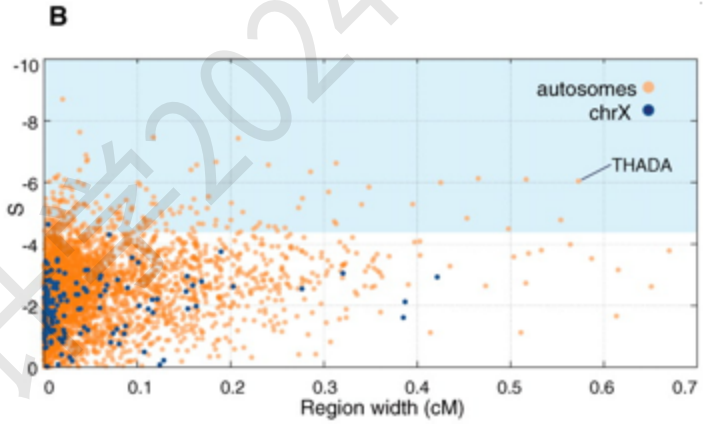
Human evolution

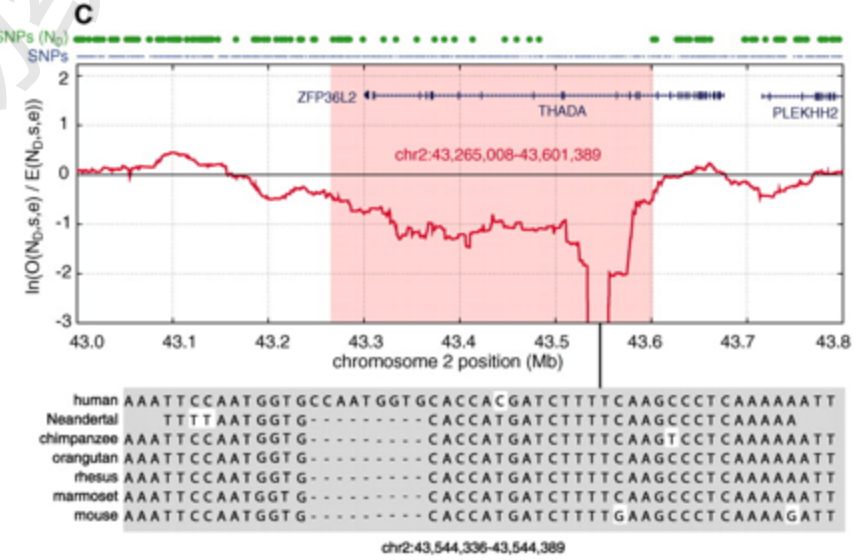


进化树构建的经典案例

Human evolution







SVANTE PÄÄBO, *Science*, 2010

进化树构建的经典案例

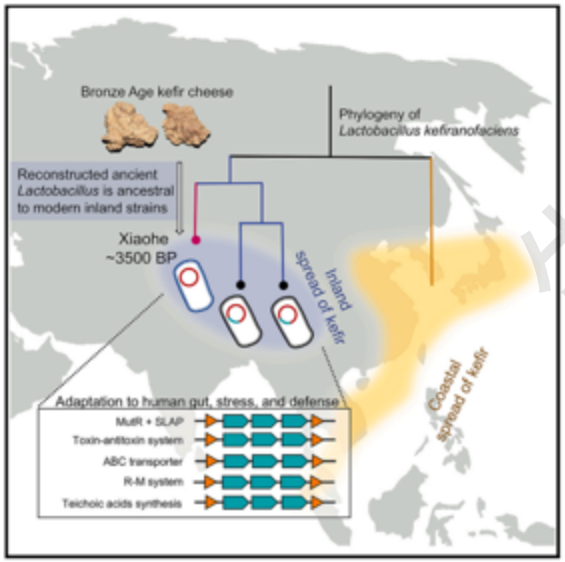
Microbe evolution

Cell

Article

Bronze Age cheese reveals human-*Lactobacillus* interactions over evolutionary history

Graphical abstract



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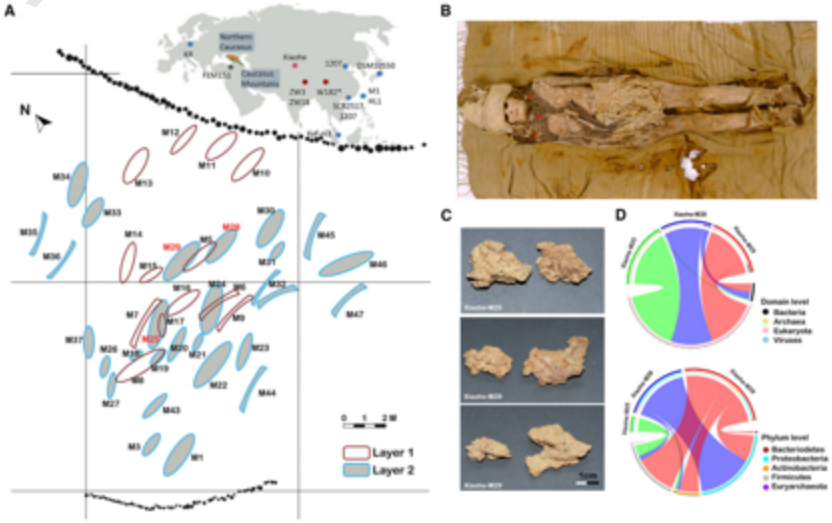
In brief

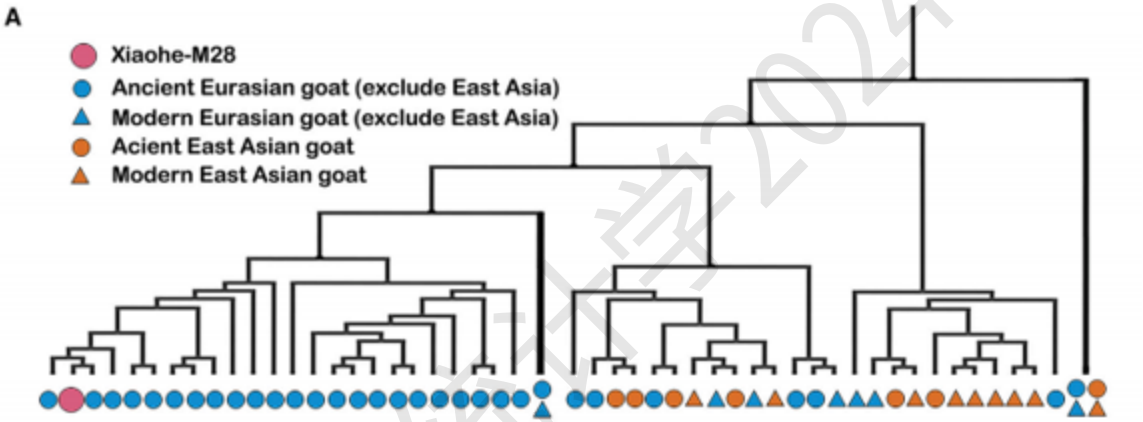
Ancient DNA has been recovered from Bronze Age cheese residue, revealing cultural communication, the spread of fermenting techniques, and the domestication of microorganisms by the Xinjiang Xiaohe population.

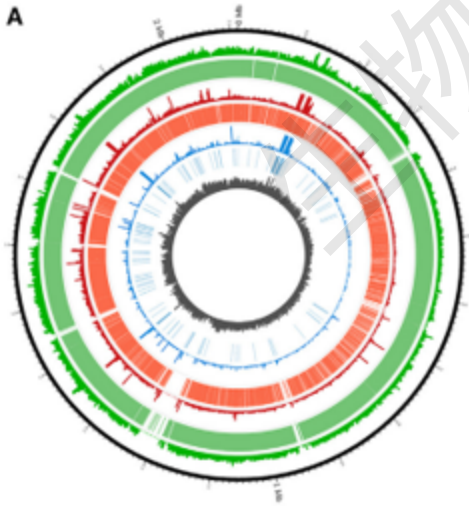


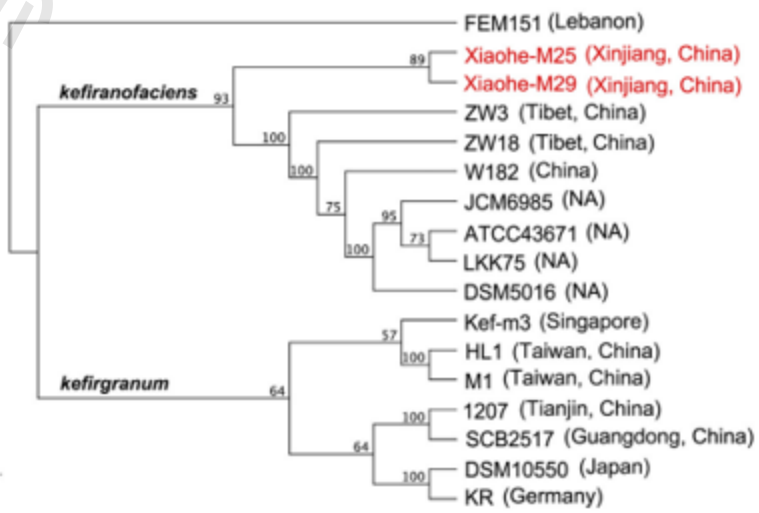
FU, *Cell*, 2024

进化树构建的经典案例

Microbe evolution



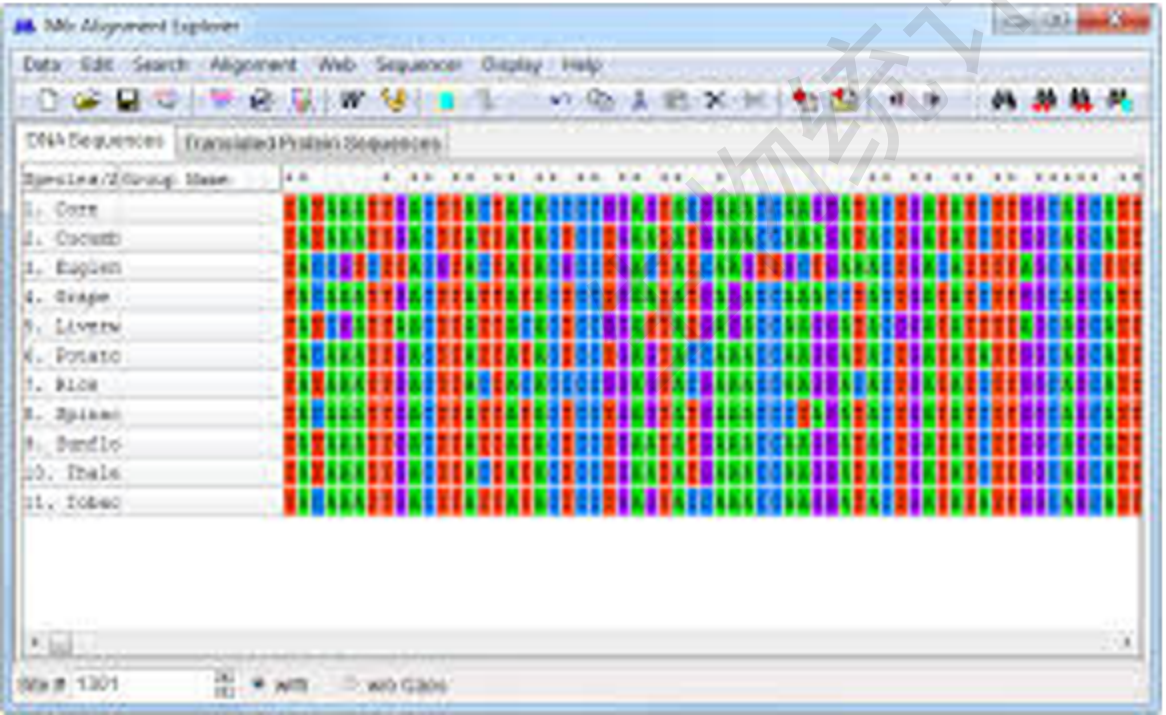


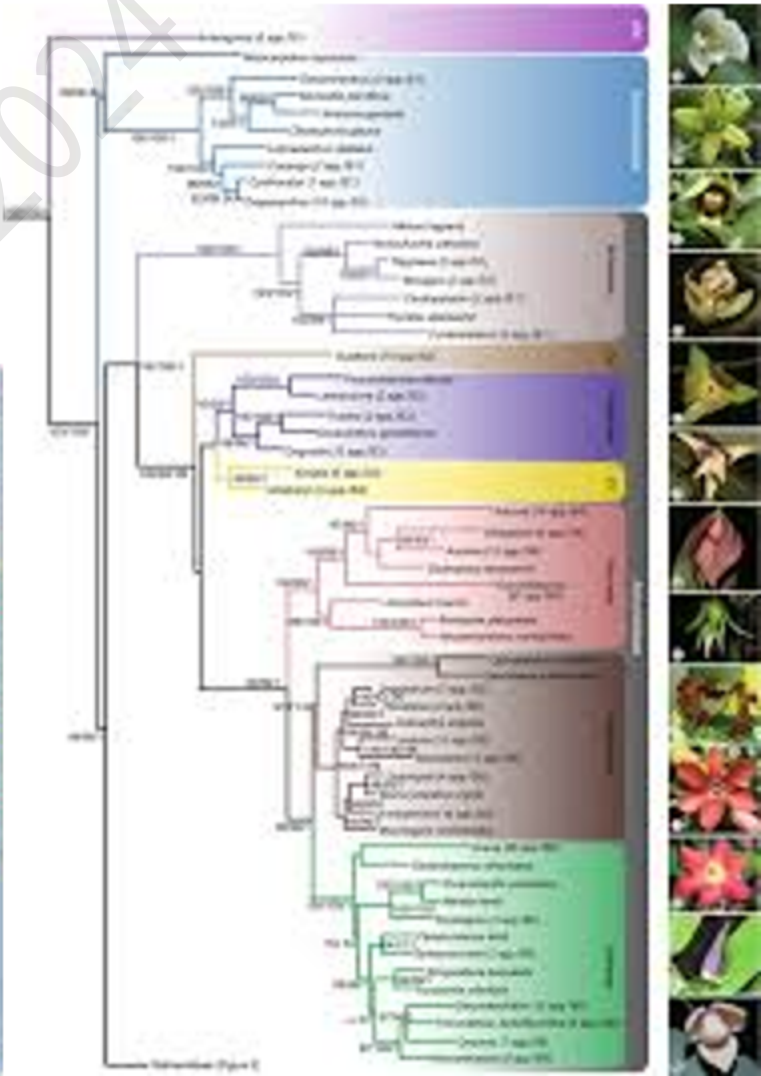


构建分子进化树相关的软件

软件	网址	说明
ClustalX	http://bips.u-strasbg.fr/fr/Documentation/ClustalX/	图形化的多序列比对工具
ClustalW	http://www.cf.ac.uk/biosi/resear ... loads/clustalw.html	命令行格式的多序列比对工具
GeneDoc	http://www.psc.edu/biomed/genedoc/	多序列比对结果的美化工具
BioEdit	http://www.mbio.ncsu.edu/BioEdit/bioedit.html	序列分析的综合工具
MEGA	http://www.megasoftware.net/	图形化、集成进化分析工具，不包括ML
PAUP	http://paup.csit.fsu.edu/	商业软件，集成的进化分析工具
PHYLIP	http://evolution.genetics.washington.edu/phylip.html	免费的、集成的进化分析工具
PHYML	http://atgc.lirmm.fr/phyml/	最快的ML建树工具
PAML	http://abacus.gene.ucl.ac.uk/software/paml.html	ML建树工具
Tree-puzzle	http://www.tree-puzzle.de/	较快的ML建树工具
MrBayes	http://mrbayes.csit.fsu.edu/	基于贝叶斯方法的建树工具
MAC5	http://www.agapow.net/software/mac5/	基于贝叶斯方法的建树工具
TreeView	http://taxonomy.zoology.gla.ac.uk/rod/treeview.html	进化树显示工具

MEGA：建树平台





FastTree：建树平台

FastTree 2

Speed

Computing maximum-likelihood trees

			FastTree 2.0.0		RAxML	PhyML 3
Alignment	# Distinct Sequences	#Positions	Settings	Hours	Memory (GB)	Hours	Hours
Efflux permeases (COG2814)	8,362	394 a.a.	JTT+CAT	0.25	0.35	>1,200	>1,200
ABC transporters (PF00005)	39,092	214 a.a.	JTT+CAT	1.0	0.96	--	--
16S ribosomal RNAs, distinct families	15,011	1,287 nt.	GTR+CAT	0.66	0.56	99	>360
16S ribosomal RNAs, distinct families	15,011	1,287 nt.	JC+CAT	0.49	0.36	--	--
16S ribosomal RNAs	237,882	1,287 nt.	JC+CAT, -fastest	21.8	5.8	--	--

All of the timings are on a single CPU. The FastTree times include the SH-like local support values. For huge alignments, FastTree 2.1 with -fastest is about twice as fast as 2.0, and the multi-alignment I ran RAxML 6 with the fast hill-climbing option (not RAxML 7), and I ran PhyML was run with the fastest settings (no variation in rates across sites and no SPR moves).

In theory, FastTree takes $O(N\ L\ a + N^{1.5})$ space and $O(N^{1.5}\ \log(N)\ L\ a)$ time, where N is the number of unique sequences, L is the width of the alignment, and a is the size of the alphabet. W time complexity are dominated by initializing the top-hits lists and maintaining them during the neighbor-joining phase. The minimum-evolution NNIs and SPRs take $O(N\ L\ a)$ time per roun $O(N\ \log(N)\ L\ a^2)$ time total, and $O(N\ L\ a)$ space. Similarly, the local supports take $O(N\ L\ a^2)$ time and $O(N\ L\ a\ )$ space. In practice, the maximum likelihood NNIs are usually the slowest step.

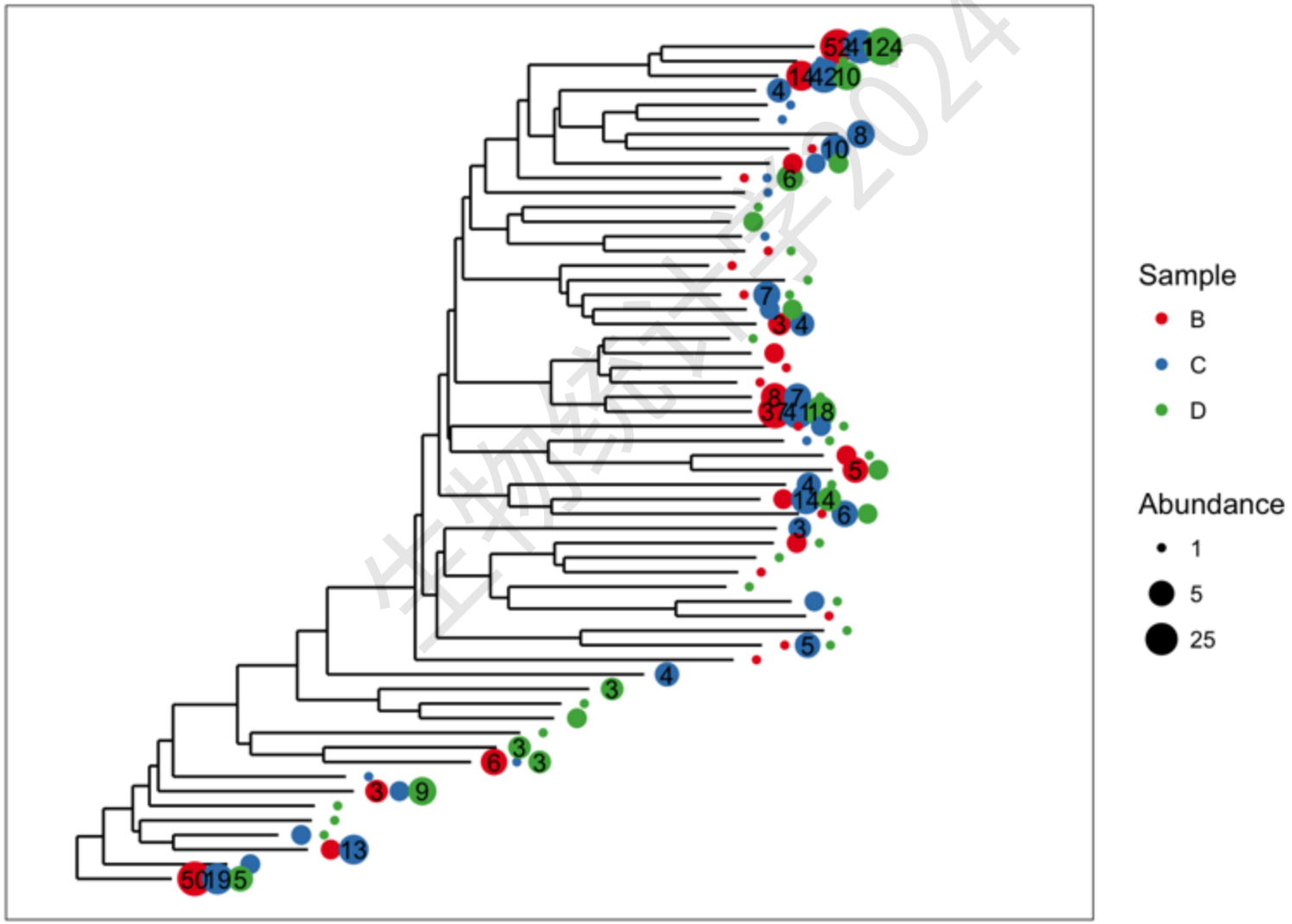
Accuracy

FastTree is slightly more accurate than PhyML3 with NNI moves because it has a better starting tree (thanks to the minimum-evolution SPR moves). FastTree is much more accurate than mi likelihood methods that do a more intensive search of topology space, such as PhyML with SPR moves or RAxML. However, for large alignments, the more accurate methods are orders-of-r poor support.

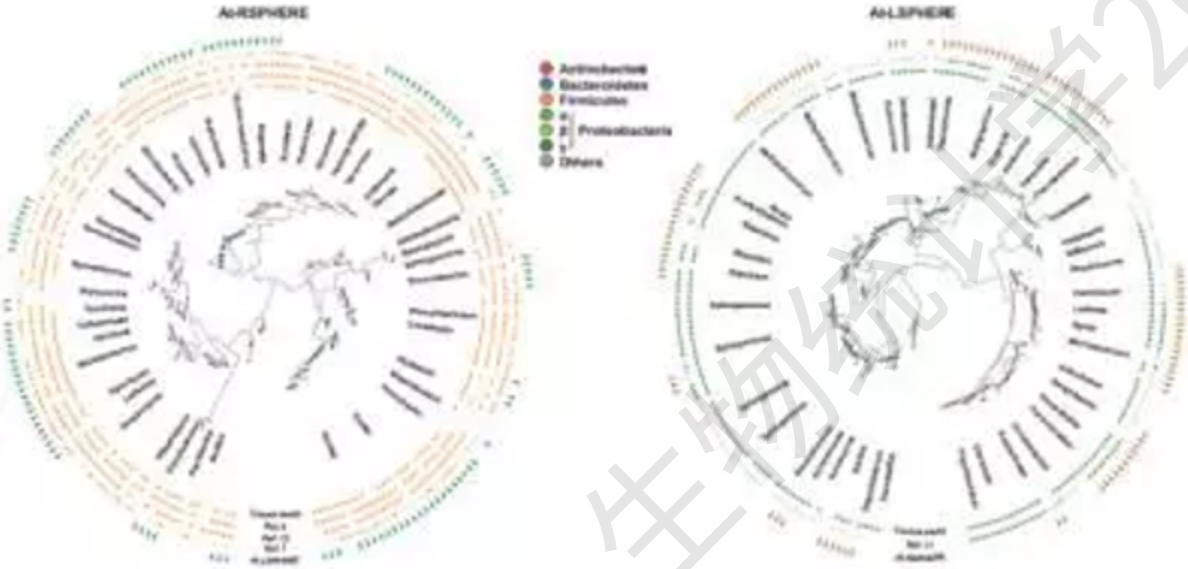
Topological accuracy for simulated alignments with varying numbers of sequences

#Sequences	250	1,250	5,000	78,132
Type	a.a.	a.a	a.a.	nt
RAxML 7 (JTTCAT + SPRs)	90.5%	88.4%	88.4%	--
PhyML 3.0 (Γ_4 + SPRs)	89.9%	--	--	--
FastTree 2.0.0 (JTT+CAT or JC+CAT)	86.9%	83.7%	84.3%	92.1%
PhyML 3.0 (Γ_4, no SPR)	86.0%	--	--	--
PhyML 3.0 (no gamma, no SPR)	81.7%	80.1%	--	--
FastME 1.1 (log-corrected distances)	79.6%	77.7%	75.3%	--
BIONJ (max-lik. distances)	77.7%	73.7%	73.1%	--
Parsimony (RAxML)	76.8%	76.5%	69.4%	--
BIONJ (log-corrected distances)	76.6%	73.0%	72.3%	--
Neighbor-joining (log-corrected distances)	76.0%	72.6%	71.6%	66.1%
Clearcut 1.0.8 (log-corrected distances)	75.5%	72.3%	71.5%	58.1%

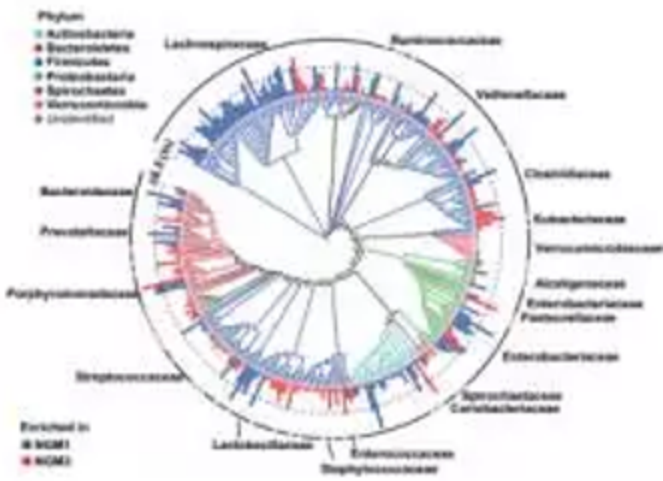
ggplot：物种进化关系分析



iTOL：物种进化关系分析



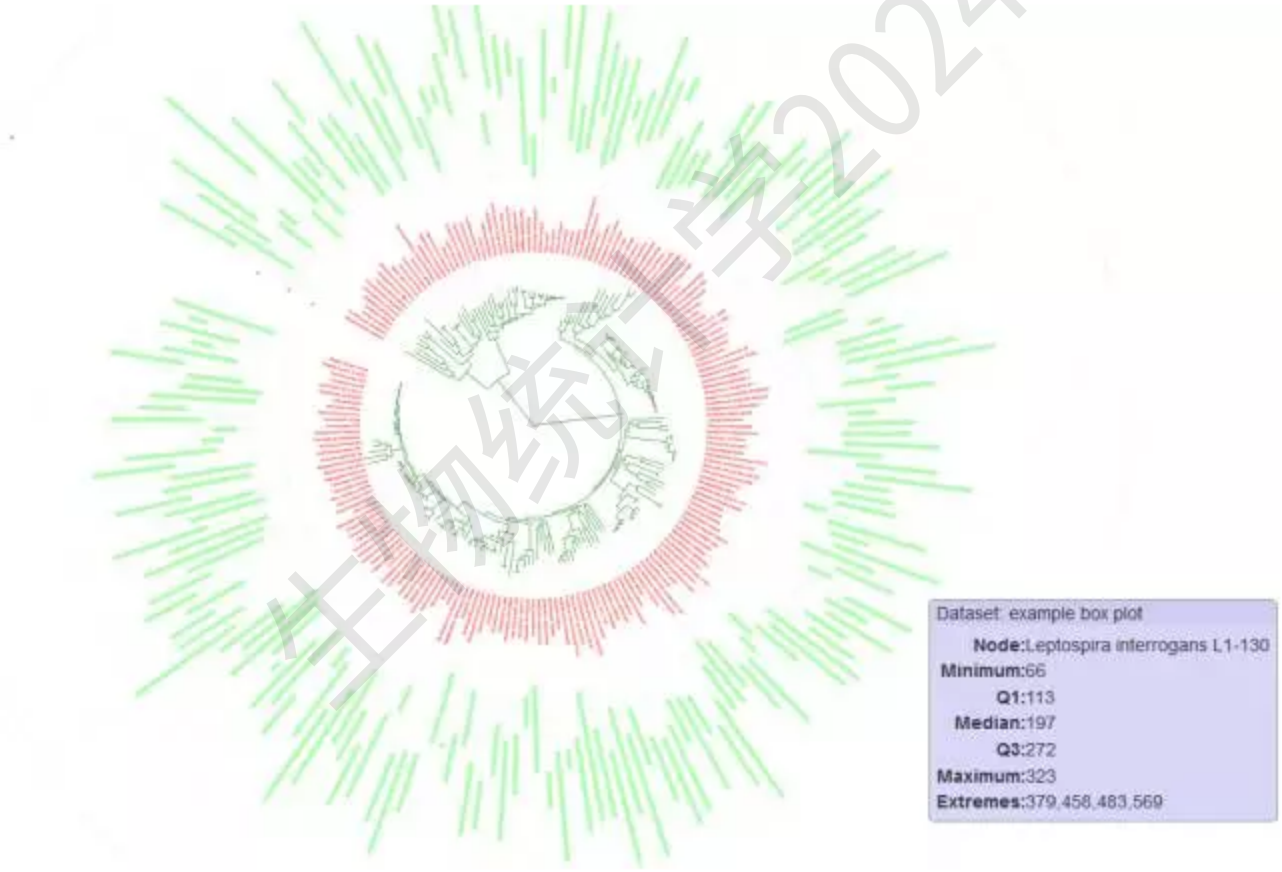
Nature 528, 364–369 (2015)



Nature Medicine 22, 1187–1191 (2016)

iTOL: https://itol.embl.de/

iTOL：物种进化关系分析



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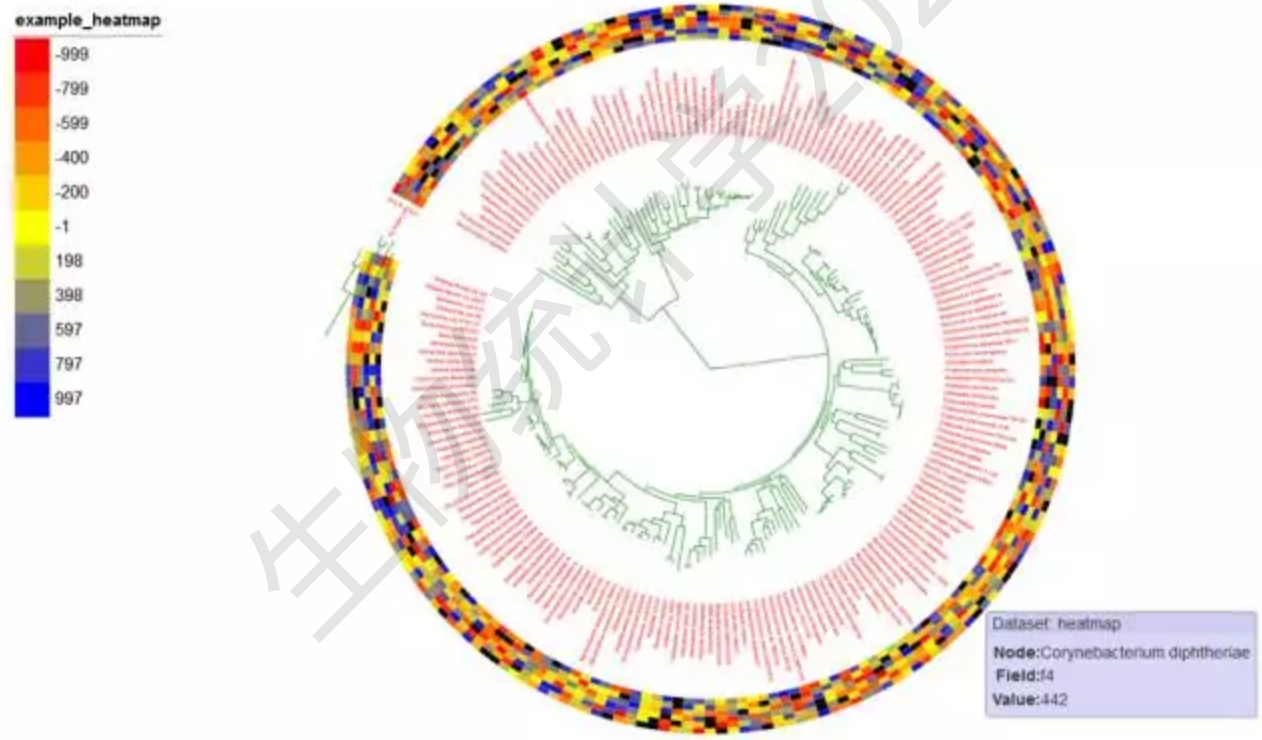
iTOL：物种进化关系分析



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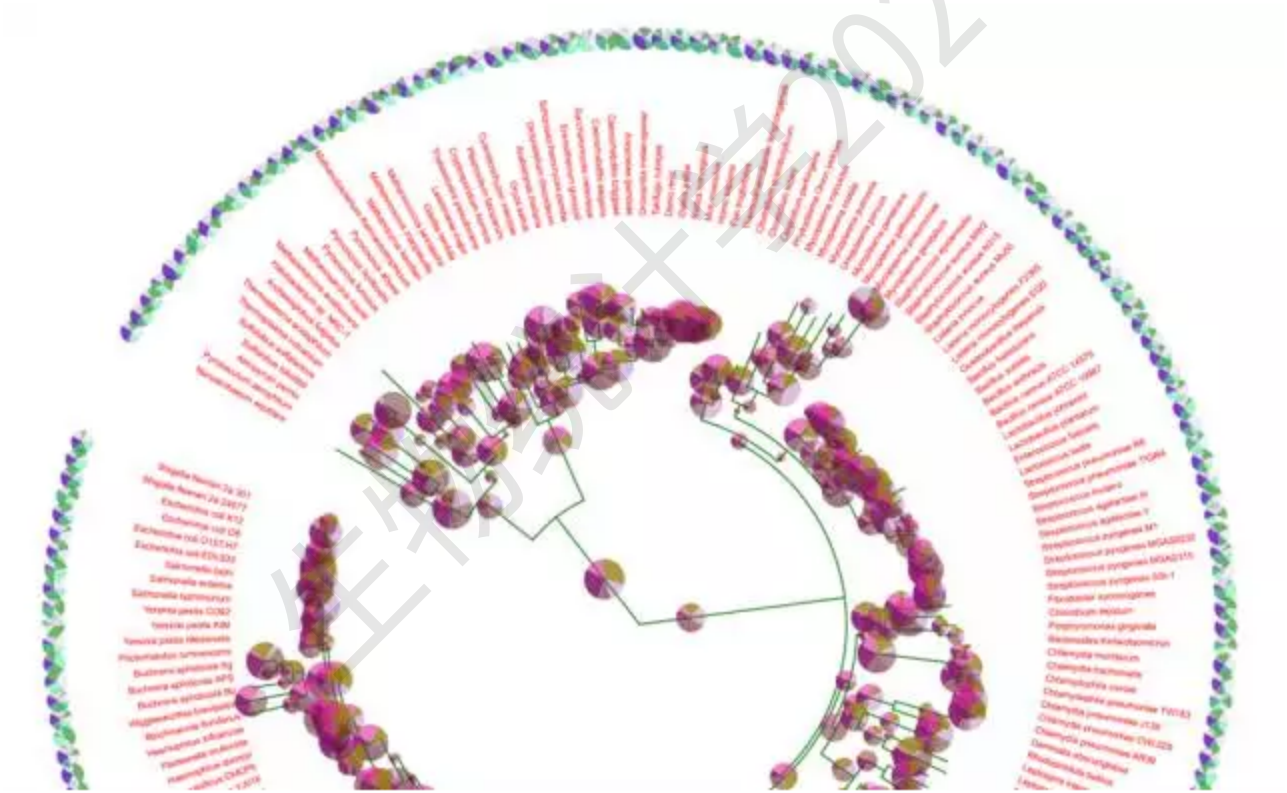
iTOL：物种进化关系分析



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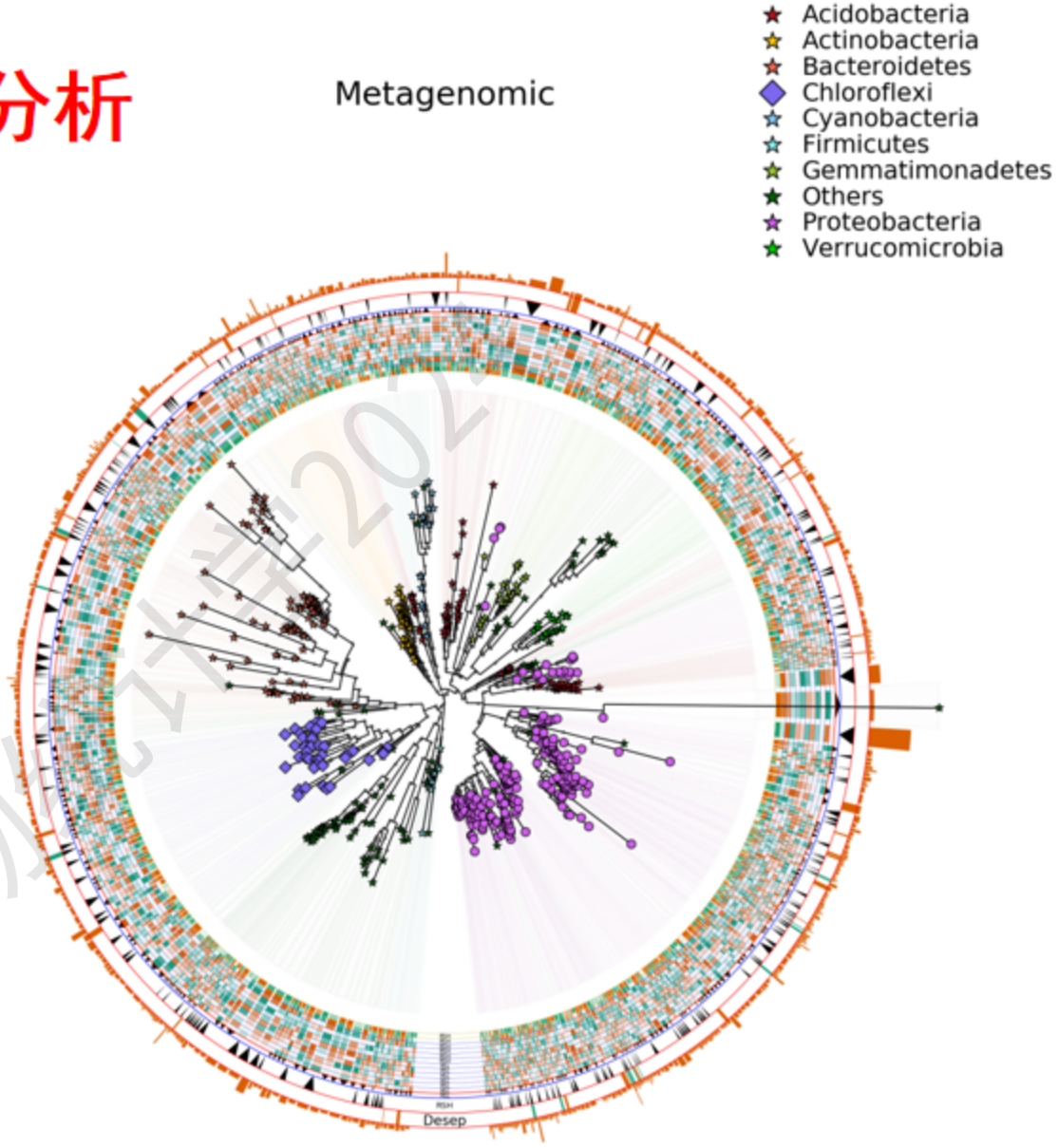
iTOL：物种进化关系分析

iTOL: https://itol.embl.de/

GraPhlAn：分类树分析



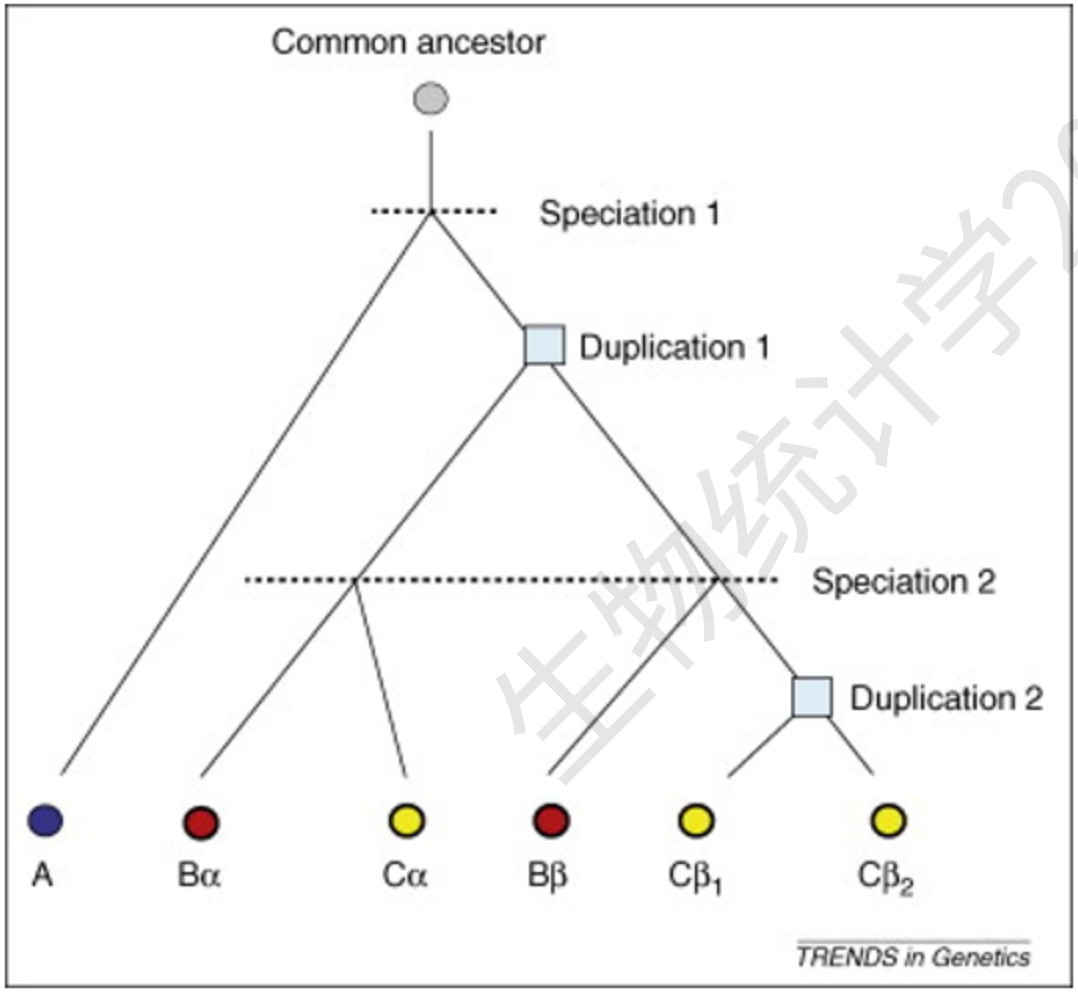
构建分子进化树相关的软件

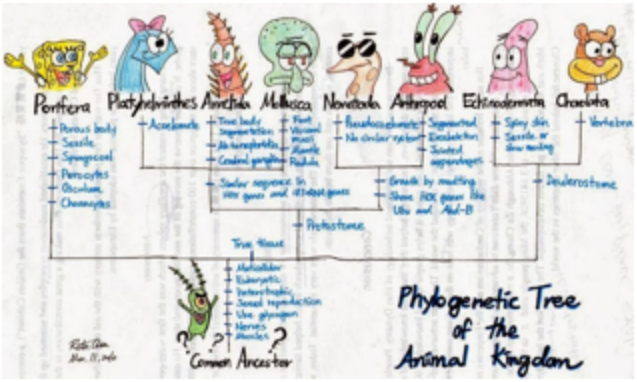
- 就进化树而言，iTOL功能最为全面。iTOL无限制添加的数据集，外环可以制作各种图形包括箱线图等，可以使用多种符号填充外环。但Graphlan就不能这么随便了，只能使用两个符号填充外环。再多的环属性也就是设置环数量和颜色，透明度了。

- ggtree最容易上手，但是就一张圈图来说，它不能添加除了热图以外的其他图形，但是在非圈图的模式下，可以对多种数据进行合并，方法将更为简单，操作也容易一些。

- Graphlan可以制作分类树，是它不同于R包ggtree和iTOL的地方。

Gene: ortholog and paralog

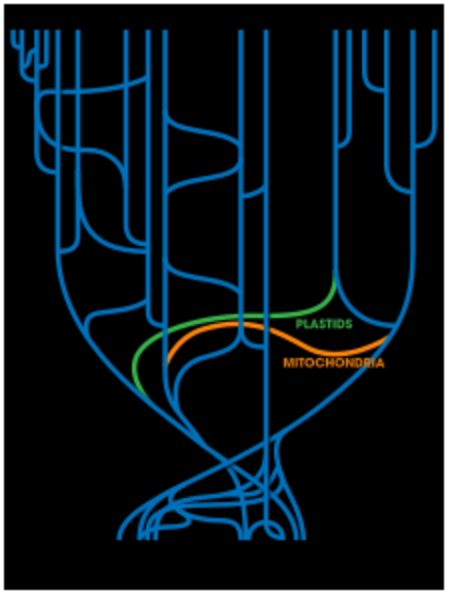


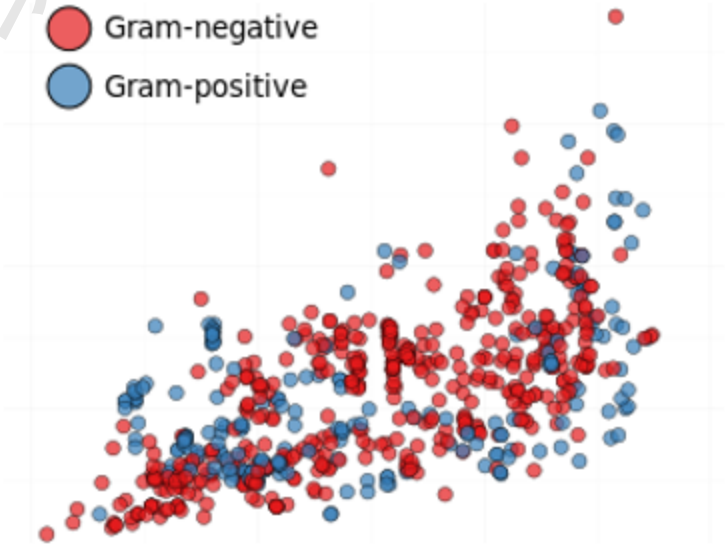


Gene: HGT

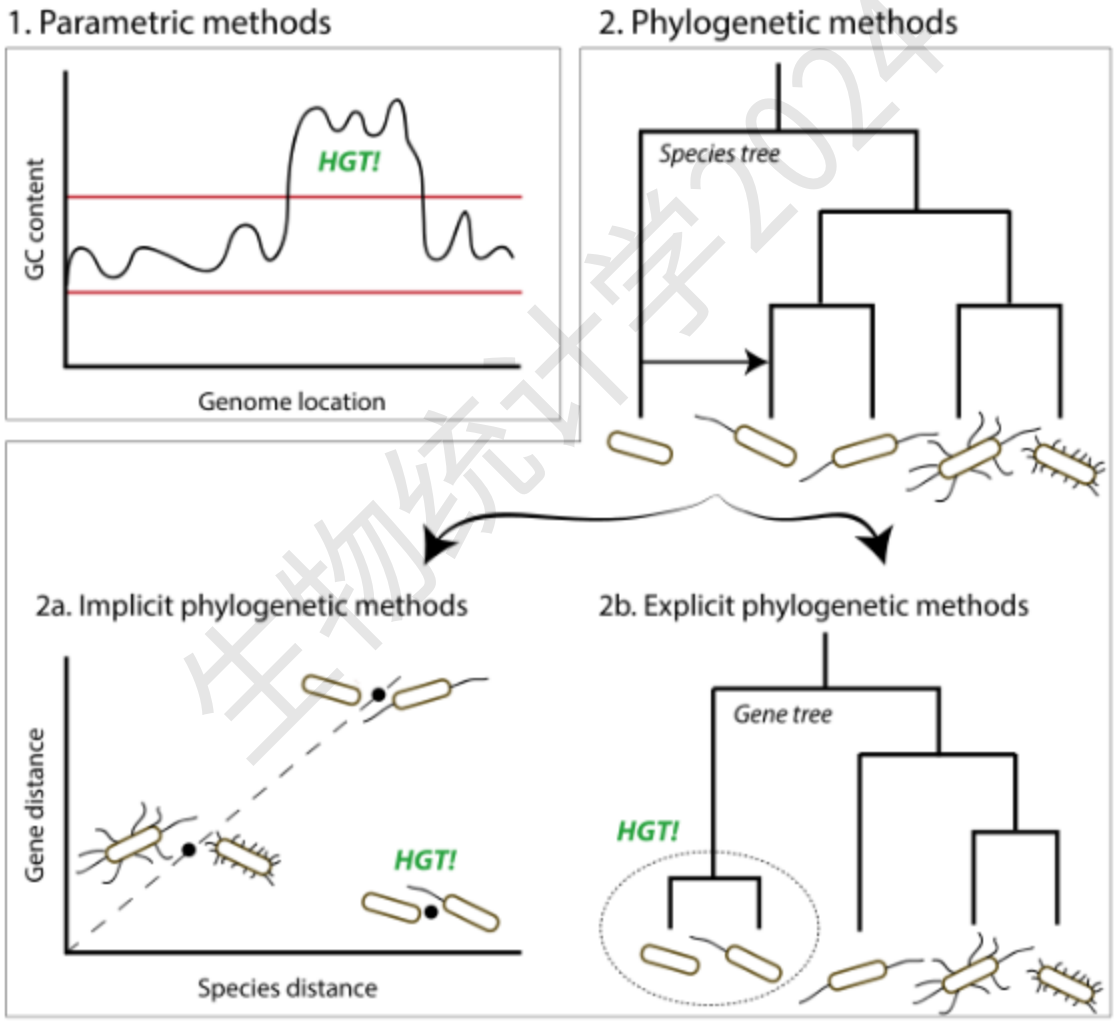
Gene: HGT

Think about it:
how does HGT affect the molecular clock calculation?





HGT identification methods (phylogeny analysis)



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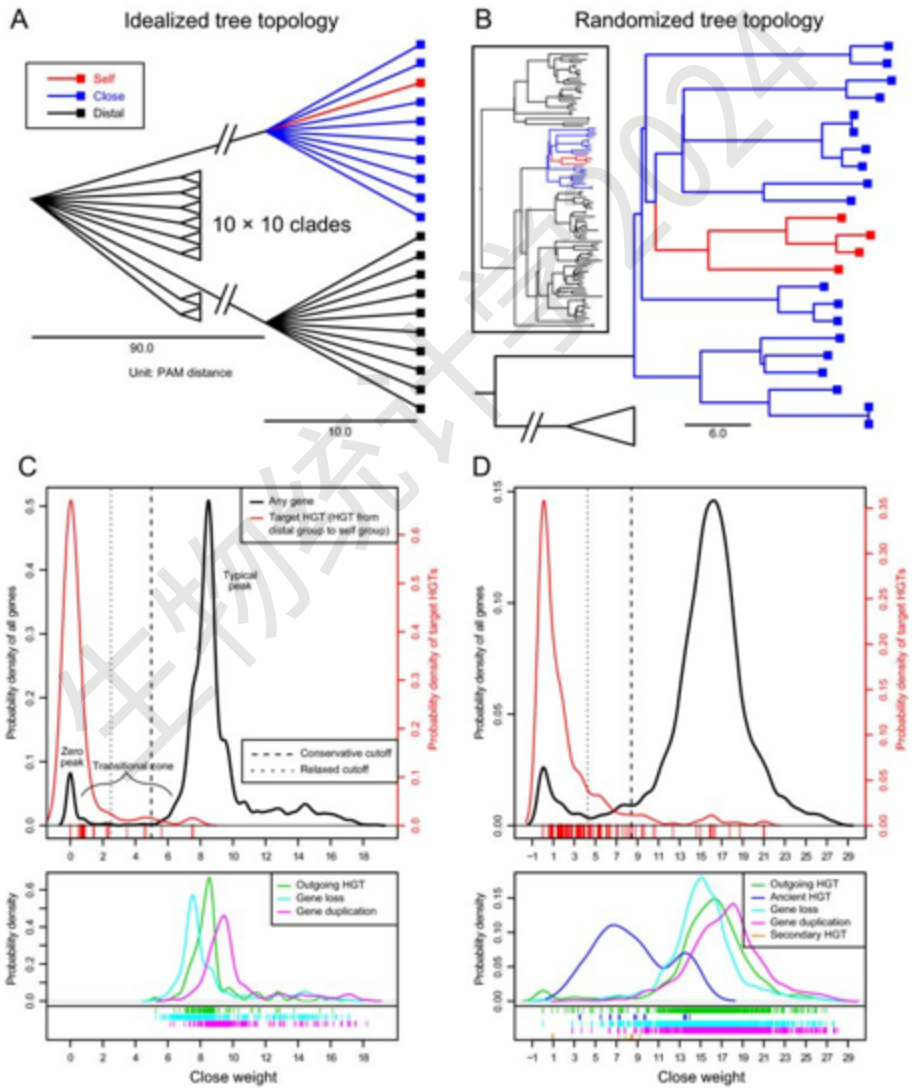

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- R. Durbin, S. Eddy, A. Krogh and G. Mitchison. Biological Sequence Analysis—Probabilistic Models of Proteins and Nucleic Acids. 1998, Cambridge University Press.

References


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