Distribution of the genomic distance

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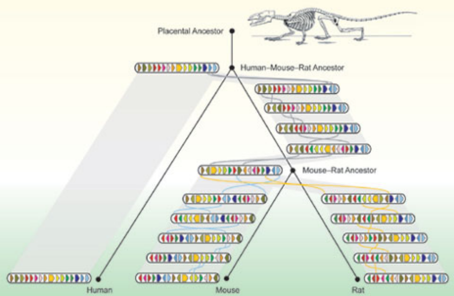
Genome comparison



Problem

Let genomes of two species have *n* common genes. What is the evolutionary scenario for transforming one genome into the other?

Rearrangment

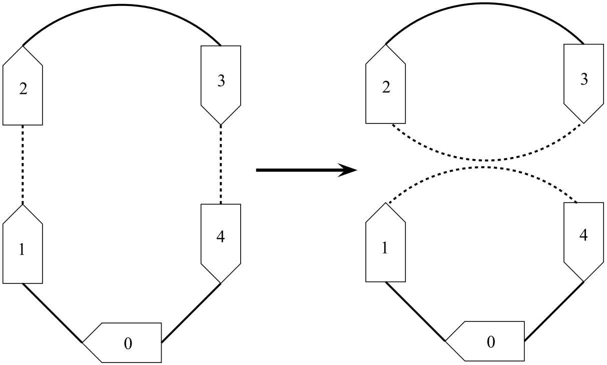


Figure : Allowed rearrangment: 2-break

Definition

The 2-break distance $d_2(A, B)$ between genomes A and B is the minimal number of 2-breaks needed to transform A to B.

Breakpoint graph

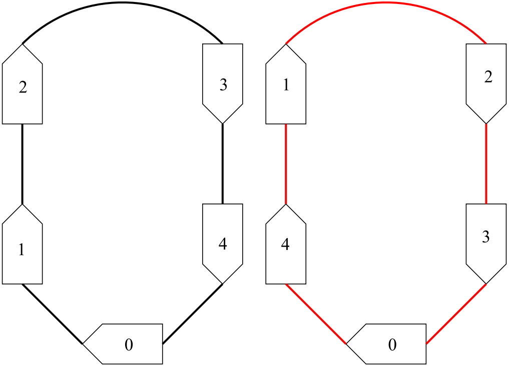


Figure : Let genomes *A* and *B* contain *n* common genes.

Breakpoint graph

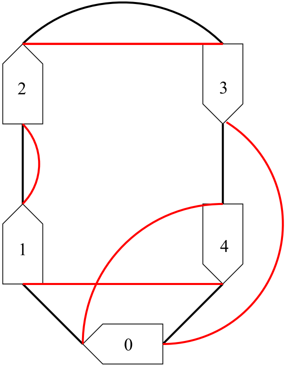


Figure : Draw both genomes *A* and *B* on the same graph.

Breakpoint graph

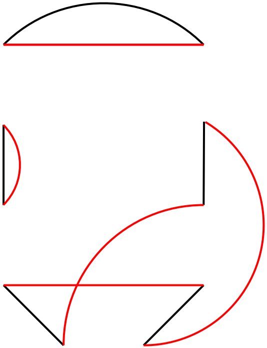


Figure : Erase all “genes” edges. *The breakpoint graph $G(A, B)$ consists of several alternating cycles.*

Bafna–Pevzner theorem

Theorem (Bafna and Pevzner ’98)

Let A and B be two genomes with n common genes, and the breakpoint graph $G(A, B)$ consists of k alternating cycles. Then the 2-break distance $d_2(A, B)$ between A and B is equal to

$$d_2(A, B) = n + 1 - k.$$

example

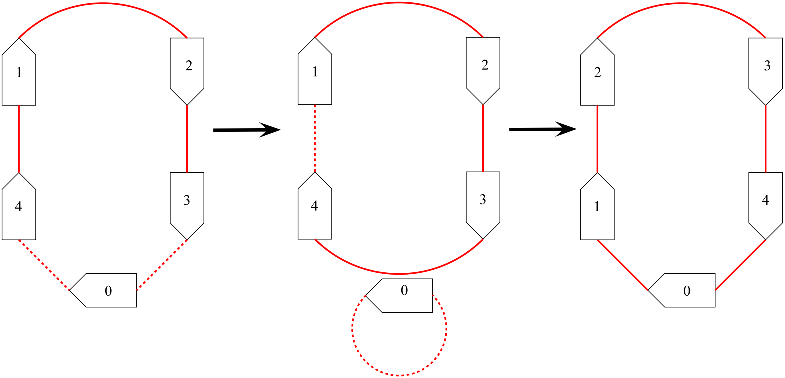


Figure : The 2-break distance between (1234) and (4123) is 2.

Topologocal interpretation

The metric d_2 on the permutation group S_n is naturally induced by the metric d_2 on the set of genomes.

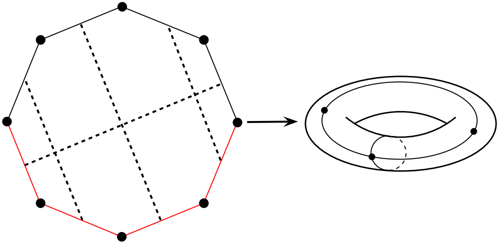


Figure : An octagon is glued according to the permutation $\pi = (4123)$.

Remark

The distance $d_2(\pi, id)$ between some permutation π and the identity is twice the genus of the surface glued according to π.

Random matrix

Definition

Hultman numbers $H(n,k) = \#\{\pi \in S_n : d_2(\pi, id) = k\}$.

$$p_n(N) = \sum_{k=1}^{n+1} H(n,k) N^k$$

Theorem (Alexeev and Zograf '11)

Let X be an $N \times N$ random matrix, whose entries x_{ij}, $1 \leq i,j \leq N$ are independent standard Gaussian complex random variables. Then

$$\mathbb{E}\,\mathrm{Tr}\,X^n X^{n*} = p_n(N).$$

$$
\begin{aligned}
p_0(N) &= N,\\
p_1(N) &= N^2,\\
p_2(N) &= N^3 + N,\\
p_3(N) &= N^4 + 5N^2,\\
p_4(N) &= N^5 + 15N^3 + 8N,\\
p_5(N) &= N^6 + 35N^4 + 84N^2,\\
p_6(N) &= N^7 + 70N^5 + 469N^3 + 180N,\\
p_7(N) &= N^8 + 126N^6 + 1869N^4 + 3044N^2,\\
p_8(N) &= N^9 + 210N^7 + 5985N^5 + 26060N^3 + 8064N,\\
p_9(N) &= N^{10} + 330N^8 + 16401N^6 + 152900N^4 + 193248N^2.
\end{aligned}
$$

Recurrence

Theorem

- *The Hultman numbers satisfy the recurrence relation*

$$(n+2)H(n,k) = (2n+1)H(n-1,k-1)- \\ -(n-1)H(n-2,k-2) + n^2(n-1)H(n-2,k);$$

- *The polynomials $p_n(N) = \sum_{k=1}^{n+1} H(n,k)N^k$ satisfy the recursion*

$$(n+2)p_n(N) = (2n+1)Np_{n-1}(N)+ \\ +(n-1)(n^2-N^2)p_{n-2}(N)$$

with $p_0 = N$, $p_1 = N^2$;

Generating function

Theorem

Let $F(x,t)$ be the generating function of the sequence $H(n,k)$

$$F(x,t) = \sum_{n=0}^{\infty} \sum_{k=1}^{n+1} H(n,k) t^k \frac{x^n}{n!} \tag{1}$$

Then

$$F(x,t) = \frac{1}{x^2} \left(\frac{1}{(1-x)^t} - (1+x)^t \right);$$

Asymptotic distribution

Consider the symmetric group S_n equipped with the uniform measure. Then the number of alternating cycles in the breakpoint graph of a random permutation is a random variable that we denote by K_n. Here we study the asymptotic distribution of the random variable K_n as $n \to \infty$.

The probability $P\{K_n = k\}$ is equal to $\frac{H(n,k)}{n!}$. Therefore,

$$F(x,t) = \sum_{n=0}^{\infty} \sum_{k=1}^{n+1} x^n t^k P\{K_n = k\},$$

and the coefficient of $F(x,t)$ at x^n is the expectation of t^{K_n}:

$$\mathbb{E}t^{K_n} = \binom{t+n+1}{n+2} - \binom{t}{n+2}.$$

Result

Theorem (Alexeev and Zograf ’13)

The number K_n of alternating cycles in the cycle graph of a random permutation of length n has the expectation and the variance of order $\ln n$: $\mathbb{E}K_n = \ln n + \gamma + o(1)$ and

$$\mathbb{E}(K_n - \mathbb{E}K_n)^2 = \ln n + \gamma - \frac{\pi^2}{6} + o(1).$$

The variable $\frac{K_n - \ln n}{\sqrt{\ln n}}$ weakly converges to the standard Gaussian random variable.

Remark

In terms of genome rearrangements this theorem claims that the 2-break distance between two genomes randomly built from the same set of n genes has the mean value of order $n - \ln n$ and is asymptotically Gaussian as $n \to \infty$.

Thanks

Thank you!