Statistical Properties of Genealogical Trees

Introduction

Distribution of repetitions

Comparison between two trees

Galton Watson process and the renormalization group

Genealogy of a chromosome

PRL 99
Physica A 2000
J. Th. Biol. 2000

JSP 99

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References

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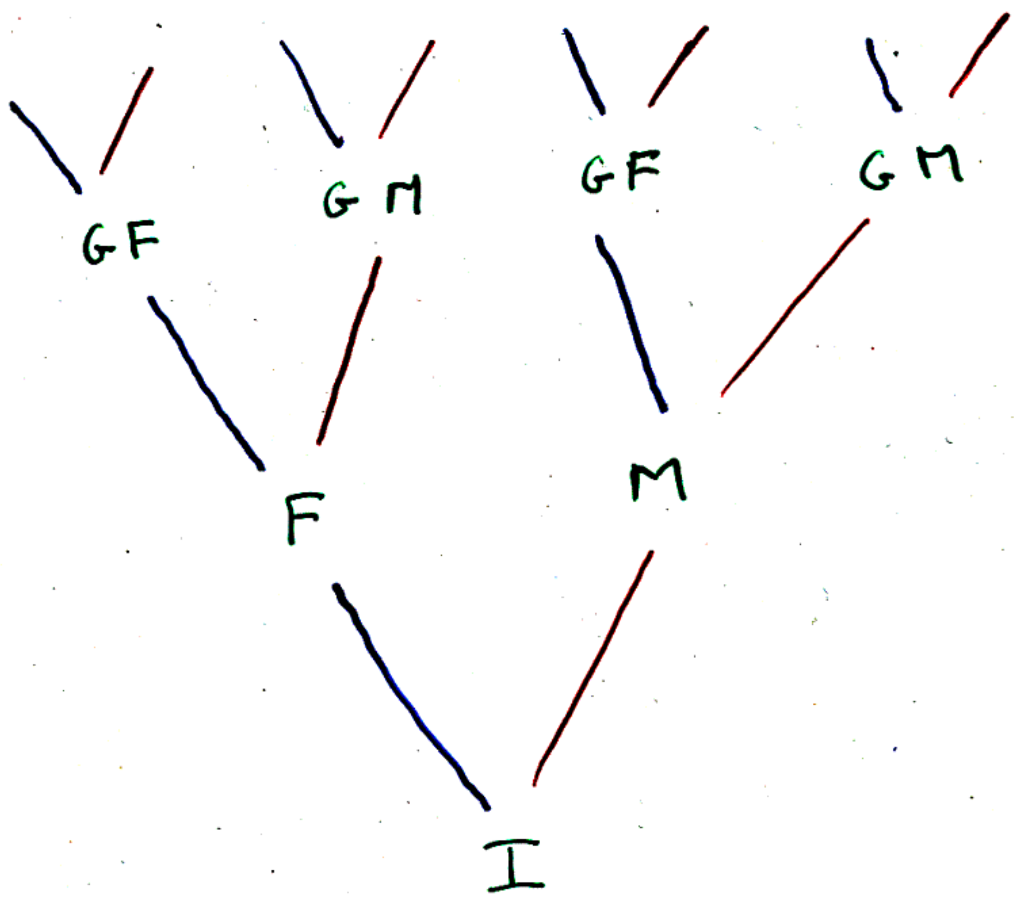

GF
GM
GF
GM
F
M
I

Repetitions in a genealogical tree

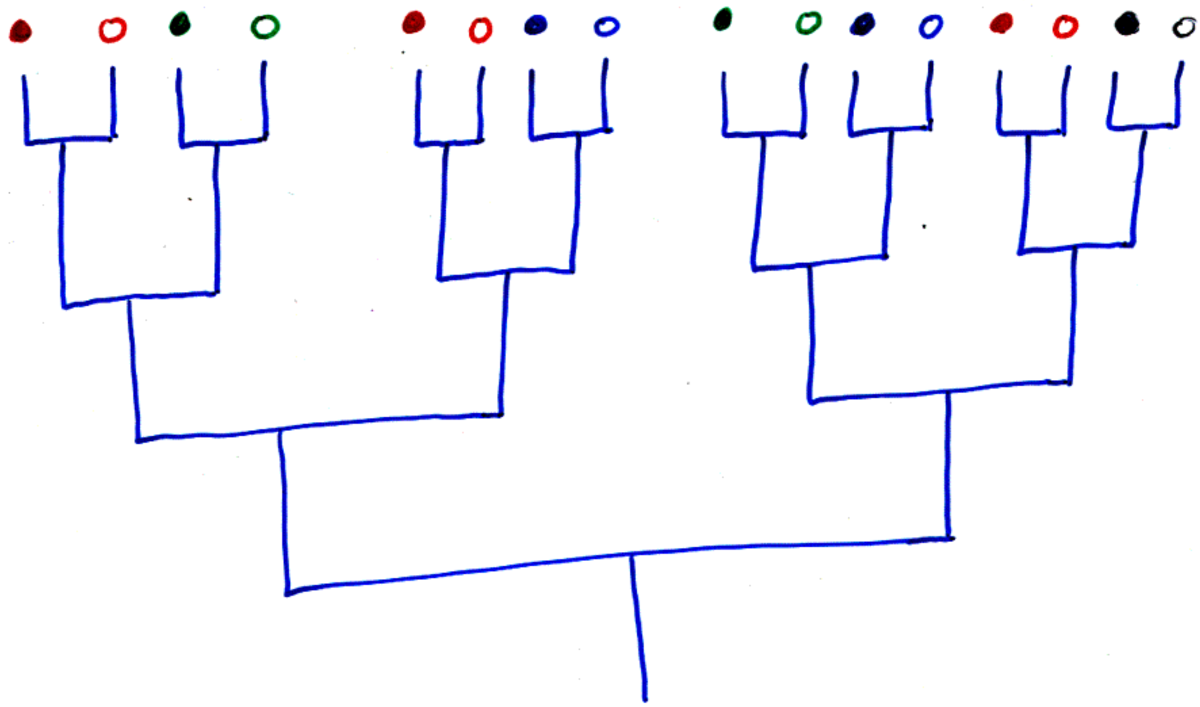
mass of earth $\sim 10^{26}$ h.b.

10^{26} ancestors $\sim$ 90 generations

90 generations $\sim$ 2000 years

$\Downarrow$

Lots of repetitions

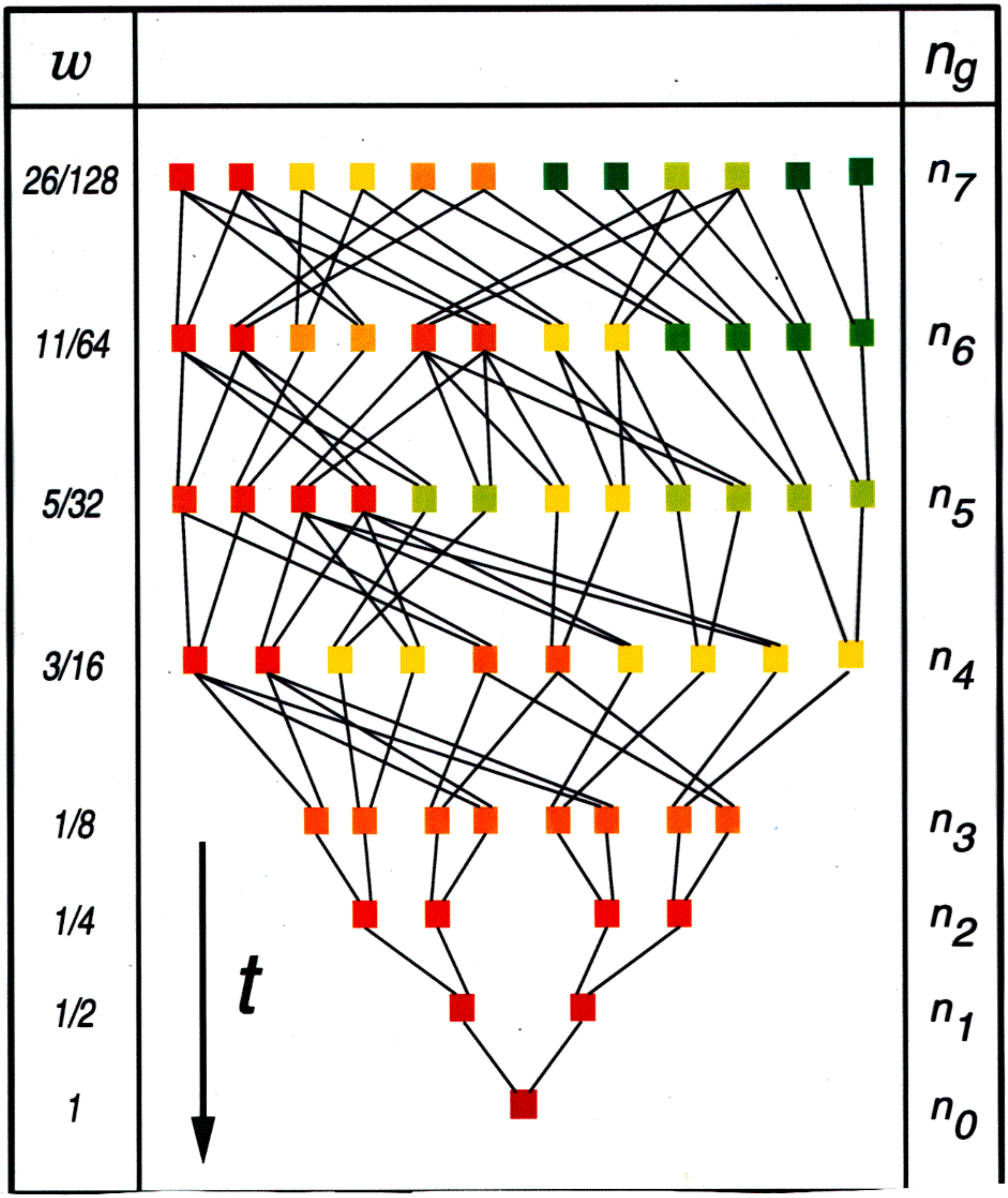


$$r(\bullet) = r(\circ) = 3$$

$$r(\bullet) = r(\circ) = 2$$

$$r(\bullet) = r(\circ) = 2$$

$$r(\bullet) = r(\circ) = 1$$



w
n_g
26/128
11/64
5/32
3/16
1/8
1/4
1/2
1
n_7
n_6
n_5
n_4
n_3
n_2
n_1
n_0
t

Model

- N individuals at each generation g
- Each individual at generation g has 2 parents chosen at random in the previous generation $g+1$

$H_g(r)$ = probability that an ancestor at generation g in the past is repeated r times

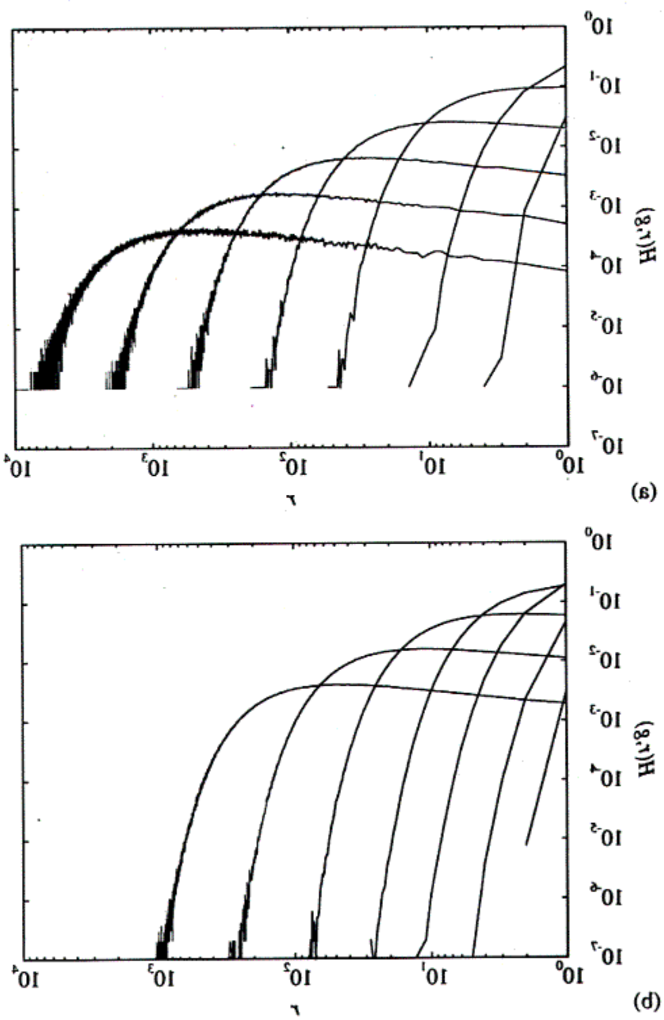


Fig. 1. Probability distribution $H(r,g)$ of r repetitions after g generations ($H(0,g)$ is not s
$g = 5, 9, 12, 14, 16, 18$, and 20 for a population of constant size. In Fig. 1a, $N = 1000$ and in
$N = 10\,000$. Both figures show averages over 1000 samples.

$H_g(r) \to$ stationary shape

r small $\quad \boxed{H(r) \sim r^{\beta}}$

$\beta = .2991138\ldots$ (exact)

Distribution of repetitions

$H_g(r)$ = probability that an ancestor is repeated r times at generation g in the past

$\boxed{\text{Large } g: \text{ all the } H_g(r) \text{ have the same shape}}$

$$r_i(g+1) = \sum_{\substack{j \text{ children} \\ \text{of } i}} r_j(g)$$

Rescaling:

$$w_i(g) = \frac{N}{2^g} r_i(g)$$

$$\boxed{w_i(g+1) = \frac{1}{2} \sum_{\substack{j \text{ children} \\ \text{of } i}} w_j(g)}$$

$$\boxed{w_i(g+1) = \frac{1}{2} \sum_{\substack{j \text{ children} \\ \text{of } i}} w_j(g)}$$

Large N:

- the $w_j(g)$ become uncorrelated
- the probability p_n of having n children is

$$\boxed{p_n = \frac{2^n}{n!} e^{-2}}$$

Generating function

$$F_g(\lambda) = \langle e^{\lambda w_i(g)} \rangle$$

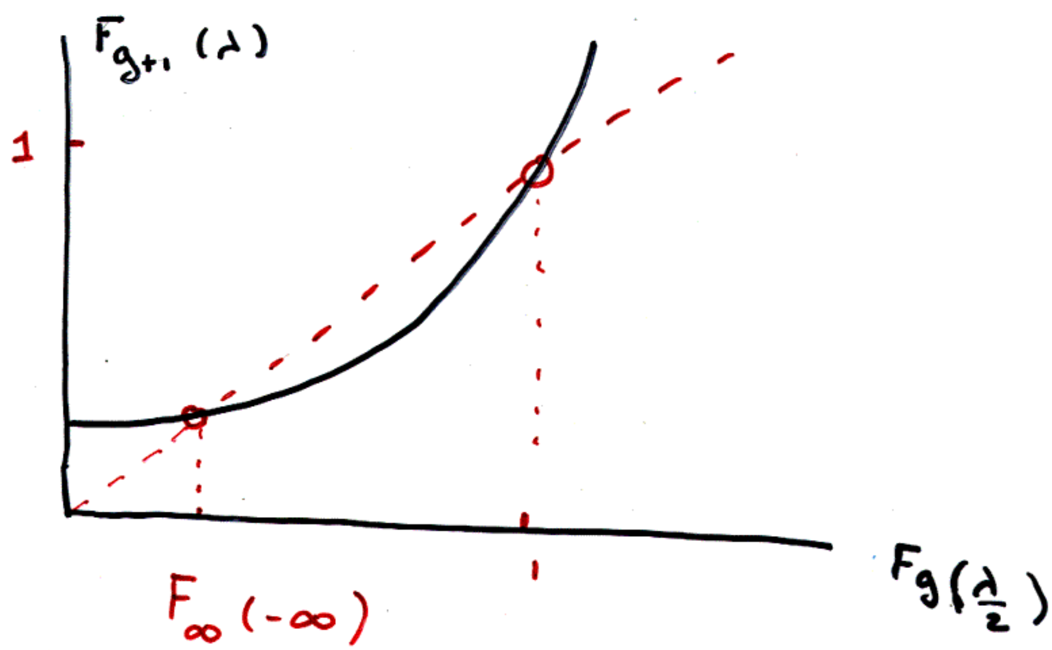
Then

$$F_{g+1}(\lambda) = \sum_n p_n \left[F_g\left(\frac{\lambda}{2}\right) \right]^n$$

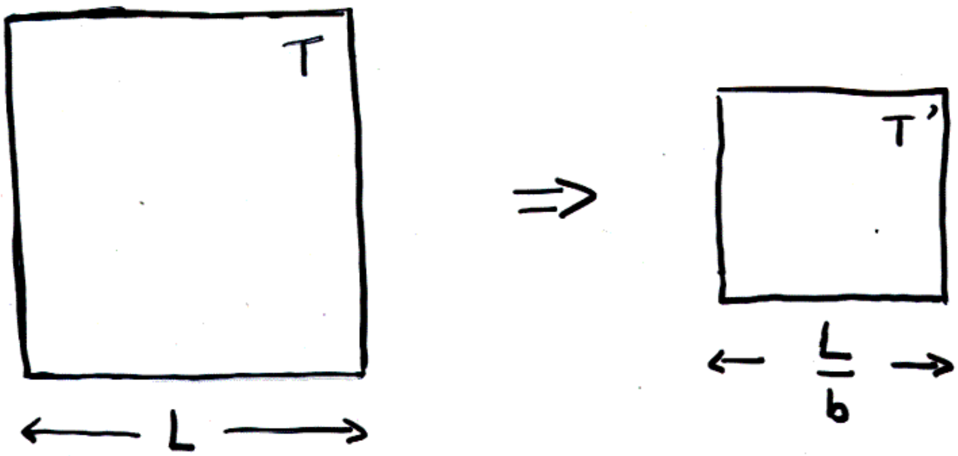
Generating function

$$F_g(\lambda) = \langle e^{\lambda w_i(g)} \rangle$$

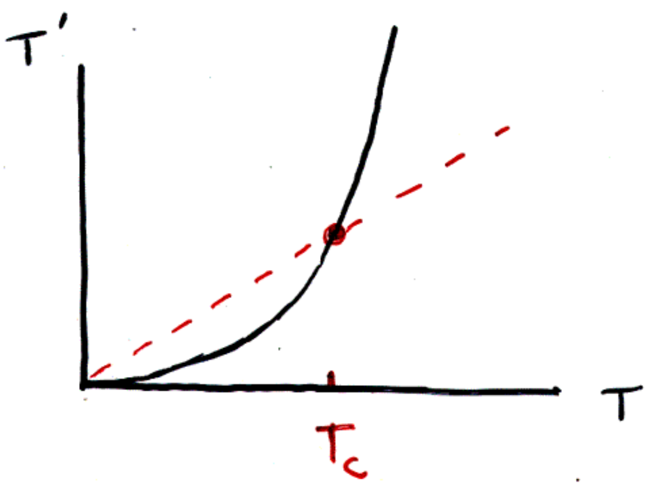
$$\boxed{F_{g+1}(\lambda) = \exp\left[2 F_g\left(\frac{\lambda}{2}\right) - 2 \right]}$$



Renormalisation



$$\boxed{T' = R_b(T)}$$



Unstable fixed point $\equiv T_c$

Exponent $\boxed{b^{1/\nu} = \left.\frac{dT'}{dT}\right|_{T_c}}$

Generalisation

$2 \longrightarrow p$ parents

$$F_{g+1}(\lambda) = e^{p F_g\left(\frac{\lambda}{p}\right) - p}$$

$p = 1 + \epsilon \Rightarrow \epsilon$ expansion . . .

$\Longleftrightarrow$ • 2 parents

• Population increasing exponentially

$$N_t = \frac{p}{2} N_{t-1}$$

Comparing two trees

$w_i^{(\alpha)}(g)$: weight of ancestor i at generation g in the pas in the tree of α

$$q_{\alpha\beta}(g) = \frac{\sum_i w_i^{(\alpha)}(g)\, w_i^{(\beta)}(g)}{\left(\sum_i w_i^{(\alpha)}(g)\right)^{1/2}\left(\sum_i w_i^{(\beta)}(g)\right)^{1/2}}$$

$$\boxed{g_c = \frac{\log N}{\log 2} - 1}$$

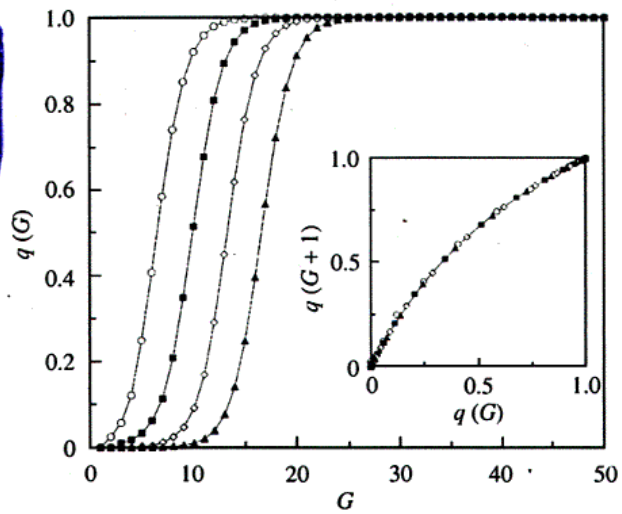


FIG. 4. The averaged overlap $q(G)$ as a function of the number of generations G. The results of simulations for different sizes of the population $N = 100$ (○), 1000 (■), 10000 (◇), 100 000 (▲) agree with this prediction, up to small finite-size corrections only visible for $N = 100$. The inset shows the results of simulations and the prediction (8).

$$q(g) = \frac{1}{1 + 2^{g_c - g}}$$

Galton Watson process 1874

T.E. Harris:
"The Theory of Branching Processes" 1963

Each individual has n descendants with probability p_n

	children	
	0	p_0
Parent	1	p_1
	2	p_2
	$\vdots$	

What is the number N_g of descendants after g generations?

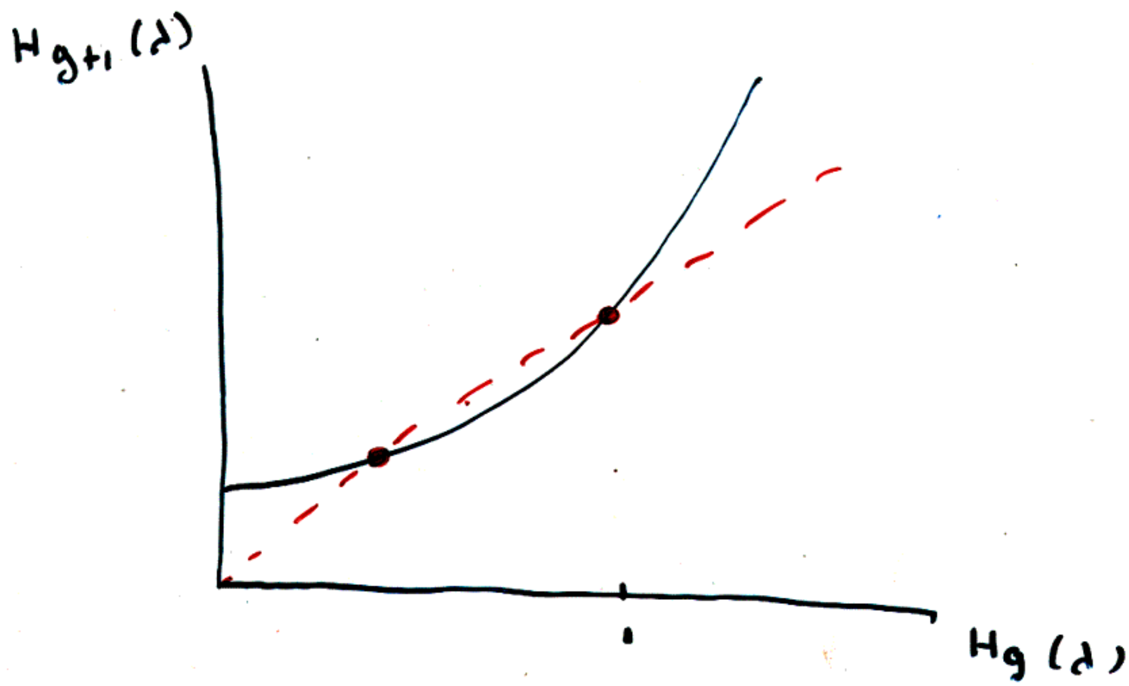
Generating function:

$$H_g(\lambda) = \langle \lambda^{N_g} \rangle$$

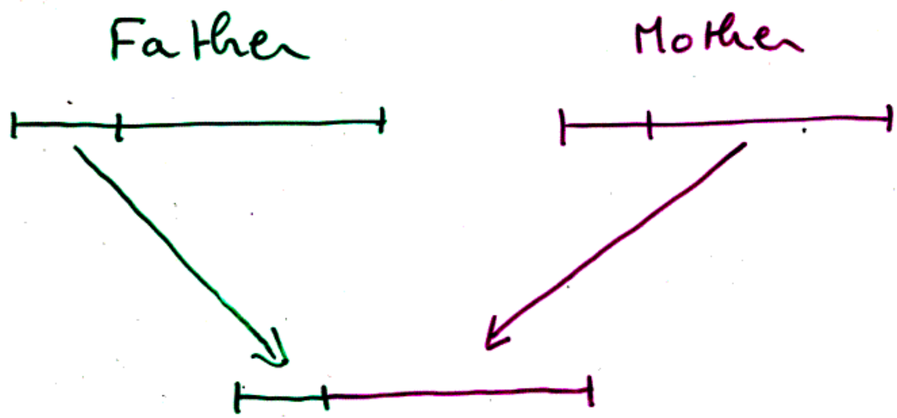
If: $f(\lambda) = \sum_n p_n \lambda^n$

Then

$$\boxed{H_{g+1}(\lambda) = f(H_g(\lambda))}$$



Genealogy of a chromosome



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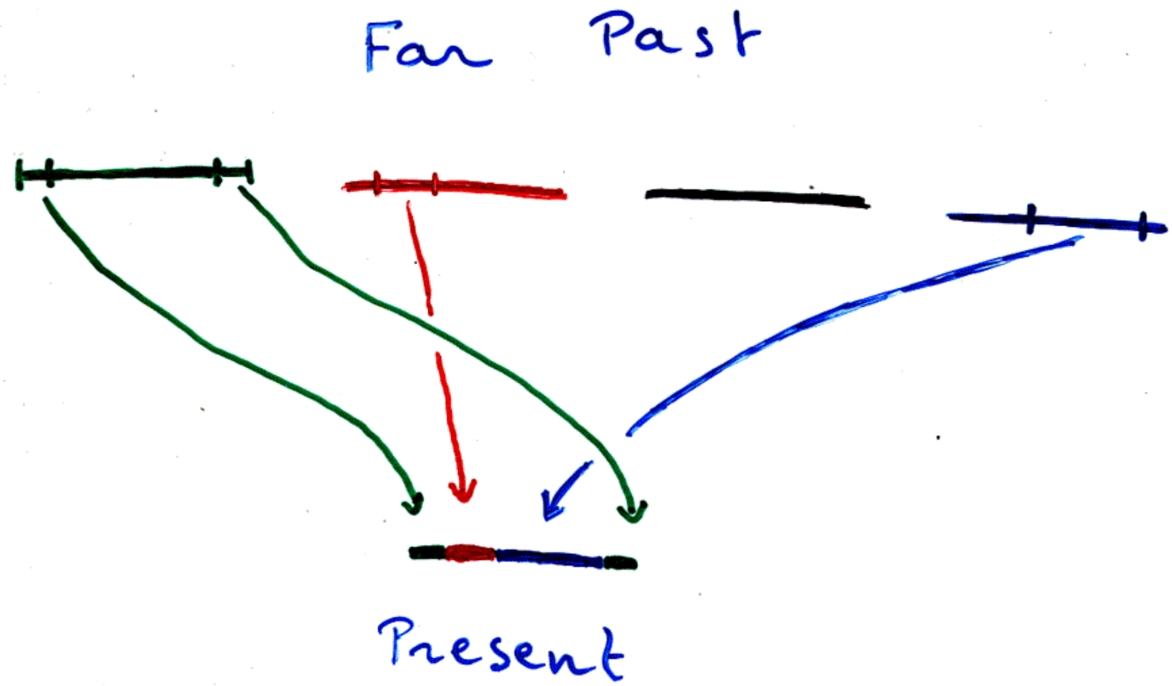
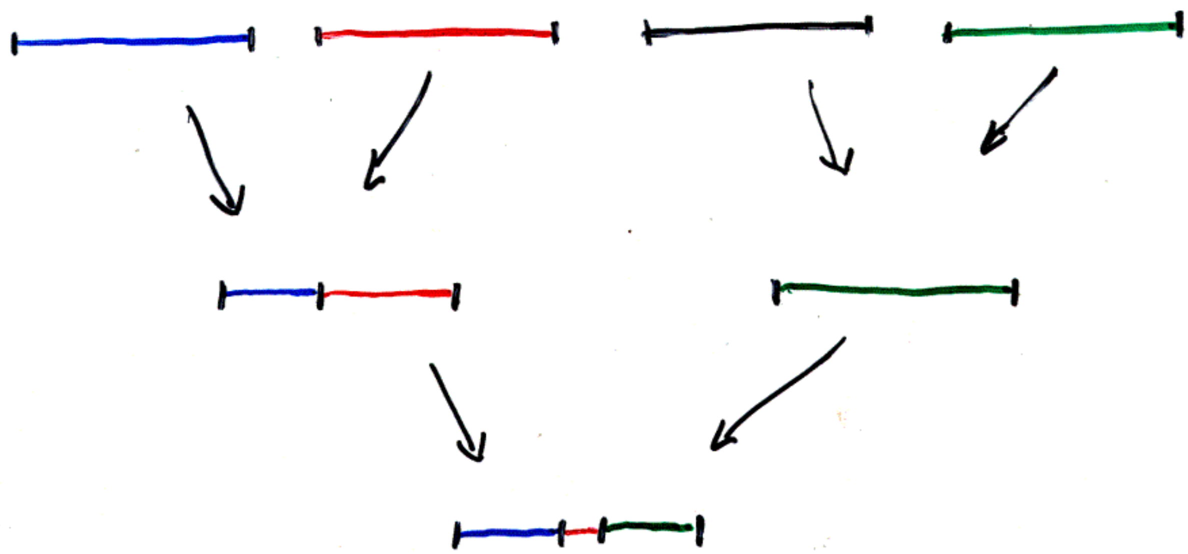


Example



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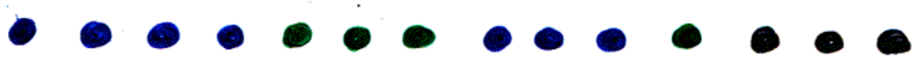
Dynamics during time dt ($dt \ll 1$)



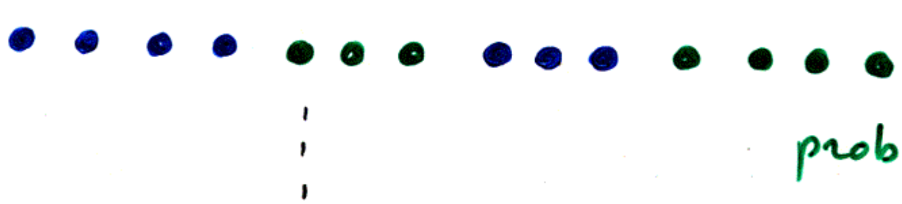
recombination : prob $17\, r\, dt$

($17 = 9 + 6 + 2$)

prob. $4\, r\, dt$

coalescence : prob $3\, dt$

(3 = nb of pairs of colors)



prob. dt

unchanged : prob $1 - (17 r + 3)\, dt$

L sites , Ω_L configurations

L	1	2	3	4	...	10	...
Ω_L	1	2	5	15	...	115975	...

- Solve exactly for L small

- Calculate the small r expansion for all L

- Calculate exactly simple correlation functions

Correlation functions

$$P_{ij} = \frac{1}{1 + r\,|j-i|}$$

$$P_{ijk} = F^{n}(r, |j-i|, |k-j|)$$

Quantities of interest

Q = number of ancestors
(≡ nb of colors)

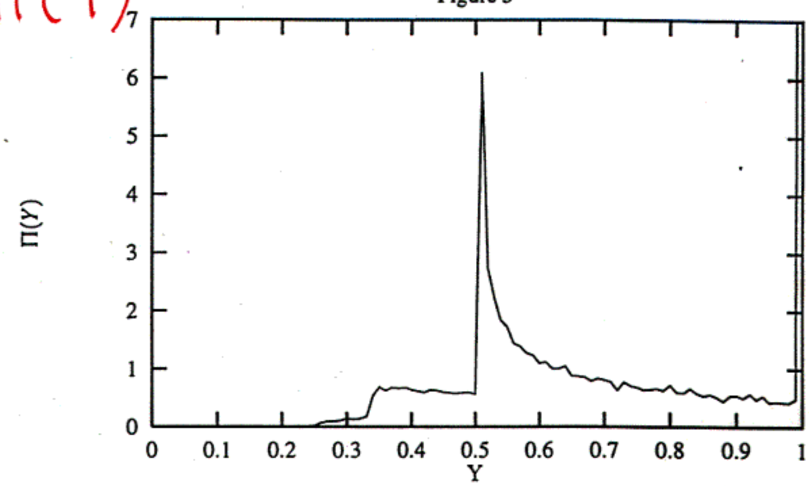
$$Y = \sum_{\alpha} (W_\alpha)^2$$

W_α : fraction of the length having color α

rL = 1

Π(Y)

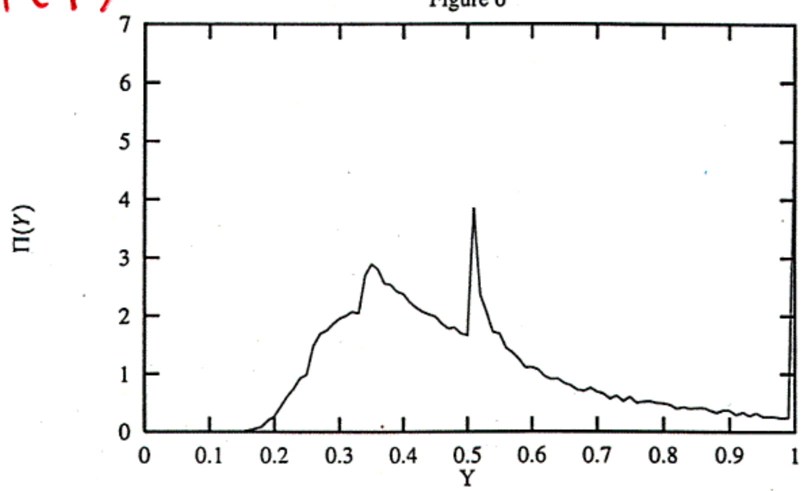
Figure 5



Y

Π(Y)

Figure 6



Y

rL = 4