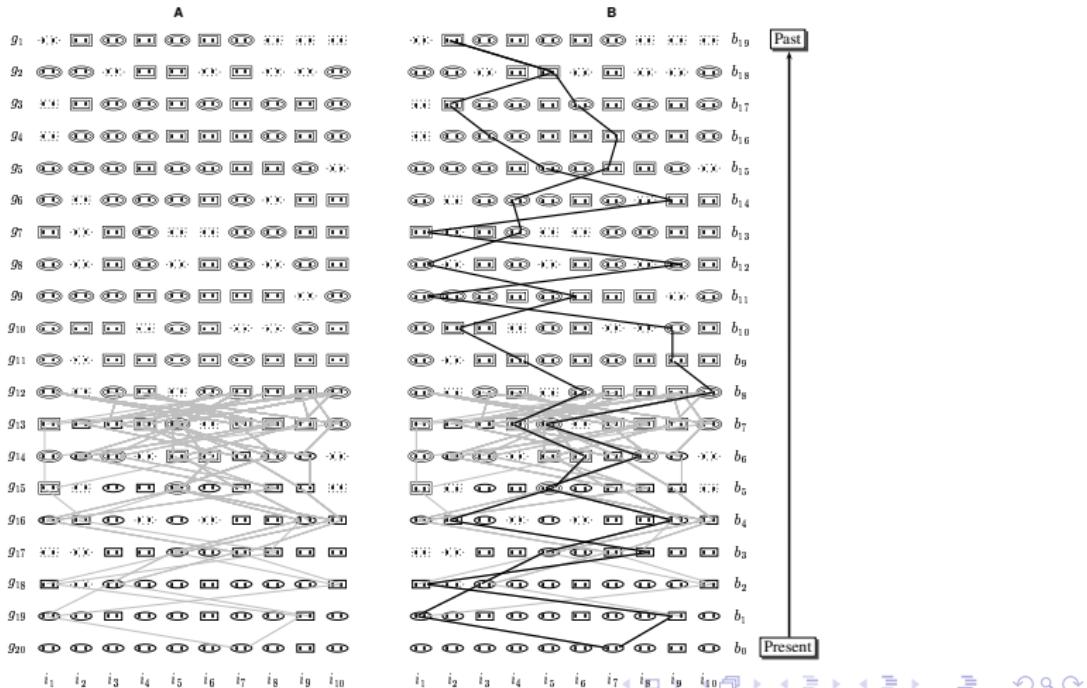


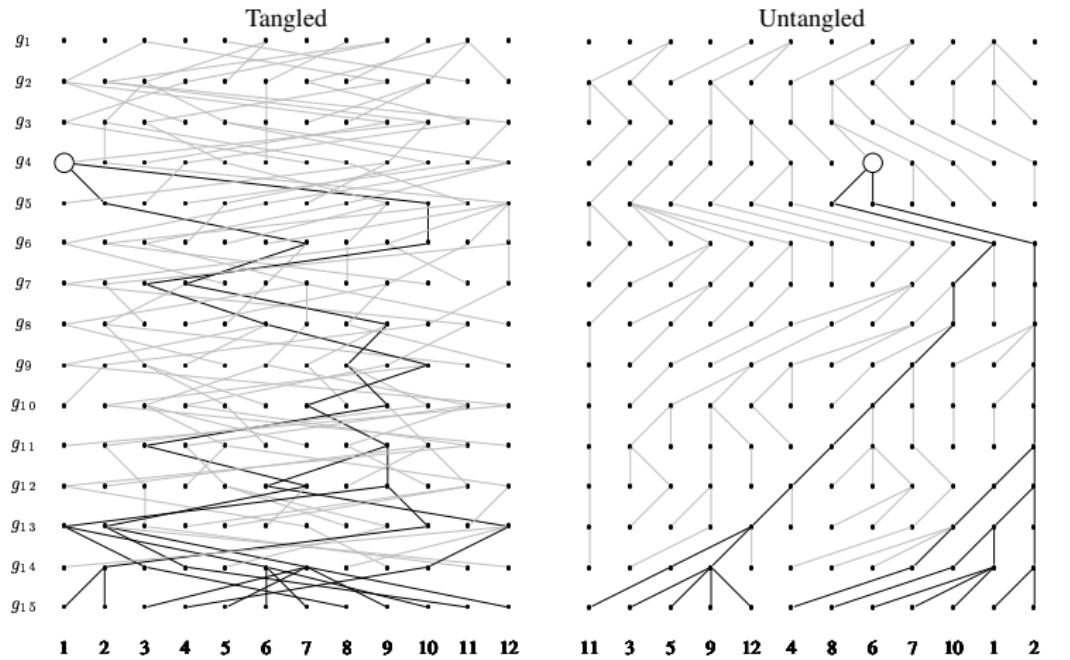
# *Introduction to Computational Biology; An Evolutionary Approach: Genes in Populations: Backward in Time*

Bernhard Haubold & Thomas Wiehe

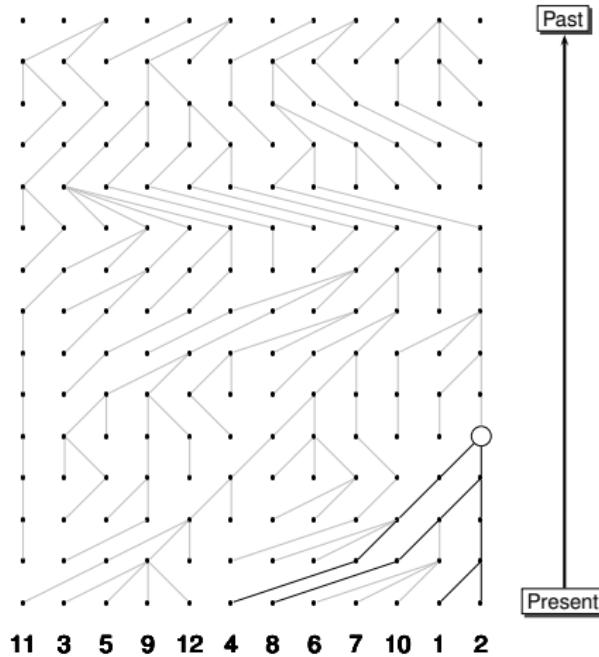
# Genealogy of Individuals



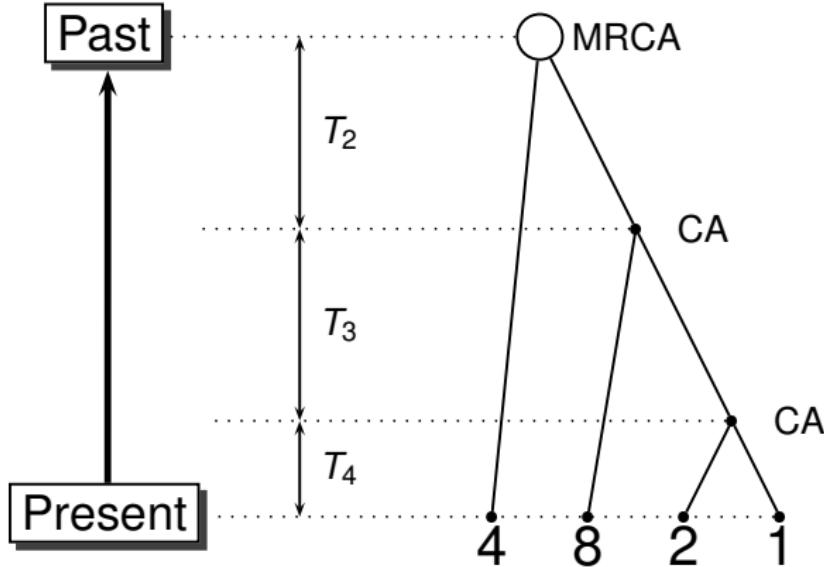
# Genealogy of Genes



# Sample Genealogy

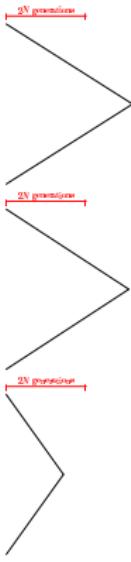


# The Coalescent

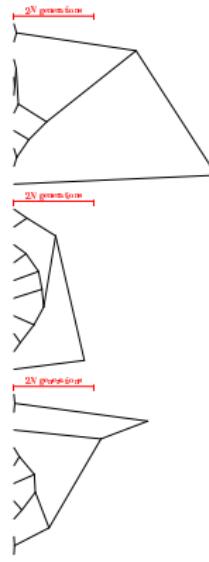


# Coalescent Trees

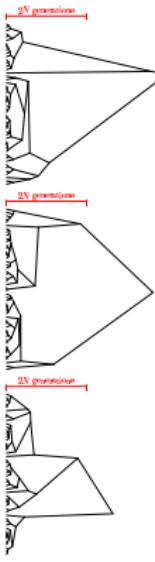
$n = 2:$



$n = 10:$



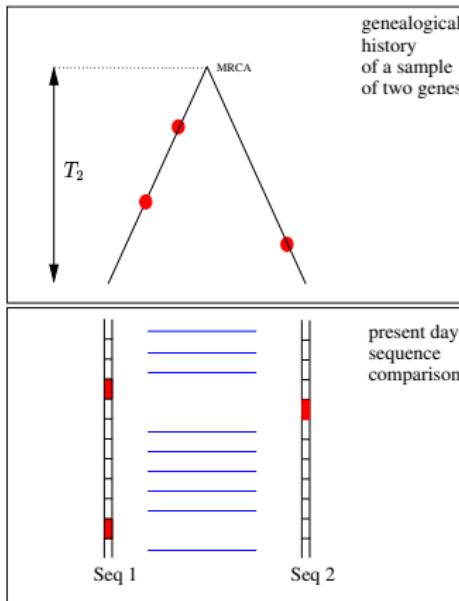
$n = 50:$



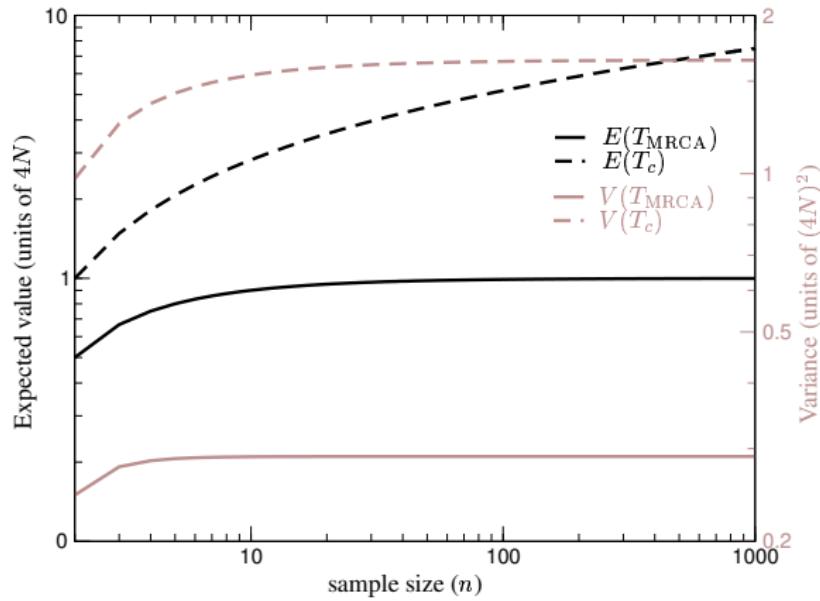
# Coalescent vs. Phylogeny

Feature	Phylogeny	Coalescent
Level of comparison	Inter-species gene history	Intra-species gene history
Purpose	Reconstruct the true species history	Simulate sets of potential gene histories
Observation of interest	Tree topology	Frequency spectrum and distribution of segregating sites
Data source	Comparative data	Model parameters
Multiplicity	Single	Many

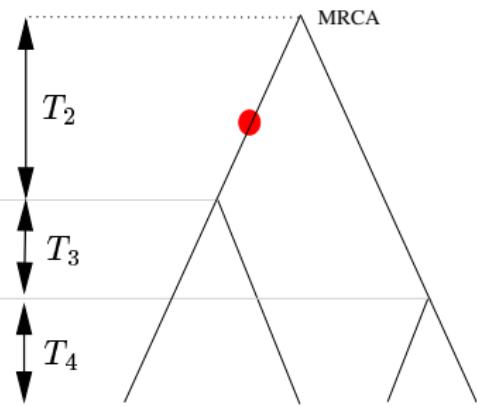
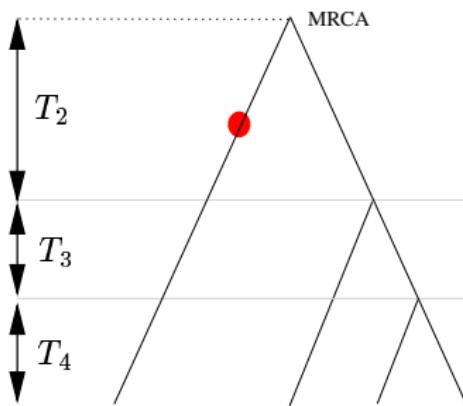
# Genealogy & Polymorphisms



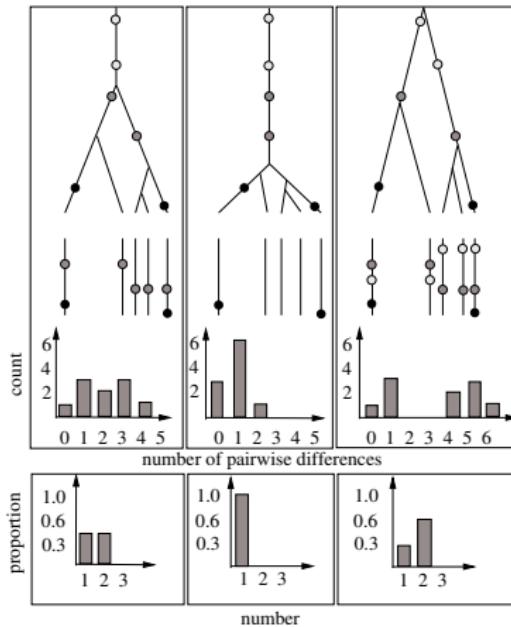
# $T_{\text{MRCA}}$



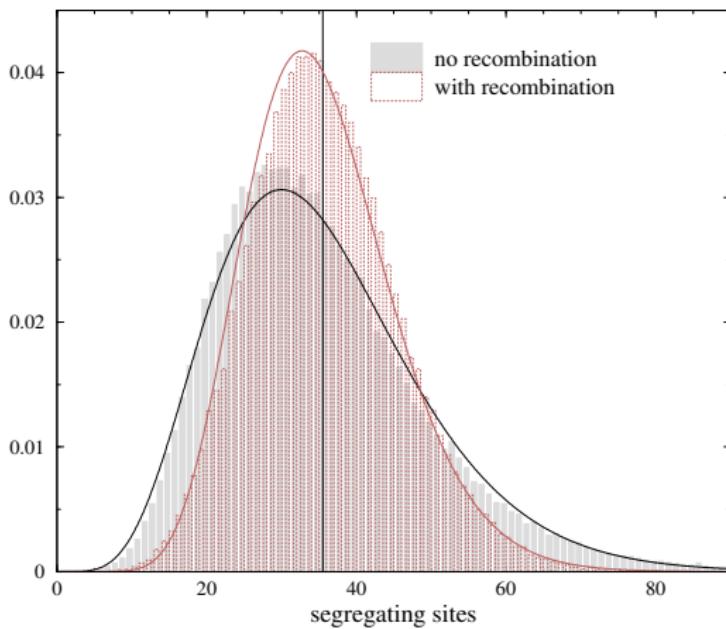
# Topology & Frequency Spectrum



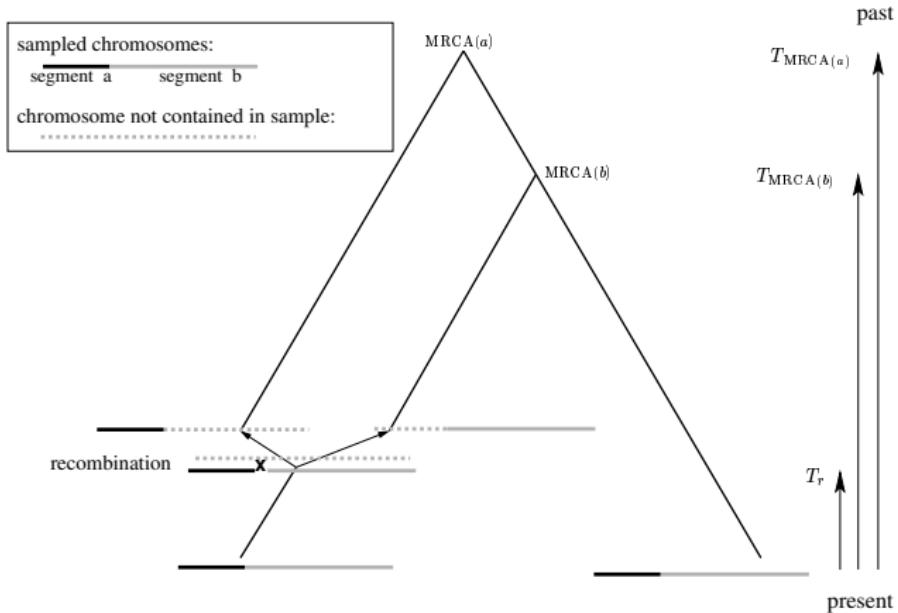
# Coalescent and SNPs



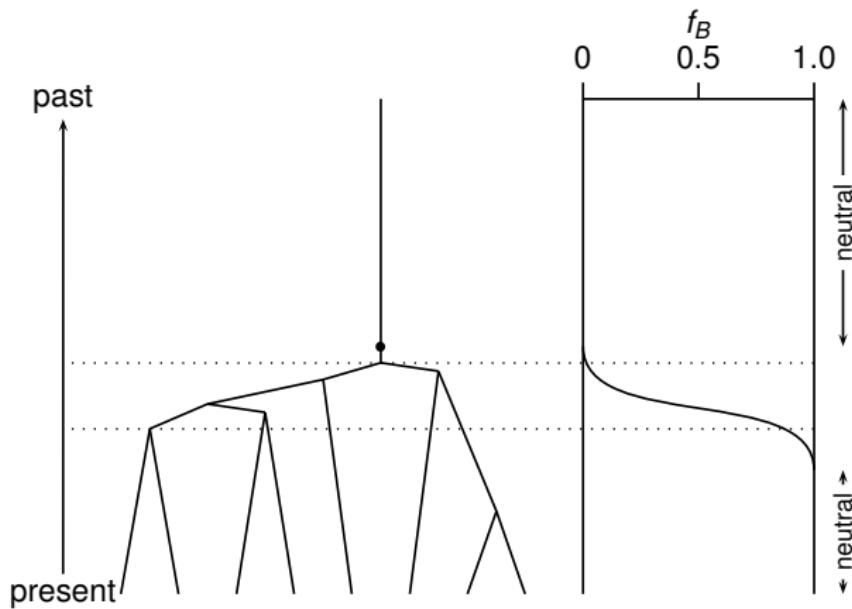
# SNPs $\pm$ Recombination



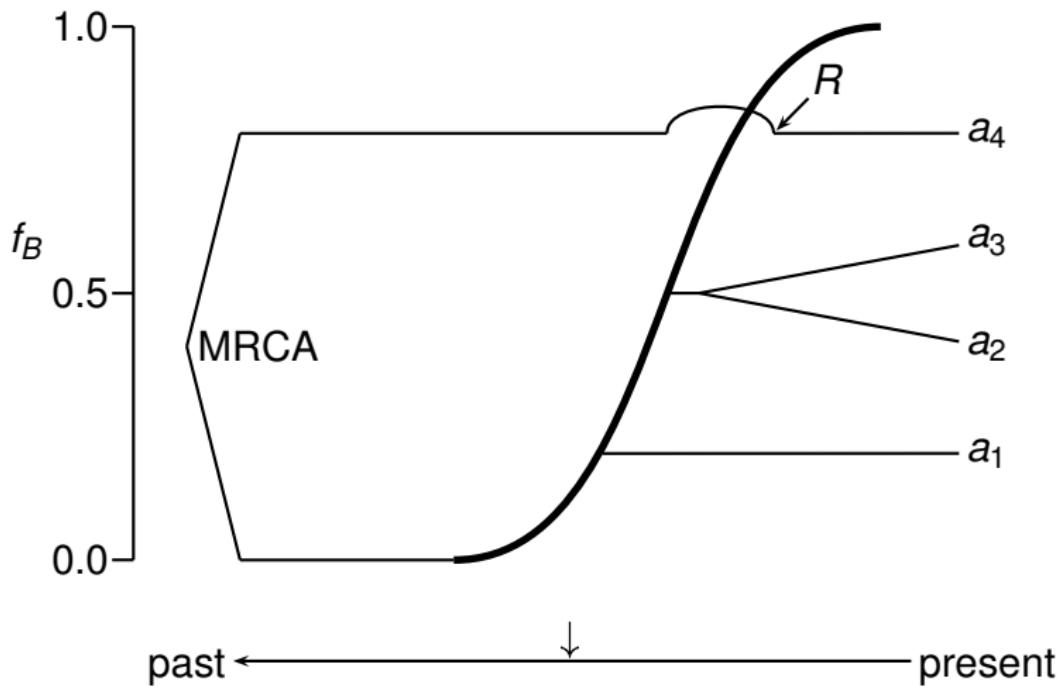
# Coalescent with Recombination



# Selective Sweep



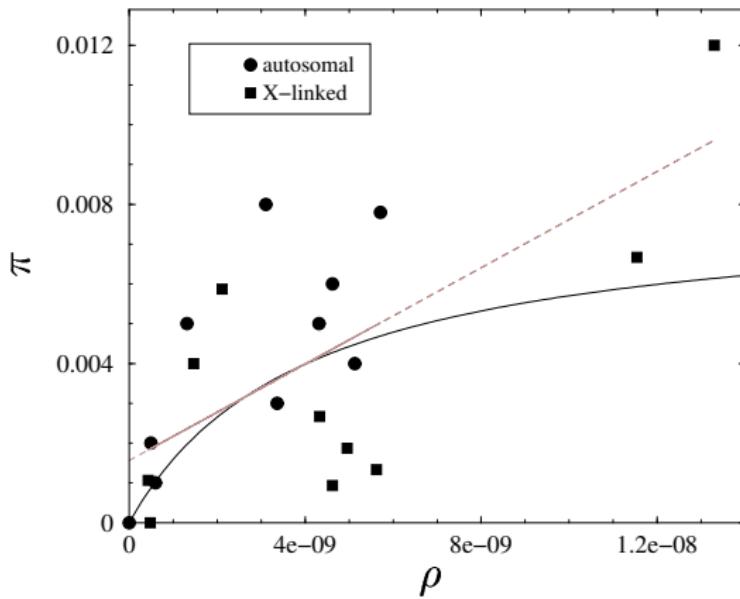
# Recombination & Selection



# Recombination & Genetic Diversity in *D. melanogaster*

locus	$\rho \times 10^{-9}$	$\pi$	reference
X-linked loci			
<i>Yellow,Achaete</i>	0.429	0.0008	[3]
<i>Pgd</i>	1.466	0.0030	[3]
<i>Z,Tko</i>	2.114	0.0044	[1]
<i>Per</i>	4.952	0.0014	[3]
<i>White</i>	13.30	0.0090	[13]
<i>Notch</i>	11.54	0.0050	[14]
<i>Vermilion</i>	5.619	0.0010	[4]
<i>Forked</i>	4.330	0.0020	[9]
<i>Zw</i>	4.619	0.0007	[6]
<i>Su(F)</i>	0.476	0.0000	[9]
autosomal loci			
<i>Gpdh</i>	5.714	0.0078	[15]
<i>Adh</i>	4.621	0.0060	[10]
<i>Ddc</i>	1.314	0.0050	[4]
<i>Amy</i>	3.107	0.0080	[11]
<i>Pu</i>	5.129	0.0040	[15]
<i>Est6</i>	4.314	0.0050	[7]
<i>MtnA</i>	0.593	0.0010	[8]
<i>Hsp70A</i>	0.493	0.0020	[12]
<i>Ry</i>	3.364	0.0030	[2]
<i>Ci<sup>D</sup></i>	0.000	0.0000	[5]

# Quantifying Selection



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