# Construction of coalescent trees on partially fixed pedigrees 

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## Genealogies

- $\Phi$ : Phenotypes

A : Affected, $\mathbf{N}$ : Not Affected
■ $\mathcal{H}$ : Haplotypes
$\square$ : Mutant, $\square$ : Non-Mutant

- $\theta$ : Unknown parameter

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\mathcal{L}(\theta)=P(\Phi, \mathcal{H} \mid \theta)
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- $\mathcal{G}$ : Genealogy

$$
\begin{aligned}
\mathcal{L}(\theta) & =P(\Phi, \mathcal{H} \mid \theta) \\
& =\int_{\mathcal{G}} P(\Phi, \mathcal{H} \mid \mathcal{G}, \theta) P(\mathcal{G} \mid \theta) \mathrm{d} \mathcal{G}
\end{aligned}
$$



## Diploid, Two-Sex, Wright-Fisher Model

Population size $2 N ; \quad N$ males $O O ; \quad N$ females $O O ; 4 N$ genes.

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## $\infty \infty \infty \infty \infty \infty \infty \infty \infty \infty \infty \infty$ $\infty \infty \infty \infty \infty \infty \infty \infty \infty \infty \infty \infty \infty \infty$

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Population size $2 N ; \quad N$ males $O O$; $N$ females $O O ; 4 N$ genes.



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Convergence to the n -coalescent (Möhle [1998])

$$
T_{1} / 4 N \sim \mathcal{E} \times p(3), T_{2} / 4 N \sim \mathcal{E} \times p(1) ; \quad N \text { large }
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## Population Pedigree



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Population Pedigree (Wakeley et al. [2012])
The set of all family relationships among members of the population for every generation.

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Pedigree Genealogy


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Meiosis Indicator (Thompson [2000])

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S_{i} \sim \text { i.i.d. Bernoulli (0.5) . Mendel's } 1^{\text {st }} \text { Law }
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Partition of genes into subsets that are IBD

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$$
\begin{array}{llllllllllll}
0 & 0 & 1 & 0 & 1 & 1 & 1 & 0 & 0 & 1 & 0 & 1
\end{array}
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## SNP Data






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$k$－locus Meiosis Indicator

$$
S_{i} \in\{0,1\}^{k}
$$

e．g．No interference（Allen and Darwiche［2008］）：

$$
P\left(S_{i}=011\right)=P\left(S_{i}=100\right)=0.5 p_{12}\left(1-p_{23}\right) .
$$

## SNP Data




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$\varepsilon_{1}$




Evidence ： $\boldsymbol{\varepsilon}$（Koller and Friedman［2009］）
An instantiation of a subset of random variables．

$$
P\left(S_{1}, S_{2}, \ldots, S_{n} \mid \varepsilon\right) \neq \prod_{i=1}^{n} P\left(S_{i} \mid \varepsilon\right)
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## P－Coalescent




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Perspectives

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## Pedigree Censorship

Big Pedigree $\Leftrightarrow$ High Complexity.
Deviations from the coalescent decreases the more distant the ancestry. (Wakeley et al. [2012])

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- Non-interfering recombinations
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## Founder Prior

- Uniform prior
- Linkage equilibrium
- Linkage disequilibrium


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