Construction of coalescent trees on partially fixed pedigrees

Renaud Alie, Sorana Froda & Fabrice Larribe

Université du Québec à Montréal

7 August 2018

Genealogies

- $\blacksquare \ \Phi \ : \ Phenotypes$
 - $\boldsymbol{\mathsf{A}}$: Affected, $\boldsymbol{\mathsf{N}}$: Not Affected
- $\blacksquare \ \mathcal{H} : \mathsf{Haplotypes}$
 - 🔳 : Mutant, 🗖 : Non-Mutant
- θ : Unknown parameter

$$\mathcal{L}(\theta) = P(\Phi, \mathcal{H}|\theta).$$

Genealogies

- $\blacksquare \ \Phi \ : \ Phenotypes$
 - $\boldsymbol{\mathsf{A}}$: Affected, $\boldsymbol{\mathsf{N}}$: Not Affected
- $\blacksquare \ \mathcal{H} : \mathsf{Haplotypes}$
 - 🔳 : Mutant, 🗖 : Non-Mutant
- θ : Unknown parameter
- $\blacksquare \ \mathcal{G} : \mathsf{Genealogy}$

$$egin{aligned} \mathcal{L}(heta) &= \mathcal{P}\left(\Phi, \mathcal{H}| heta
ight) \ &= \int_{\mathcal{G}} \mathcal{P}\left(\Phi, \mathcal{H}|\mathcal{G}, heta
ight) \mathcal{P}\left(\mathcal{G}| heta
ight) \, \mathsf{d} \, \mathcal{G}. \end{aligned}$$



Population size 2N; N males ∞ ; N females ∞ ; 4N genes.

$\infty \infty 00$

Population size 2N; N males ∞ ; N females ∞ ; 4N genes.

Population size 2N; N males ∞ ; N females ∞ ; 4N genes.





















Population size 2N; N males ∞ ; N females ∞ ; 4N genes.

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

 $T_1/4N \sim \mathcal{E}xp(3), T_2/4N \sim \mathcal{E}xp(1);$ N large.







Population Pedigree (Wakeley et al. [2012])



Population Pedigree (Wakeley et al. [2012])



Population Pedigree (Wakeley et al. [2012])



Population Pedigree (Wakeley et al. [2012])



Population Pedigree (Wakeley et al. [2012])



Population Pedigree (Wakeley et al. [2012])



Population Pedigree (Wakeley et al. [2012])

The set of all family relationships among members of the population for every generation.



Population Pedigree (Wakeley et al. [2012])

The set of all family relationships among members of the population for every generation.

O O O

Population Pedigree (Wakeley et al. [2012])

The set of all family relationships among members of the population for every generation.



Population Pedigree (Wakeley et al. [2012])

The set of all family relationships among members of the population for every generation.



Population Pedigree (Wakeley et al. [2012])

The set of all family relationships among members of the population for every generation.



Population Pedigree (Wakeley et al. [2012])

The set of all family relationships among members of the population for every generation.





Meiosis Indicator (Thompson [2000]) $S_i \sim i.i.d. Bernoulli (0.5).$ Mendel's 1st Law



0 1 1 1 0 1

Meiosis Indicator (Thompson [2000]) $S_i \sim i.i.d. Bernoulli (0.5).$ Mendel's 1st Law



 $0 \ 1 \ 1 \ 1 \ 0 \ 1$

Meiosis Indicator (Thompson [2000]) $S_i \sim i.i.d. Bernoulli (0.5).$ Mendel's 1st Law



Meiosis Indicator (Thompson [2000]) $S_i \sim i.i.d. Bernoulli (0.5).$ Mendel's 1st Law

IBD Partition



Meiosis Indicator (Thompson [2000]) $S_i \sim i.i.d. Bernoulli (0.5).$ Mendel's 1st Law

IBD Partition



Meiosis Indicator (Thompson [2000]) $S_i \sim i.i.d. Bernoulli (0.5).$ Mendel's 1st Law

IBD Partition



$\begin{array}{ll} \mbox{Meiosis Indicator (Thompson [2000])} \\ S_i \sim i.i.d. \mbox{\mathcal{B}ernoulli} (0.5). & \mbox{Mendel's 1}^{\rm st} \mbox{ Law} \end{array}$

IBD Partition



Meiosis Indicator (Thompson [2000]) $S_i \sim i.i.d. Bernoulli (0.5)$. Mendel's 1st Law

IBD Partition



Meiosis Indicator (Thompson [2000]) $S_i \sim i.i.d. Bernoulli (0.5).$ Mendel's 1st Law

IBD Partition



 $0 \ 0 \ 1 \ 0 \ 1 \ 1 \ 1 \ 0 \ 0 \ 1 \ 0 \ 1$

$\begin{array}{ll} \mbox{Meiosis Indicator (Thompson [2000])} \\ S_i \sim i.i.d. \mbox{\mathcal{B}ernoulli} (0.5) . & \mbox{Mendel's 1}^{\rm st} \mbox{ Law} \end{array}$

IBD Partition



 $0 \ 0 \ 1 \ 0 \ 1 \ 1 \ 1 \ 0 \ 0 \ 1 \ 0 \ 1$

$\begin{array}{ll} \mbox{Meiosis Indicator (Thompson [2000])} \\ S_i \sim i.i.d. \mbox{\mathcal{B}ernoulli} (0.5) . & \mbox{Mendel's 1}^{\rm st} \mbox{ Law} \end{array}$

IBD Partition





IBD Partition





k-locus Meiosis Indicator

 $S_i \in \{0,1\}^k$.

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

$$P(S_i = 011) = P(S_i = 100) = 0.5p_{12}(1 - p_{23}).$$



Evidence : ε (Koller and Friedman [2009])

An instantiation of a subset of random variables.

$$P(S_1, S_2, \dots, S_n | \varepsilon) \neq \prod_{i=1}^n P(S_i | \varepsilon).$$



Evidence : ε (Koller and Friedman [2009])

An instantiation of a subset of random variables.

$$P(S_1, S_2, \ldots, S_n | \varepsilon) \neq \prod_{i=1}^n P(S_i | \varepsilon).$$









Pedigree Censorship

 $\mathsf{Big} \; \mathsf{Pedigree} \Leftrightarrow \mathsf{High} \; \mathsf{Complexity}.$

Deviations from the coalescent decreases the more distant the ancestry. (Wakeley et al. [2012])

Pedigree Censorship

Big Pedigree \Leftrightarrow High Complexity.

Deviations from the coalescent decreases the more distant the ancestry. (Wakeley et al. [2012])

Recombination Model

- Independently segregating loci
- Non-interfering recombinations
- Positive interference

Pedigree Censorship

Big Pedigree \Leftrightarrow High Complexity.

Deviations from the coalescent decreases the more distant the ancestry. (Wakeley et al. [2012])

Recombination Model

- Independently segregating loci
- Non-interfering recombinations
- Positive interference

Founder Prior

- Uniform prior
- Linkage equilibrium
- Linkage disequilibrium

References I

David Allen and Adnan Darwiche. Rc_link : Genetic linkage analysis using bayesian networks. *International journal of approximate reasoning*, 48(2) :499–525, 2008.

- Alexandre Bureau. Genetic linkage analysis based on identity by descent using Markov chain Monte Carlo sampling on large pedigrees. PhD thesis, University of California, Berkeley, 2001.
- Robert Fung and Brendan Del Favero. Backward simulation in bayesian networks. In *Uncertainty Proceedings 1994*, pages 227–234. Elsevier, 1994.
- Daphne Koller and Nir Friedman. *Probabilistic graphical models : principles and techniques.* MIT press, 2009.
- Fabrice Larribe, Sabin Lessard, and Nicholas J Schork. Gene mapping via the ancestral recombination graph. *Theoretical population biology*, 62(2) :215–229, 2002.

References II

- M Möhle. Coalescent results for two-sex population models. *Advances in Applied Probability*, 30(2) :513–520, 1998.
- Doug Speed and David J Balding. Relatedness in the post-genomic era : is it still useful? *Nature Reviews Genetics*, 16(1) :33, 2015.
- Elizabeth A Thompson. Statistical inference from genetic data on pedigrees. In *NSF-CBMS regional conference series in probability and statistics*, pages i–169. JSTOR, 2000.
- Elizabeth A Thompson. Identity by descent : variation in meiosis, across genomes, and in populations. *Genetics*, 194(2) :301–326, 2013.
- John Wakeley, Léandra King, Bobbi S Low, and Sohini Ramachandran. Gene genealogies within a fixed pedigree, and the robustness of kingman's coalescent. *Genetics*, pages genetics–111, 2012.