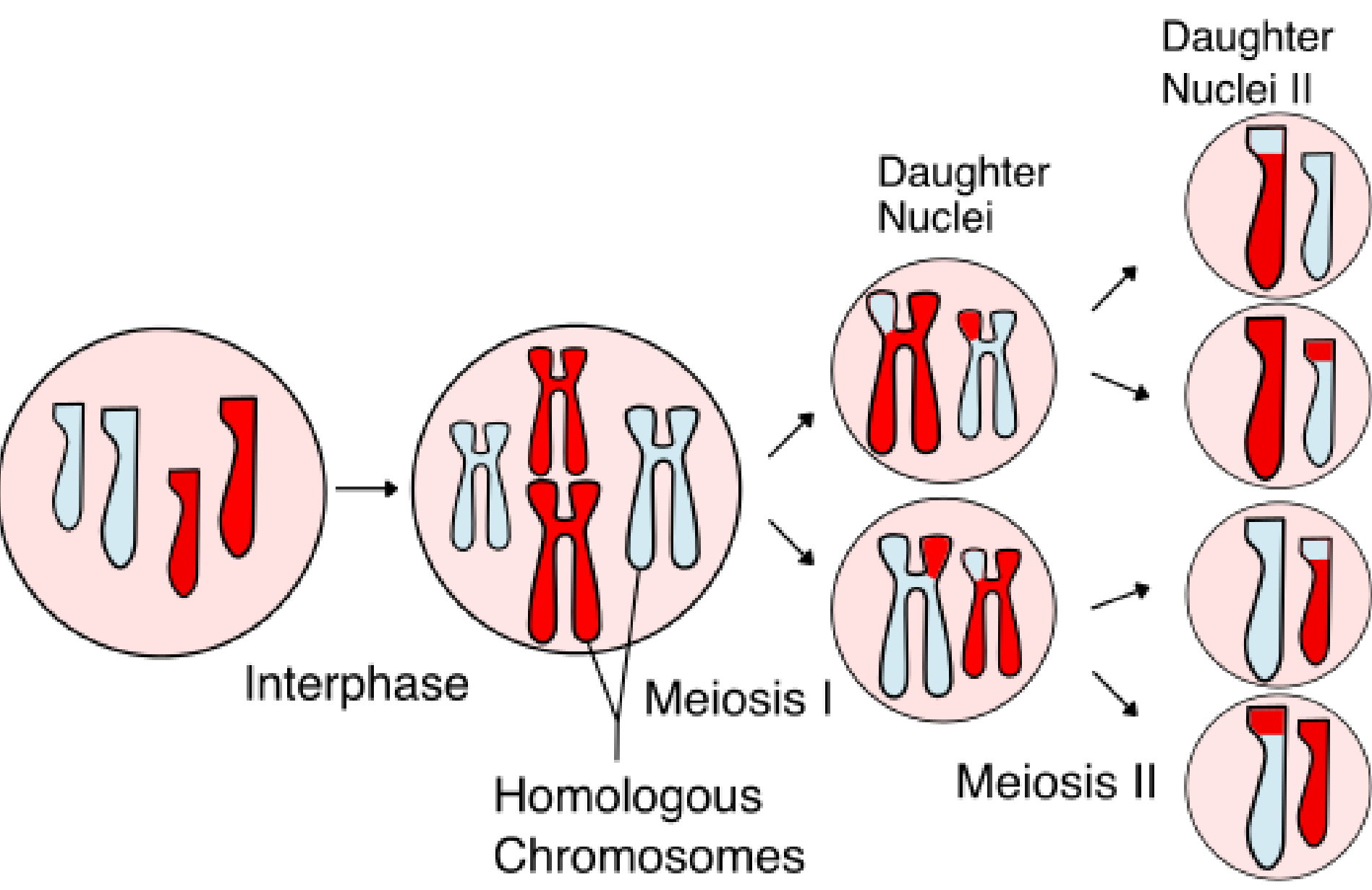


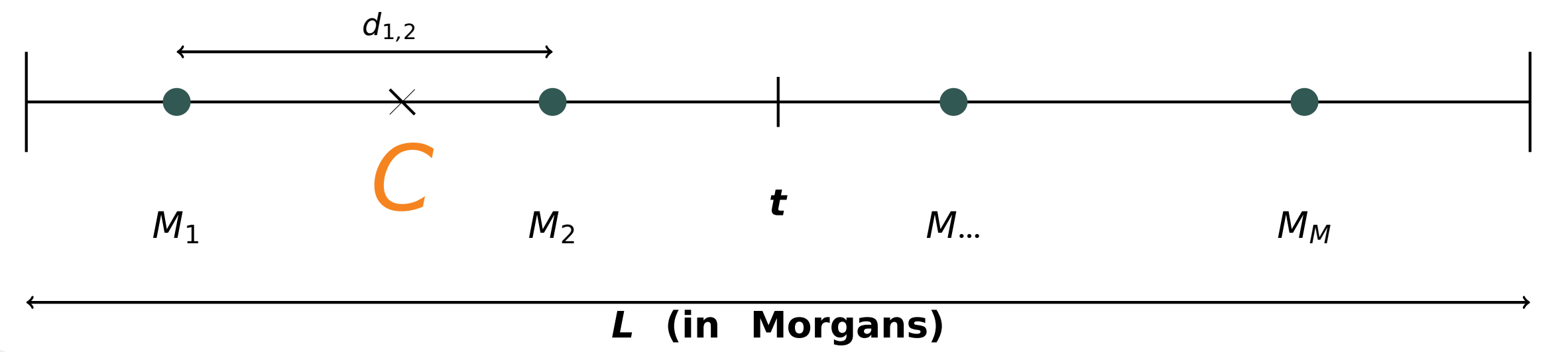
Evaluation of Simulated Meiosis Algorithms for Stochastic Simulations

Fernando H. Toledo ✉ <f.toledo@cgiar.org>, José Crossa and Juan Burgueño

- 📍 **Inheritance** of loci/genes subject to the **Mendelian** laws;
- 📍 **Meiosis** is crucial (**gametes** → new **individuals**);
- 📍 **de novo** variability:
 - (i) crossing over; and
 - (ii) independent assortment.
- 📍 **Simulation**: useful, cheap and quick answers (time/resources);
- 📍 **Models** should **properly** represent **meiosis**.

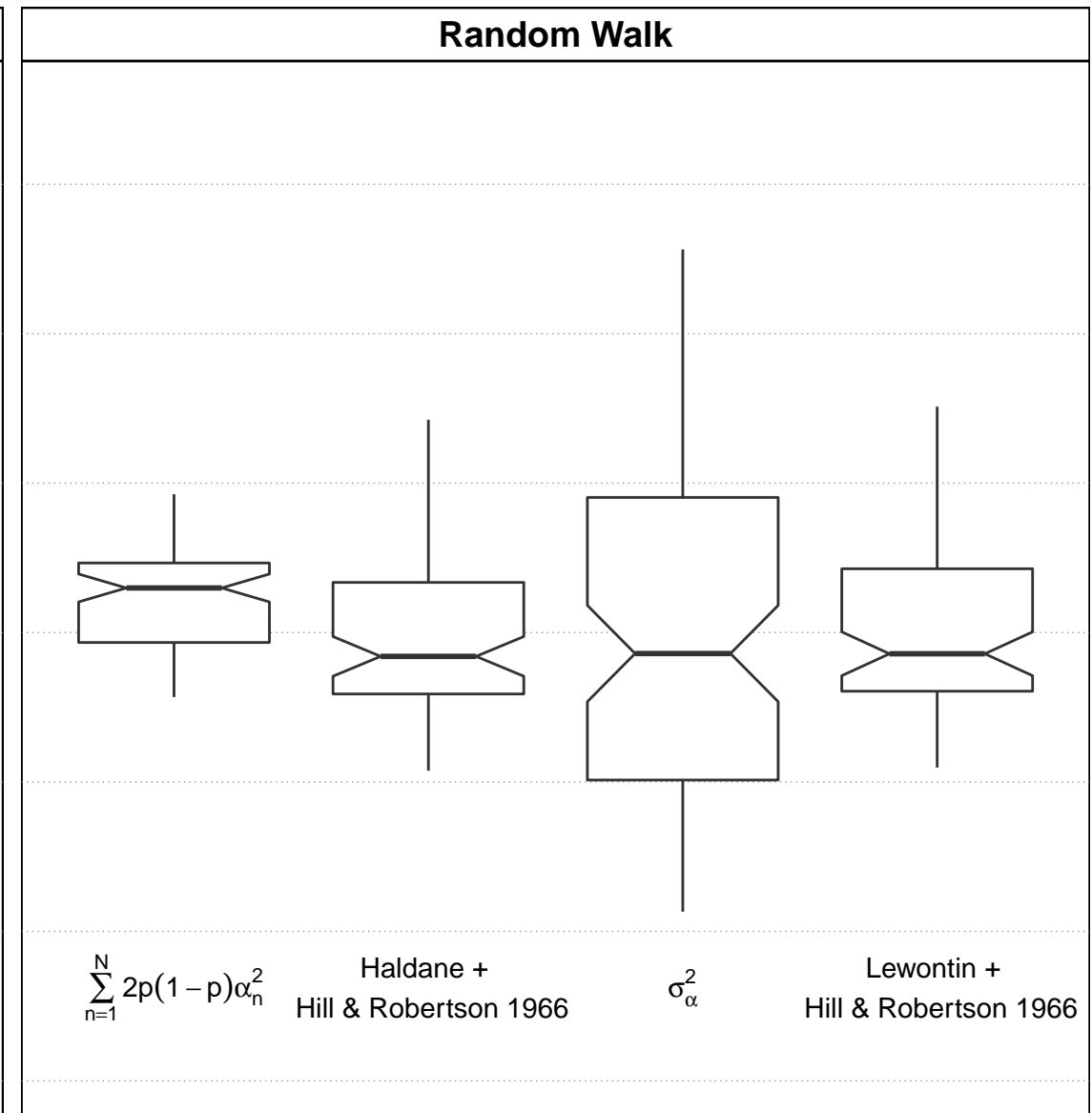
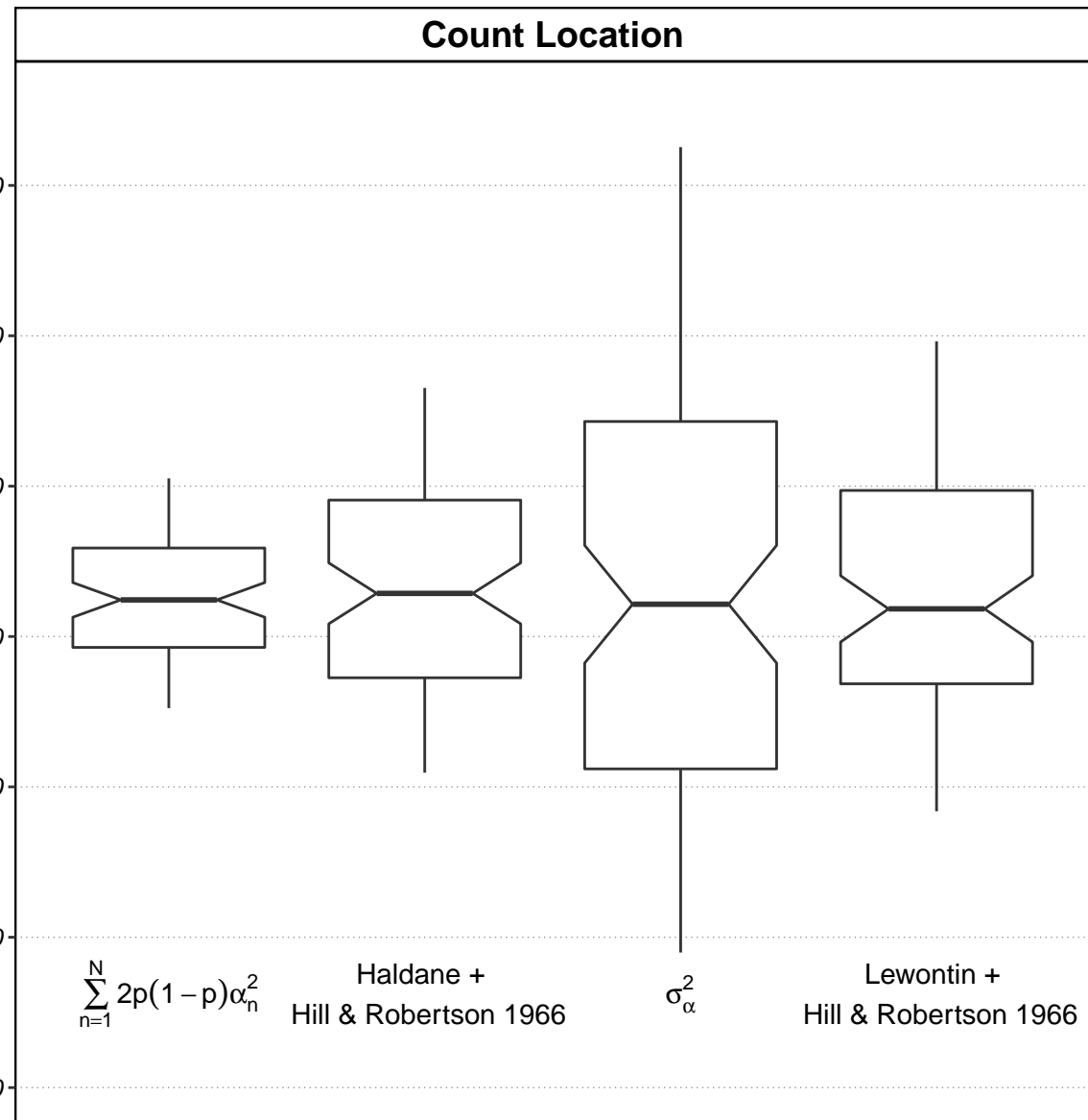
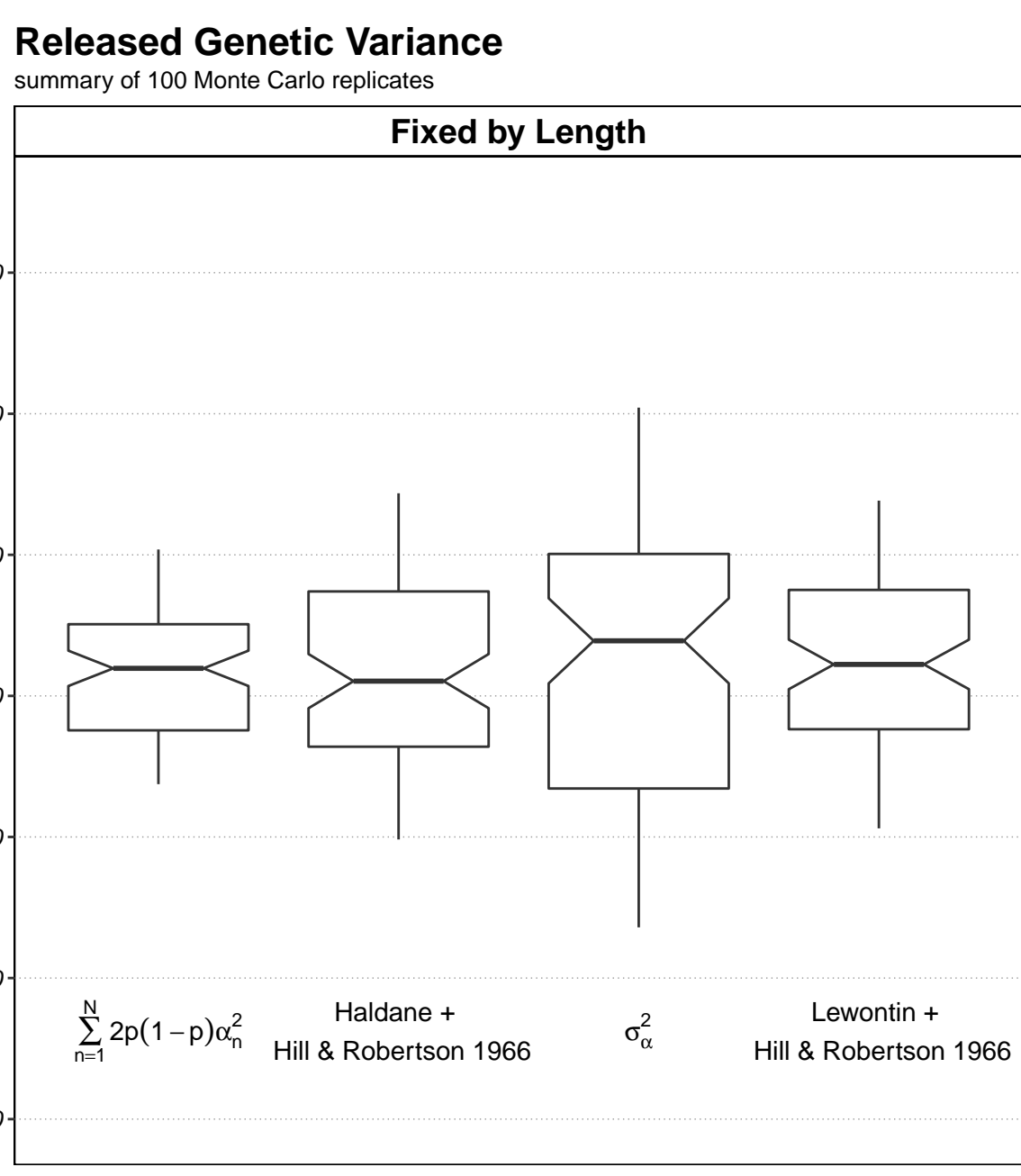


- 📖 **Algorithms:**
- > **Count Location** := $P(C|L) \sim \text{Poisson}(\lambda=L)$ & $p_C \sim \text{Uniform}(0,L)$ [1, 2]
 - > **Random Walk** := $P(C|d_{1,2}) \sim \text{Bernoulli}(\theta=d_{1,2})$ [3, 4]
 - > **Fixed by Length** := $P(C|C \in t) = 1$ & $p_C \sim \text{Uniform}(0,t)$ [5, 6]



Efficiency

(sec)	short		long		overall
	sparse	dense	sparse	dense	
CL	76.68	91.18	98.72	273.63	135.05
RW	81.64	119.84	126.89	509.73	209.52
FL	78.63	94.54	101.82	243.21	129.55



Simulation

meiosis

algorithms

Count Location

Random Walk

Fixed by Length

isqg

- ⚙️ **Advantages/Features:**
- 🔗 simulation ↔ analysis;
 - 🔗 C++ embedded (🔗);
 - 🔗 Open source (🔗);
 - 🔗 Cross-platform (🔗/🔗/🔗);
 - 🔗 Extendable; and
 - 🔗 ...

- 🔗 **Highlights:**
- 🔗 low/high interface;
 - 🔗 full flexibility;
 - 🔗 building block (🔗); and
 - 🔗 complex & customized.

- 🔗 **Thus ...:**
- 🔗 **CL** ≈ **RW**;
 - 🔗 Poisson-Binomial distribution
 - 🔗 Both allow **interference**; tuning algorithms 🔄
 - 🔗 Or even **independency**; and long or several chroms
 - 🔗 **CL** support **hotspots**. parametrizing occurrences' (~β)

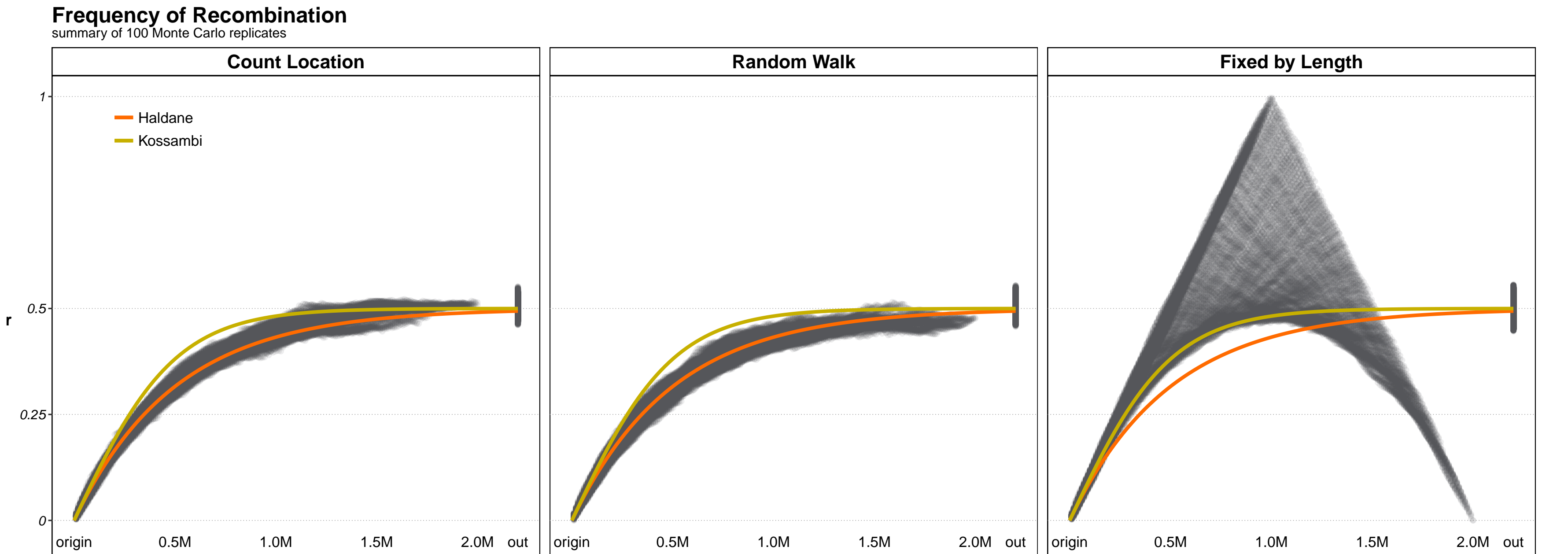
- 🔗 **TODO Further:**
- 🔗 From 🔄 to **CRAN**;
 - 🔗 Extend mating designs:
 - * Current:
 - ✓ simple cross;
 - ✓ selfing; and
 - ✓ double-haploid.
 - * **TODO**:
 - ! Diallels;
 - ! North Carolina; and
 - ! Custom Pedigree.
 - 🔗 Improve documentation 📖

Evaluations

discussion

- 💬 **Remarks & Comments:**
- 🔗 The algorithms didn't show **deviation** from the expected σ_G^2 ;
 - 🔗 Reinforce **relationship** evidences between **CL** & **RW**;
 - 🔗 **Agreement** with respect to the **Haldane's** functions;
 - 🔗 **Dangerous** side effects for **FL**:
 - 🔗 frequency of **recombination** ≠ distance in **Morgan** ⚠;
 - 🔗 attach **bias** for **short** and **long** distances;
 - 🔗 hidden **interference** among **crossing** events; and
 - 🔗 **disable** linkage between loci 🚫.
 - 🔗 **FL** slightly better in terms of computational performance 🏎;
 - 🔗 Sparse genomes & long chromosomes → **RW**; and
 - 🔗 Else → **CL** should be preferred.

Mapping



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📄 **isqg Availability:** 🌐 <www.data.cimmyt.org> 📧 @FHToledo

- 📖 **References:**
- [1] Karlin & Liberman (1978) *Proc Natl Acad Sci* 75(12):6332-6336 [w/o DOI]
 - [2] Technow (2011) *R* package: "hypred" [discontinued]
 - [3] Podlich & Cooper (1998) *Bioinformatics* 14(7):632-653 [w/o DOI]
 - [4] de los Campos et al., (2015) *PLoS Genetics* 11(5):1-21 [DOI: 10.1371/journal.pgen.1005048]
 - [5] Jenko et al., (2015) *Genetics Selection Evolution* 47(1):55 [DOI: 10.1186/s12711-015-0135-3]
 - [6] Faux et al., (2016) *The Plant Genome* (2016) 9(3):1-14 [DOI: 10.3835/plantgenome2016.02.0013]

