



# Improvement of the assembly of heterozygous genomes of non-model organisms

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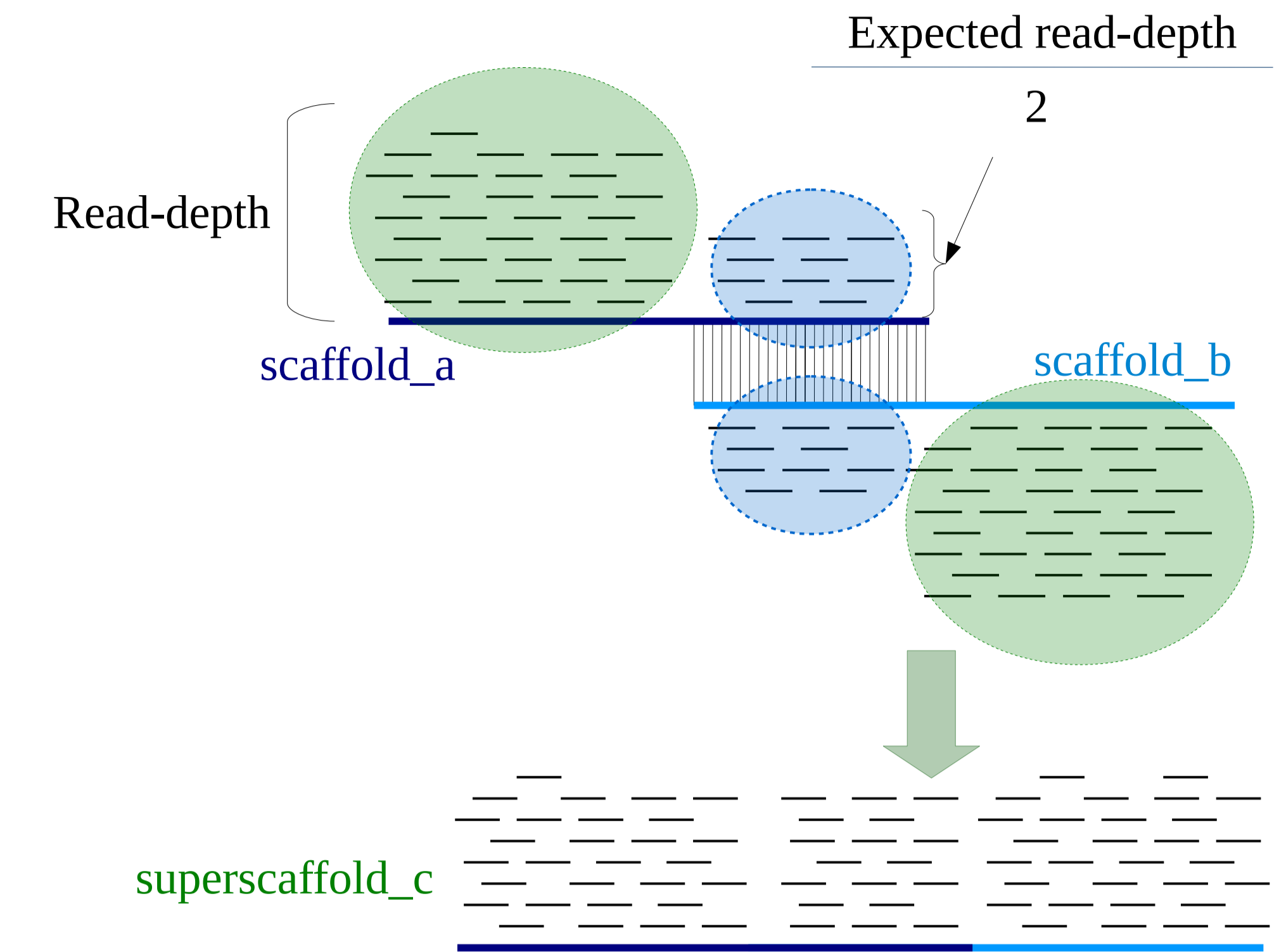
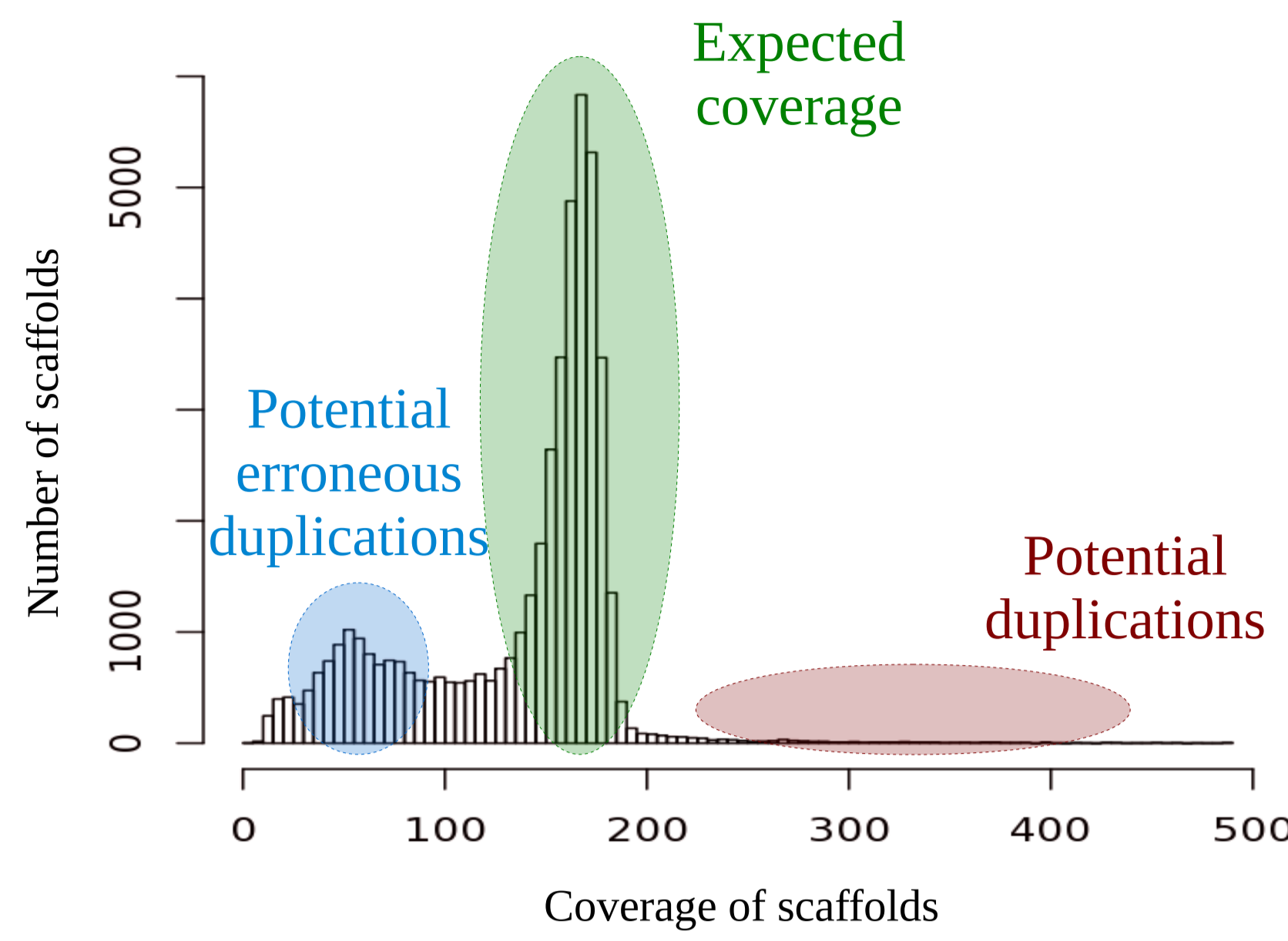
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# Improvement of the assembly of heterozygous genomes of non-model organisms

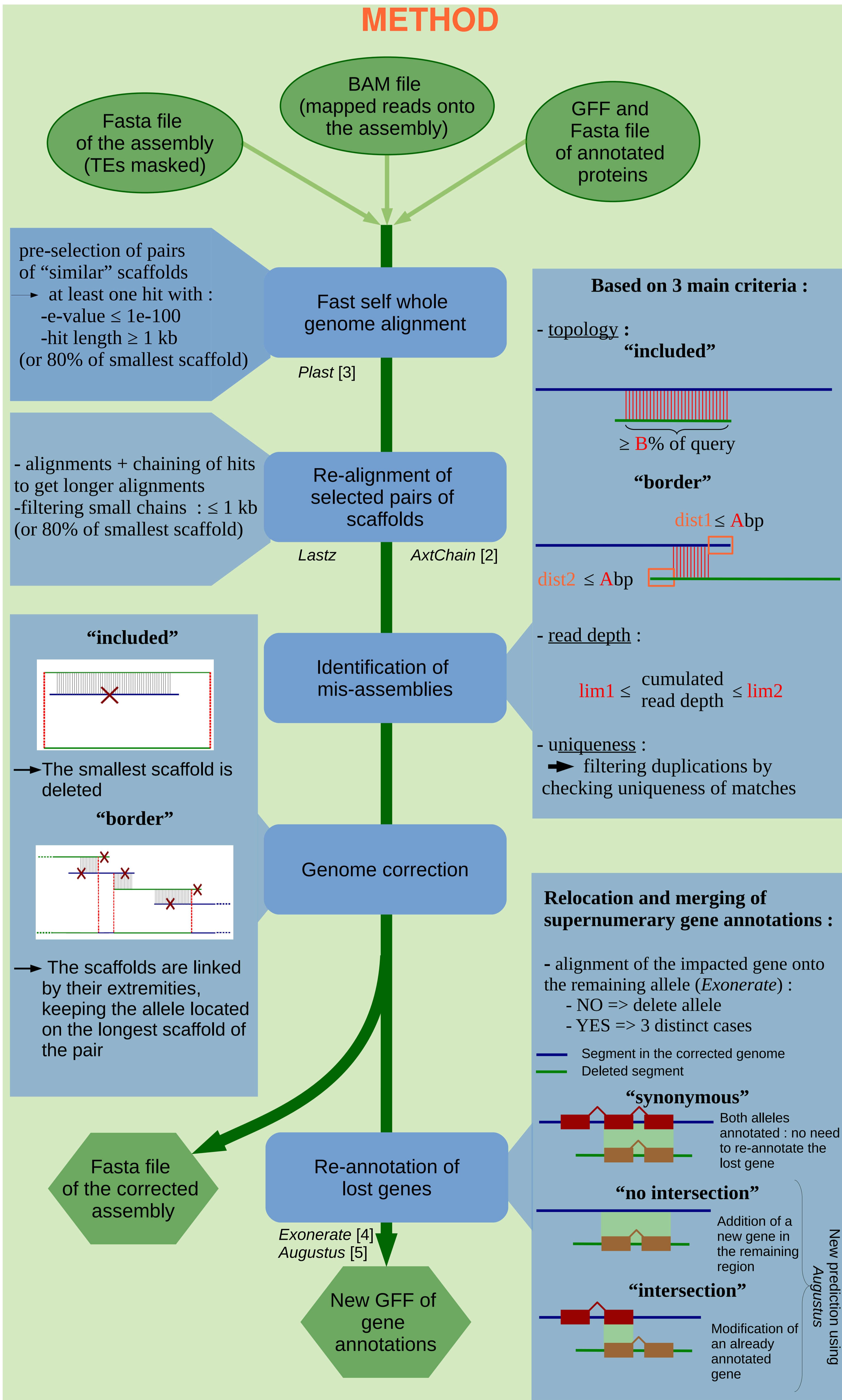
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**Motivation** : Some heterozygous regions have a significant divergence between the two haplotypes and the assembly process can lead to the construction of two different contigs, instead of one consensus sequence.

**Objective** : Set up a strategy to detect and correct false duplications in already-built assemblies.



## METHOD



## APPLICATION

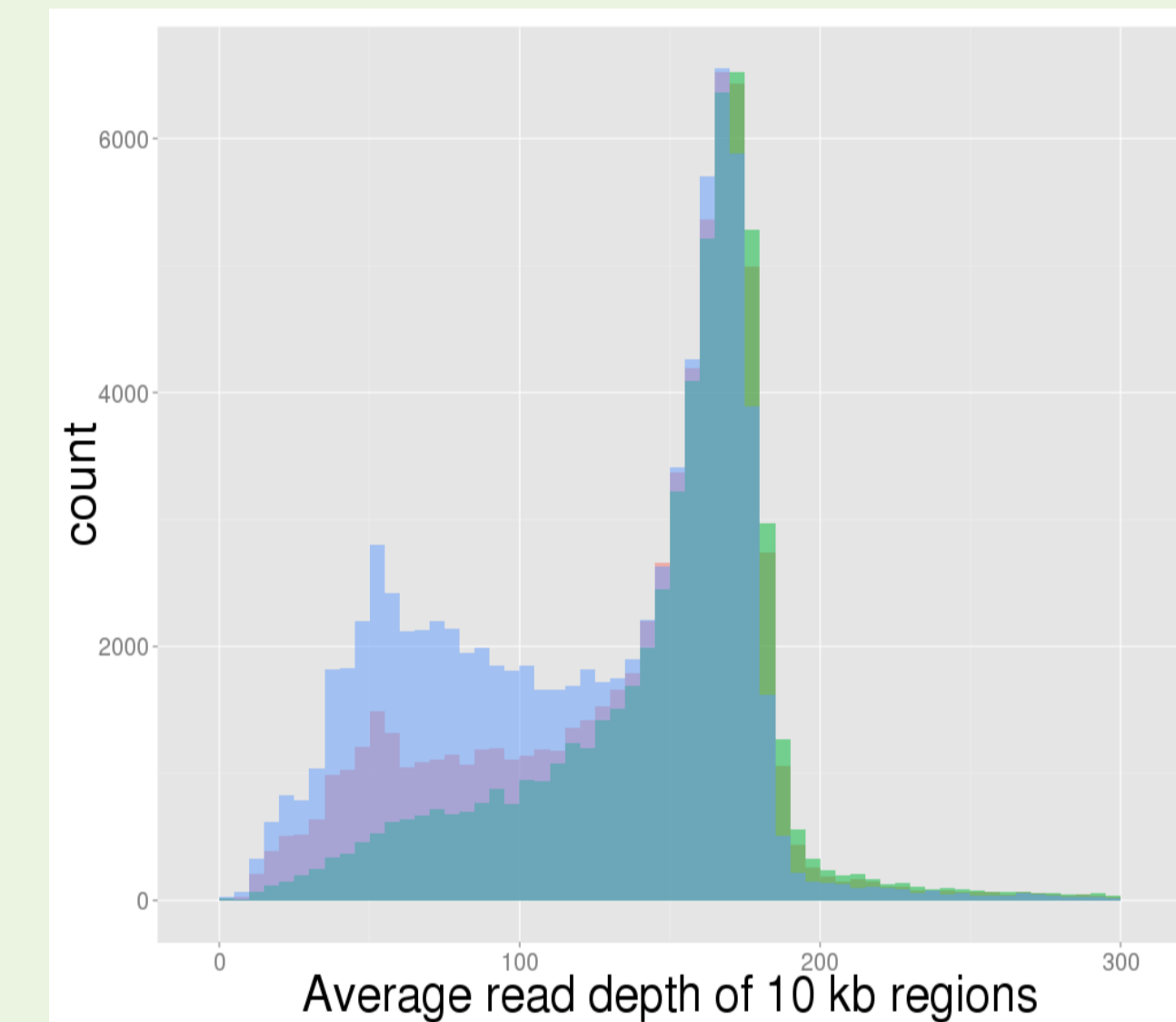
### *Spodoptera frugiperda* genome

#### Genome correction

★ Comparison with another method : *Haplomerger* [1]  
 Expected size : ~ 400 Mb

	Initial assembly <i>Allpaths</i>	Corrected assembly	<i>Haplomerger</i>
Total size (Mb)	526.0	434.9	369.5
Nb. scaffolds	48,272	41,577	37,797
N50 (kb)	39.6	52.8	58.4

★ Read depth analysis : before/after correction



- Improvement of the initial assembly for both methods
- Haplomerger* merged more regions, leading to a smaller final assembly

★ BUSCO statistics : Benchmarking sets of Universal Single-Copy Orthologs (2,675 for Arthropoda species) [6]

	Initial assembly	Corrected assembly	<i>Haplomerger</i>
Missing	363	336 *	562
Single copy	1,246	1,586 *	1,242
Fragmented	476	457 *	771
Duplicated	590	296	100 *

\* best result by category

- Reduction of the genome size (17%), increase of the N50 and more single copies for important genes
- Reduces less than *Haplomerger* → gain of numerous BUSCO genes
- Our method: more conservative, preserves genome consistency and allows easier re-annotation of impacted genes

#### Annotation stats

Previous release : 25,041 genes  
 ==> 3,746 genes to re-annotate

	# genes	% success
"no alignment"	34	0
"synonymous"	747	100
"no intersection"	643	45.4
"intersection"	2,322	86.3

==> Overall success of 80% / New release : 21,578 genes