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Anaïs Gouin, Anthony Bretaudeau, Claire Lemaitre, Fabrice Legeai

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# Identification and correction of genome mis-assemblies due to heterozygosity

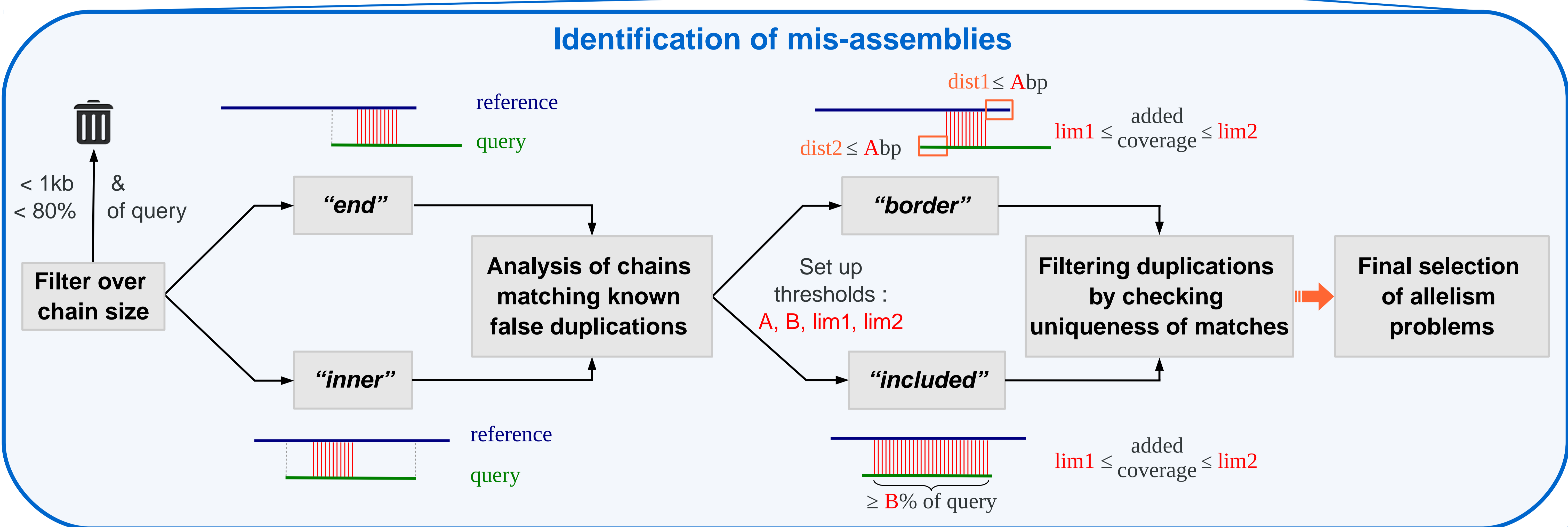
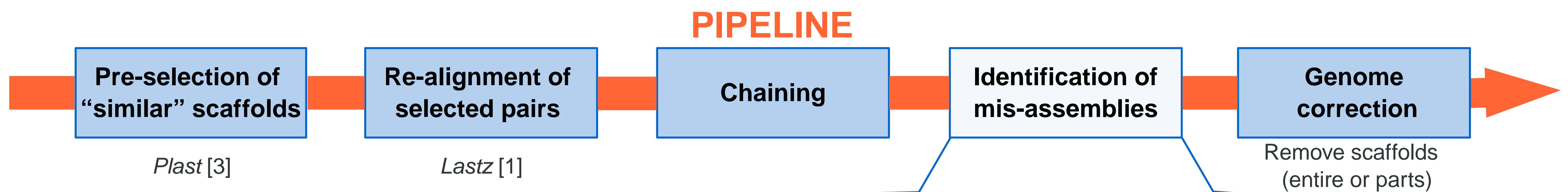
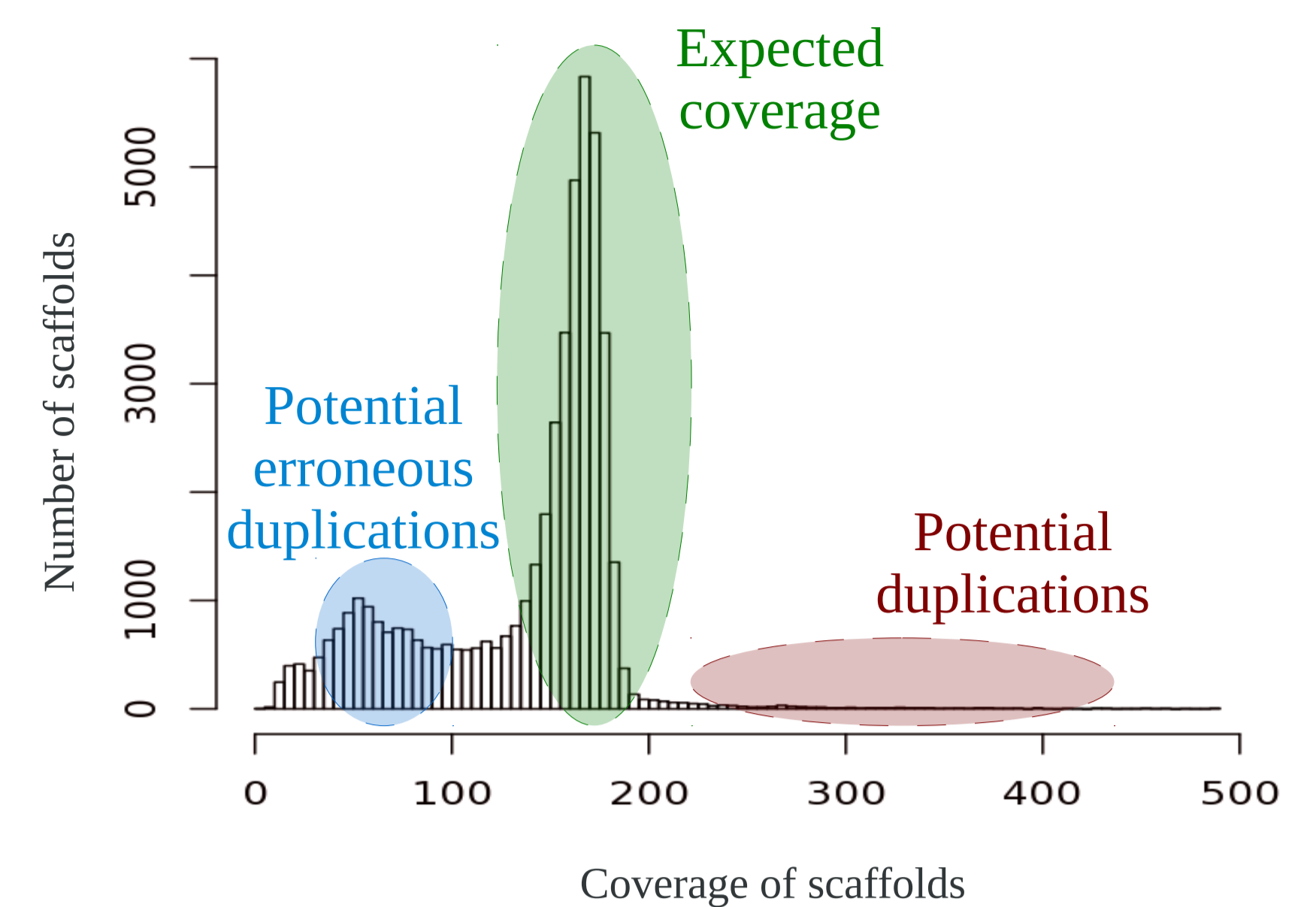
Anais GOUIN<sup>1</sup>, Anthony BRETAUDEAU<sup>2</sup>, Claire LEMAITRE<sup>1</sup> and Fabrice LEGEA<sup>1</sup>

<sup>1</sup>INRIA/IRISA/GenScale, Campus de Beaulieu, 35042 Rennes cedex, France

<sup>2</sup>INRA, Institut de Génétique, Environnement et Protection des Plantes (IGEPP), Domaine de la Motte – 35653 Le Rheu

**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.

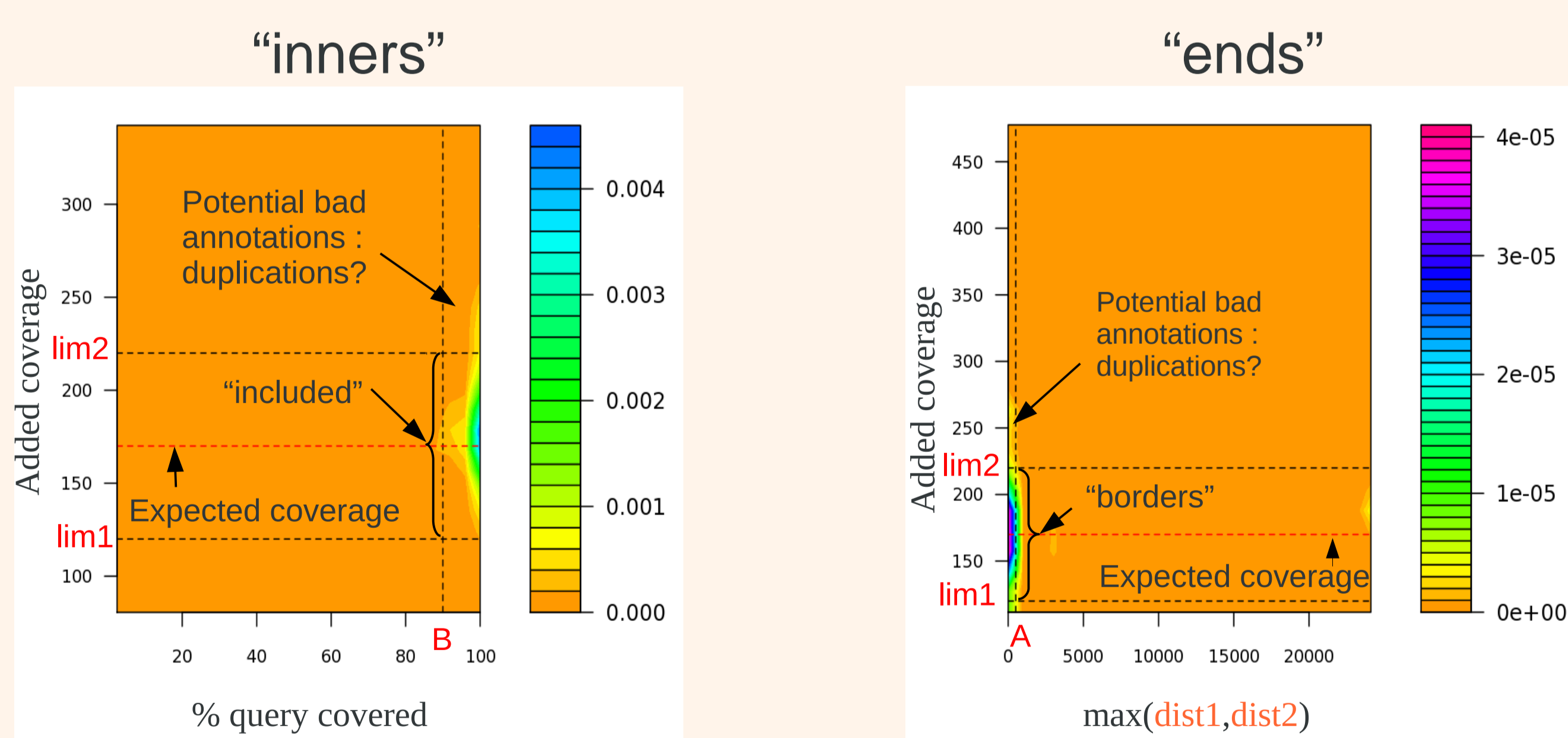


**Application : *Spodoptera frugiperda* genome**



## Set up thresholds

206 chains matching known false duplications (manually curated) :  
153 "inners" / 53 "ends"



→ 114 "included" / 38 "borders"

→ ~80% of known allelic regions with chosen thresholds

## Genome correction

Expected size : ~ 375 Mb

	Initial assembly <i>Allpaths</i>	<i>Platanus</i> [2] assembly	Corrected assembly
Total size (Mb)	526,0	470,1	434,9
Nb. scaffolds	48 272	41 633	41 536
N50 (bp)	39 593	75 578	52 733
BUSCO* stats	No hit	14	15
	Single hit	1497	2047
	Multi hit	782	374

\*BUSCO : Benchmarking sets of Universal Single-Copy Orthologs (Arthropoda species) [4]

- Our strategy allows a good improvement of the initial assembly.
- Performing a new assembly with a tool handling heterozygosity (such as *Platanus*) is still more efficient.

## Perspectives :

Non-studied here : potential problems of allelism within a scaffold, at contig level?

Other parameters to take into account : SNPs count (to select regions) / mate pairs (to validate corrected assembly)

[1] Harris RS: Improved pairwise alignment of genomic DNA. Ann Arbor: ProQuest; 2007:84

[2] Kajitani R. et al, Efficient de novo assembly of highly heterozygous genomes from whole-genome shotgun short reads, *Genome Res.* 2014; 24(8):1384-95

[3] Nguyen V.H., Lavenier D., PLAST: parallel local alignment search tool for database comparison, *BMC Bioinformatics*, vol 10, no 329, 2009

[4] Waterhouse et al, OrthoDB: a hierarchical catalog of animal, fungal and bacterial orthologs, *Nucleic Acids Research*, 2013, PMID:23180791