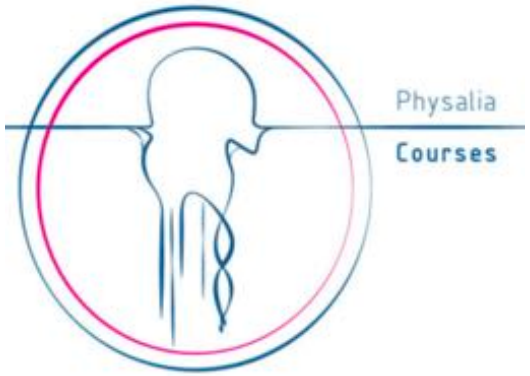

Population genomics for adaptation

Day 1 - Lecture 2

Analytical approaches

GWAS

Comparative genomics

Transcriptomics

Experimental evolution

QTL mapping

Epigenetics

Population genomics

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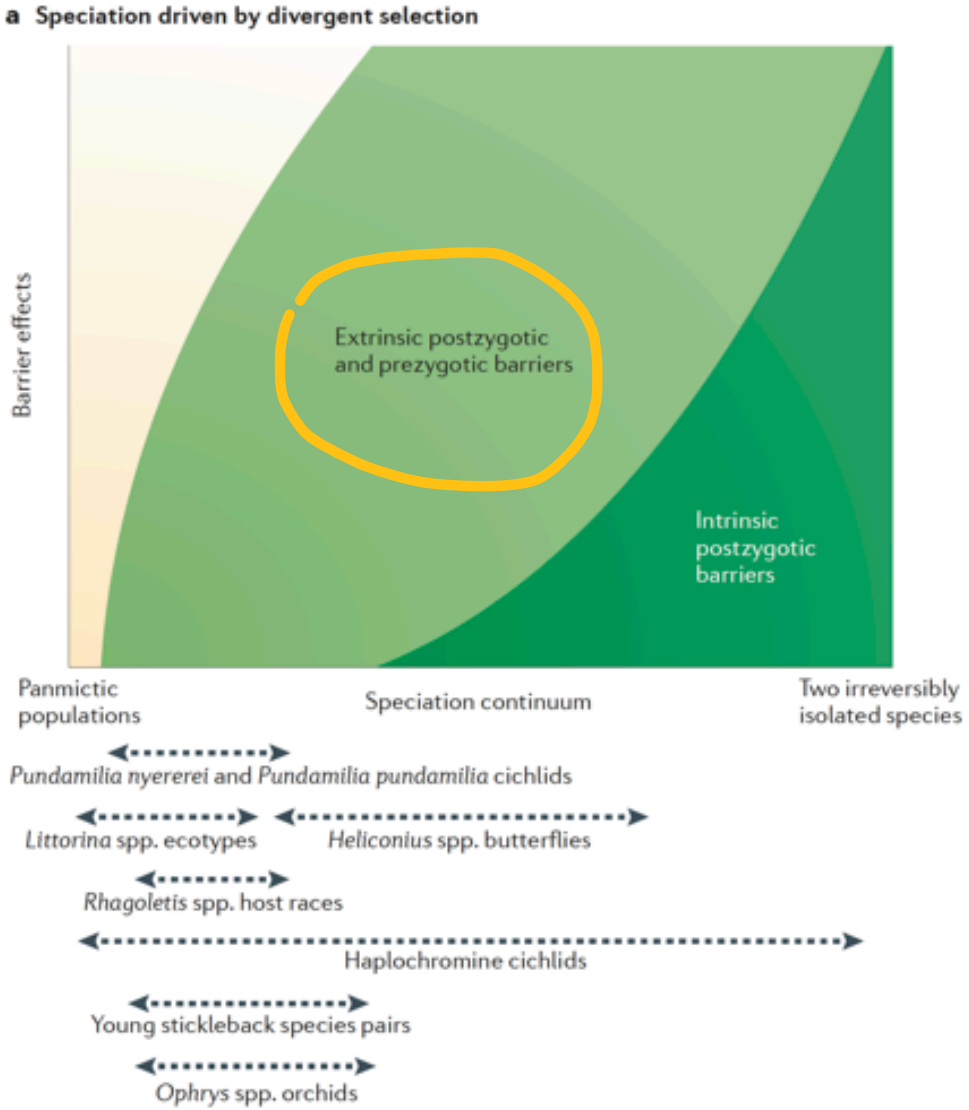
By comparing differences in genetic diversity and differentiation within species we can study population structure, speciation and adaptation.

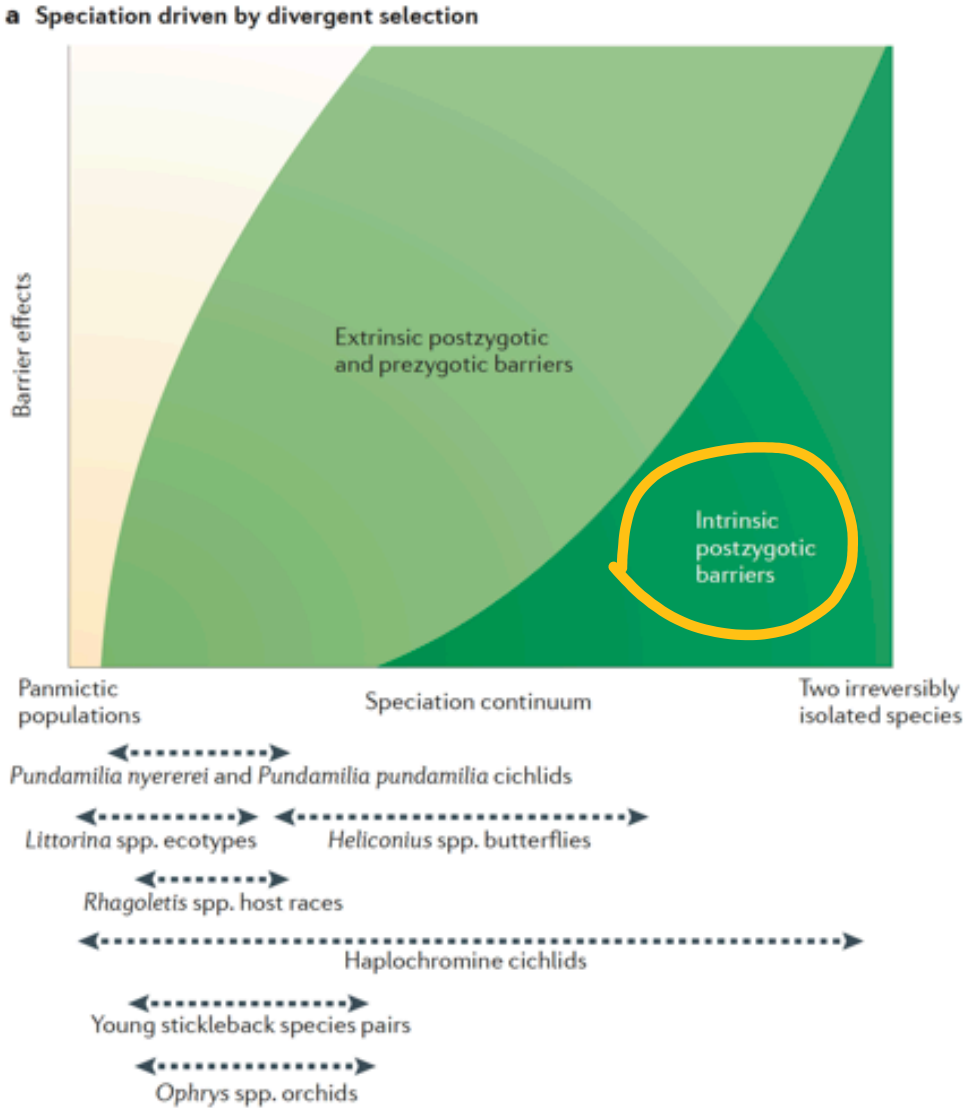
Population genomics for adaptation



Population genomics study populations early in the speciation continuum.

Seehausen et al. 2014, Nat. Gen. Rev.

Population genomics for adaptation

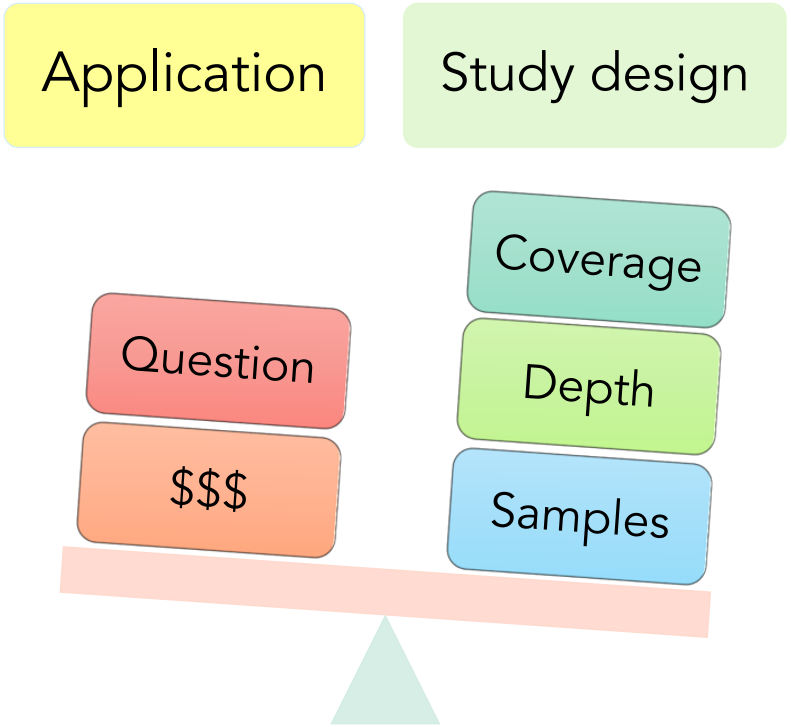


Population genomics study populations early in the speciation continuum.

Later on in the continuum, differentiation builds up and it becomes more and more difficult to distinguish whether genetic differentiation is due to ecological divergence and adaptation or to other factors.

Seehausen et al. 2014, Nat. Gen. Rev.

Population genomics with RADseq



Why RADseq?

RADseq allows to genotype thousands of loci across many individuals at a reasonable cost and can be tuned to address many different questions

Why RADseq?

- It doesn’t require extensive genomic resources: no need of a high-quality reference genome (though it helps)
- It is customizable: through choice of restriction enzyme and sequencing volumes you can tune coverage of the genome and depth of sequencing
- It samples random loci across the genome, both putative neutral and adaptive loci.

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For our adaptation genomics course

- It provides a manageable amount of data that allows quick analyses.
- It provides skills that are easily transferable for the analysis of other data type (targeted sequencing or WGS)

Bioinformatic pipeline

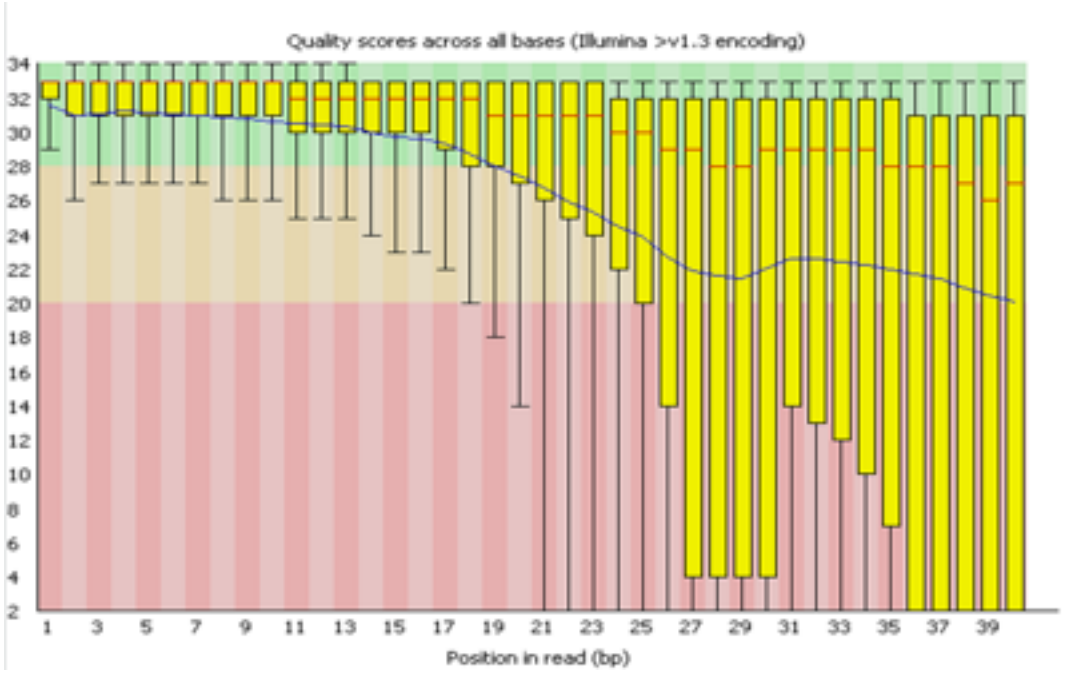
Bioinformatic pipelines

.fastq .fastq

Quality control → Adapter trimming → Read aligning → Variant calling

FASTQC

file:///Users/anna/Dropbox/genomes%20analyses/murre_hunt/completedataset/fastqc_results/lane1.Tig1_R1_fastqc.html



Bioinformatic pipeline

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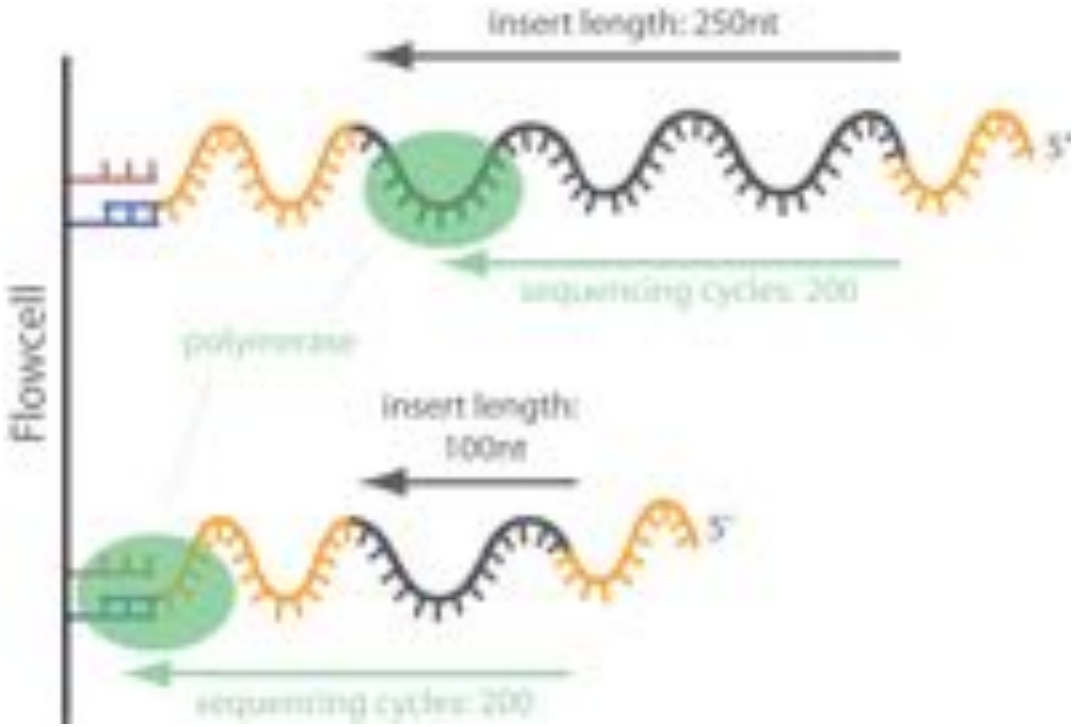
Quality control → Adapter trimming → Read aligning → Variant calling

FASTQC

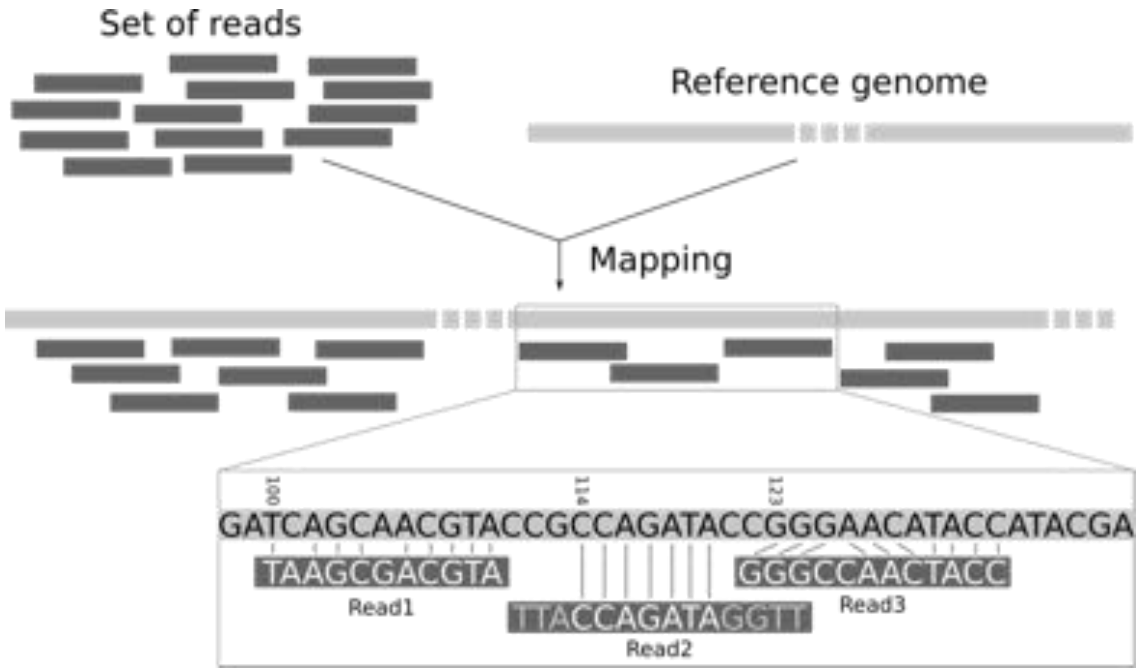
Trimmomatic
Cutadapt
Fastp



Bioinformatic pipeline

.fastq .fastq .fastq .sam/.bam

Quality control → Adapter trimming → Read aligning → Variant calling



Bowtie2
BWA

Bioinformatic pipeline

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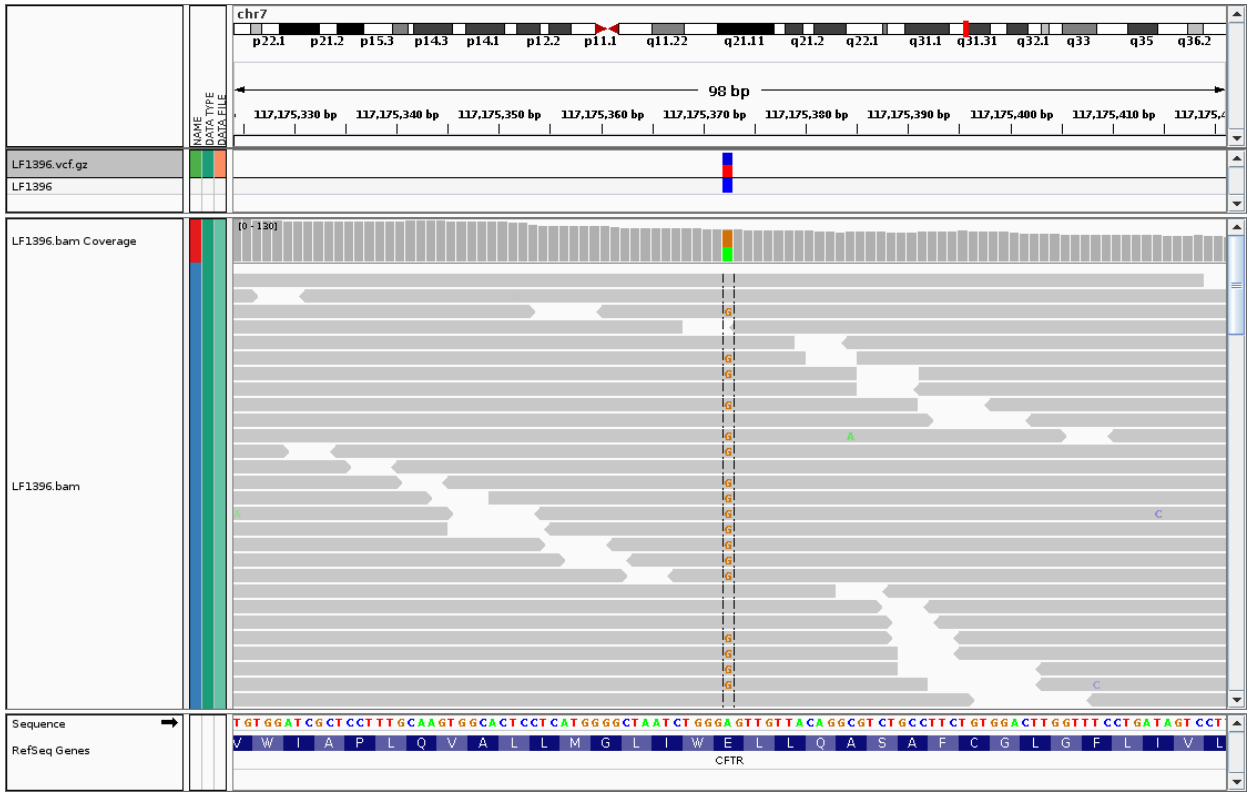
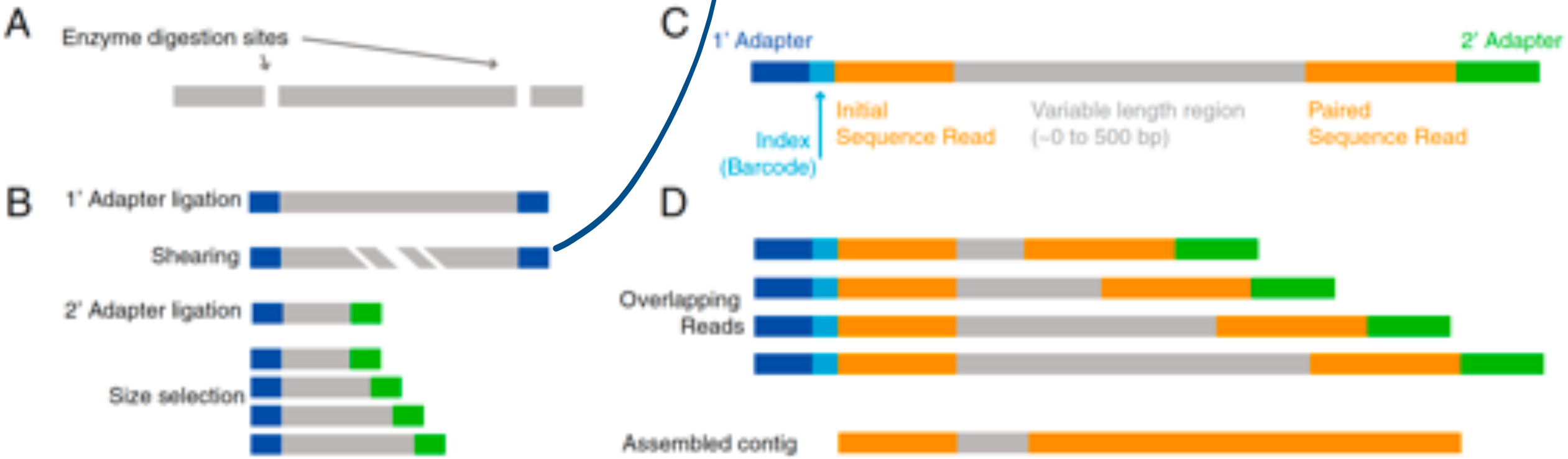


STACKS
ANGSD
GATK
SAMtools
…

RADseq pipeline

Or double digestion



RADseq pipeline

Raw reads

READ 1

Restriction site

READ 2

Restriction site

RADseq pipeline

Raw reads

In addition to potential adapter contamination,
we need to demultiplex RADseq libraries

RADseq pipelines

- STACKS (Catchen et al. 2013, Molecular Ecology)
- dDocent (Puritz et al. 2014, PeerJ)
- PyRAD (Eaton 2014, Bioinformatics)
- AftrRAD (Sovic et al. 2015, Molecular Ecology Resources)
- ANGSD (Korneliussen et al. 2014)
- GATK (McKenna et al. 2010, Genome Research)

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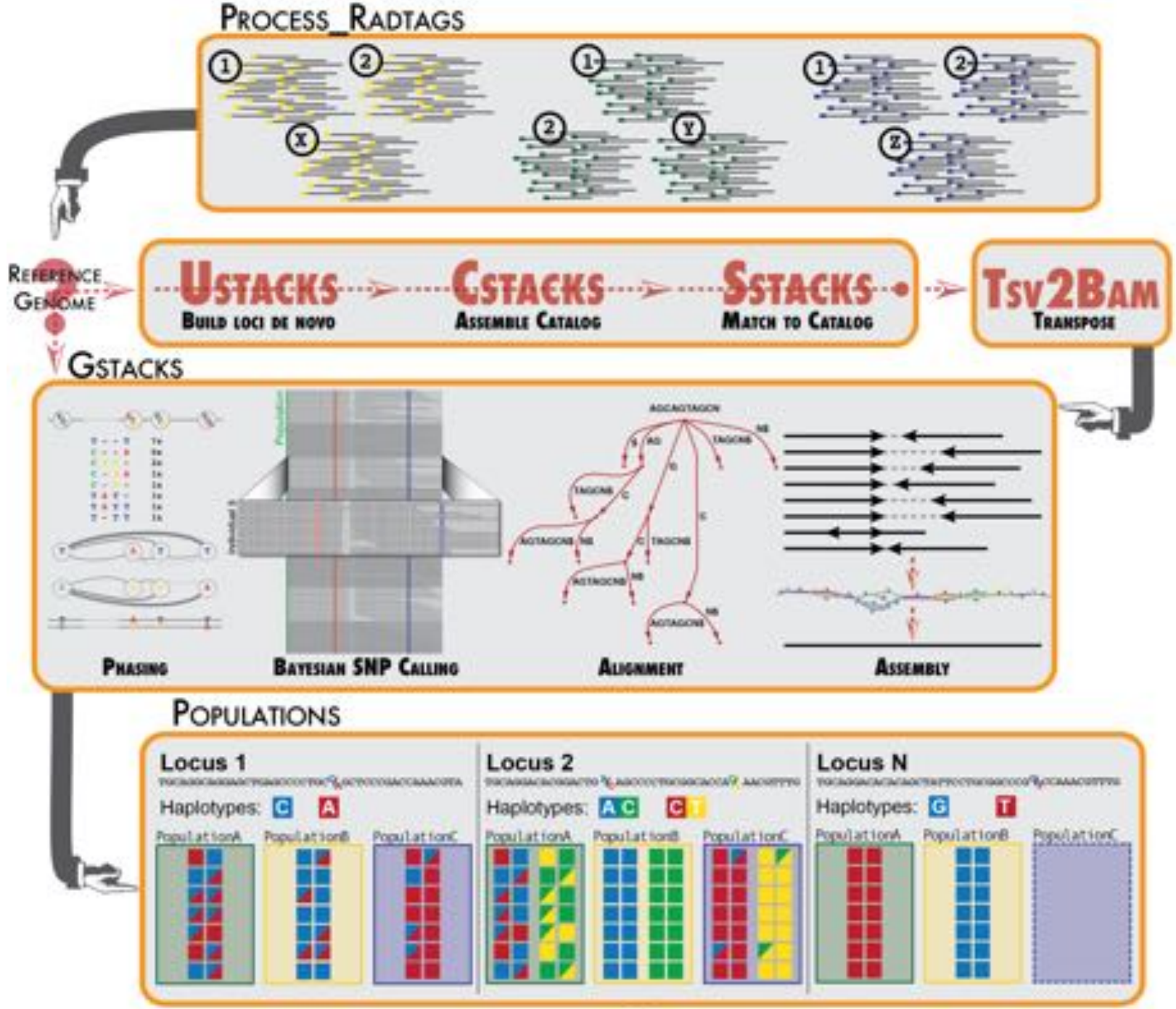
STACKS

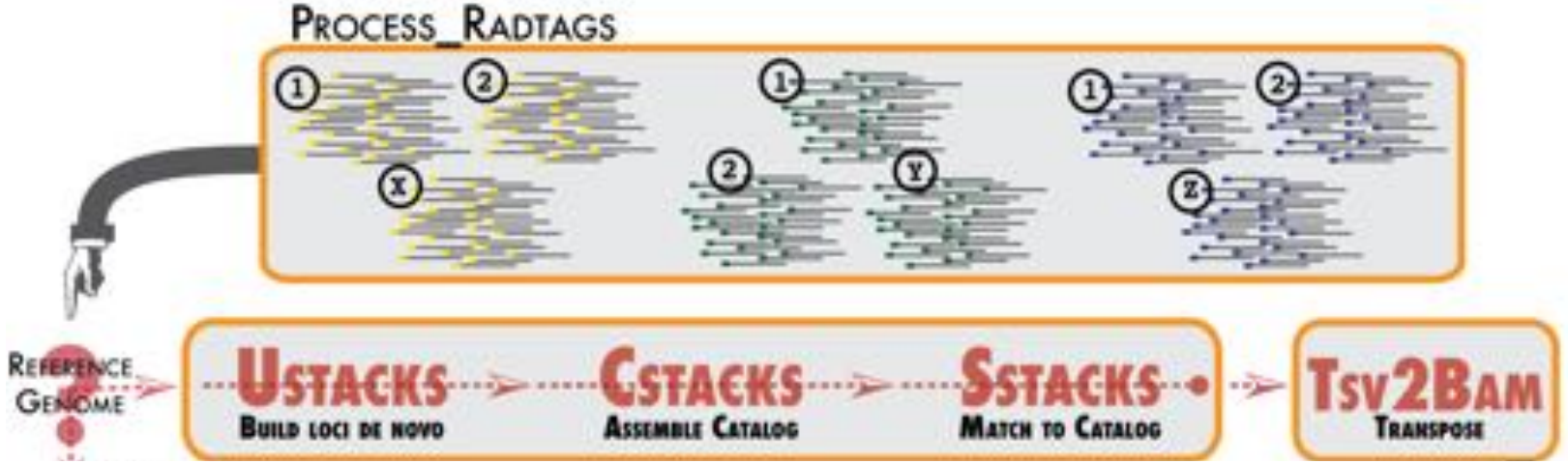

PROCESS_RADTAGS
REFERENCE GENOME
USTACKS
BUILD LOCI DE NOVO
CSTACKS
ASSEMBLE CATALOG
SSTACKS
MATCH TO CATALOG
TSV2BAM
TRANSPOSE
GSTACKS
PHASING
BAYESIAN SNP CALLING
ALIGNMENT
ASSEMBLY
POPULATIONS
Locus 1
Haplotypes: C A
Locus 2
Haplotypes: A C C T
Locus N
Haplotypes: G T
PopulationA
PopulationB
PopulationC

STACKS

To preprocess raw data

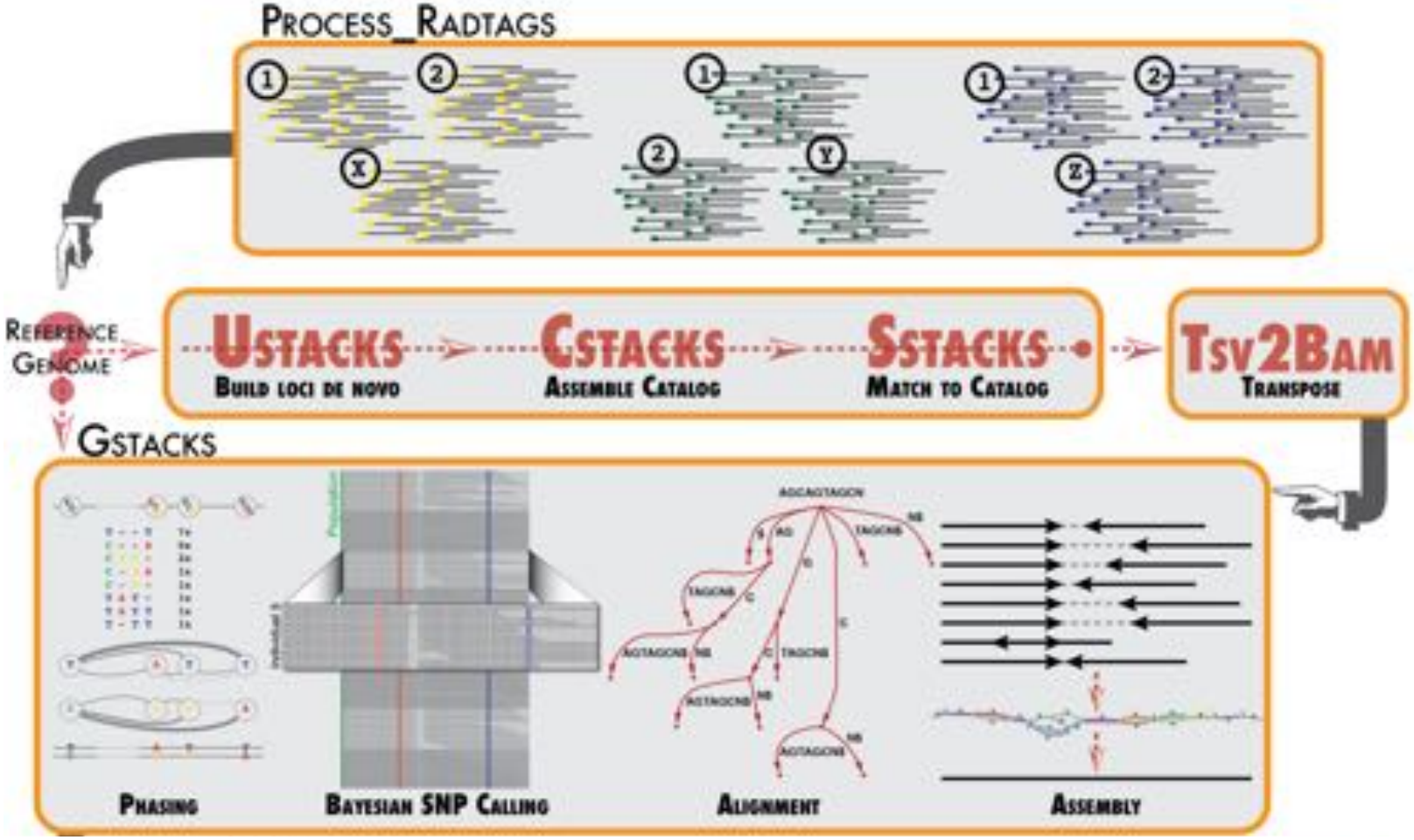
- Demultiplexing
- Adapter removal
- Quality filtering

STACKS



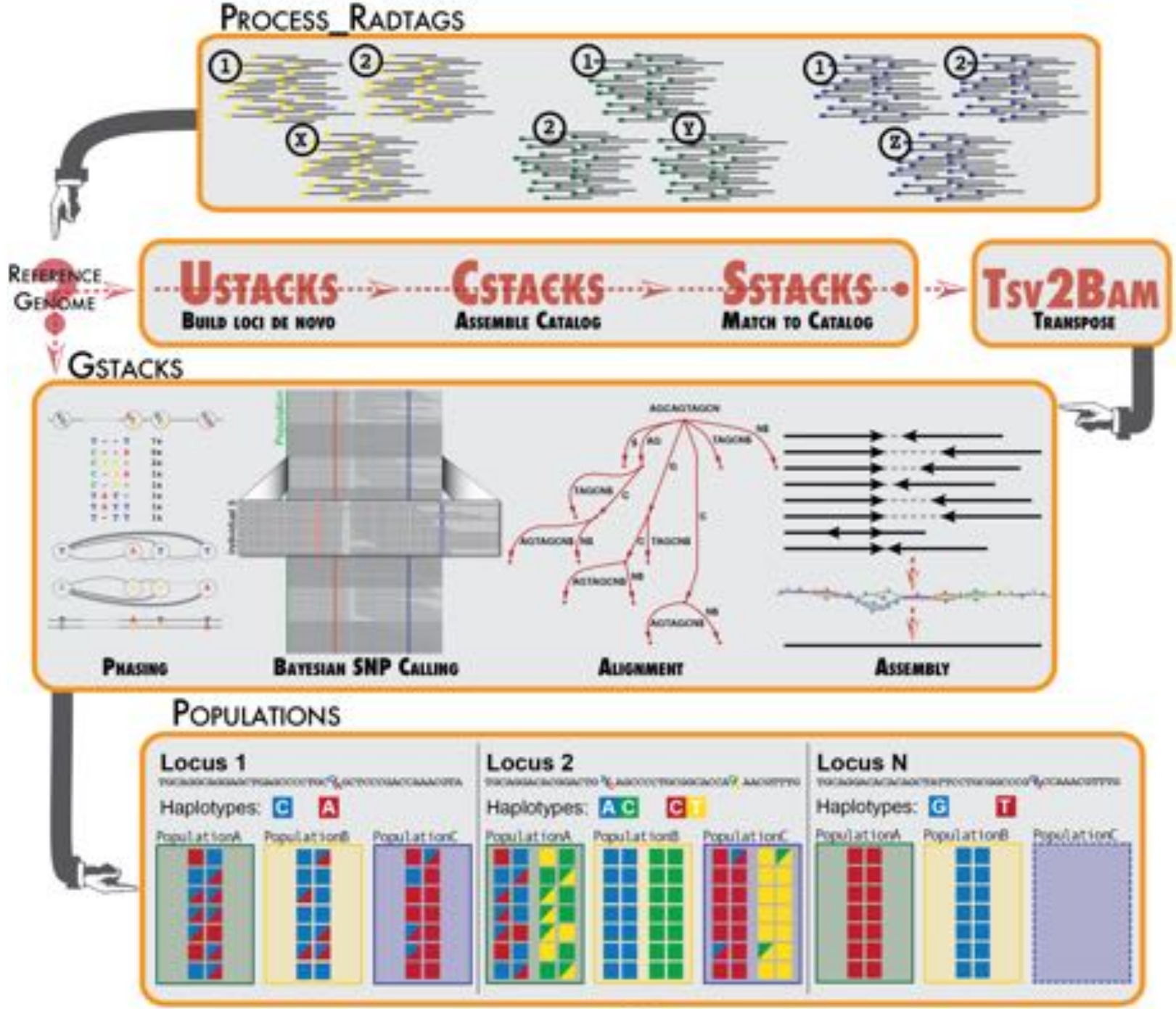
Loci assembly without reference genome

STACKS



If you have a reference genome, align RAD data with external software.
GSTACKS does different things according to data input but at end it calls variants from assembled loci.

STACKS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