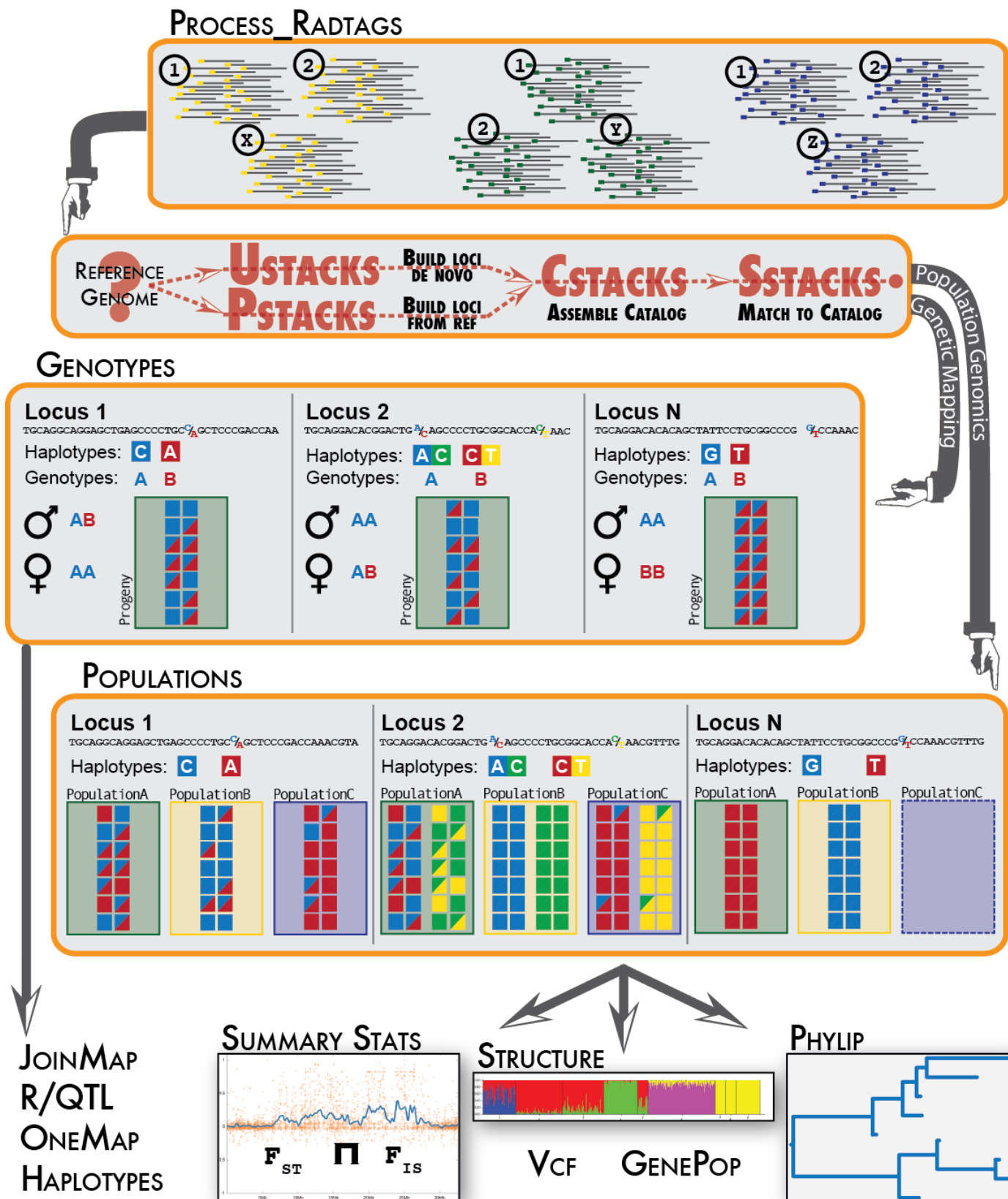


# Introduction

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The overall RAD methodology:



(c) The Stacks pipeline

Check [Stacks manual](#) to learn more in detail of how to analyze metagenomics data.

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## Have a try...

---

```
mkdir -p denovo
denovo_map.pl -M 3 -n 2 -T 2 --samples ./samples --popmap tutorial.pop.txt -o ./denovo
populations -P ./denovo -M tutorial.pop.txt -p 1 -r 0.50 -R 0.50 -t 2 --min_maf 0.01
```

Check Github [radmap](#)