

genetic
inference
of recent

fragmen-
tation

01 XII 2025

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wild
populations
are
often
structured



barriers to
gene flow
can **reduce**
or **disrupt**
their
connectivity



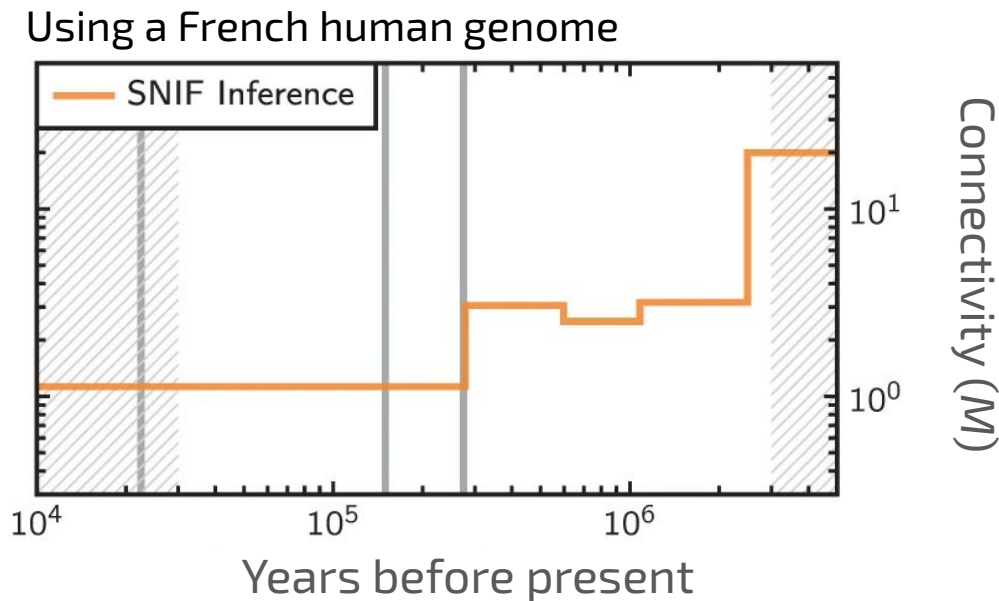
in the long
run, this can
lead to
increased
divergence



or increased
inbreeding
and
**risk of
extinction**



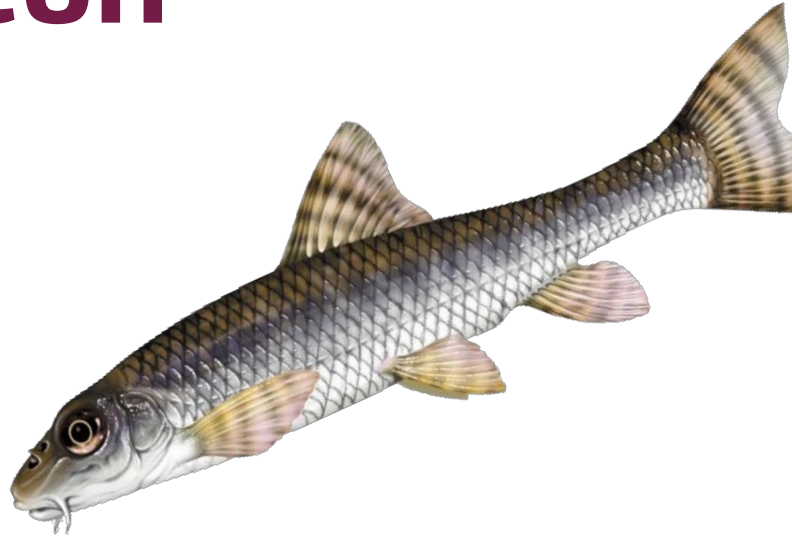
Most current genetic methods infer only **ancient** changes in connectivity

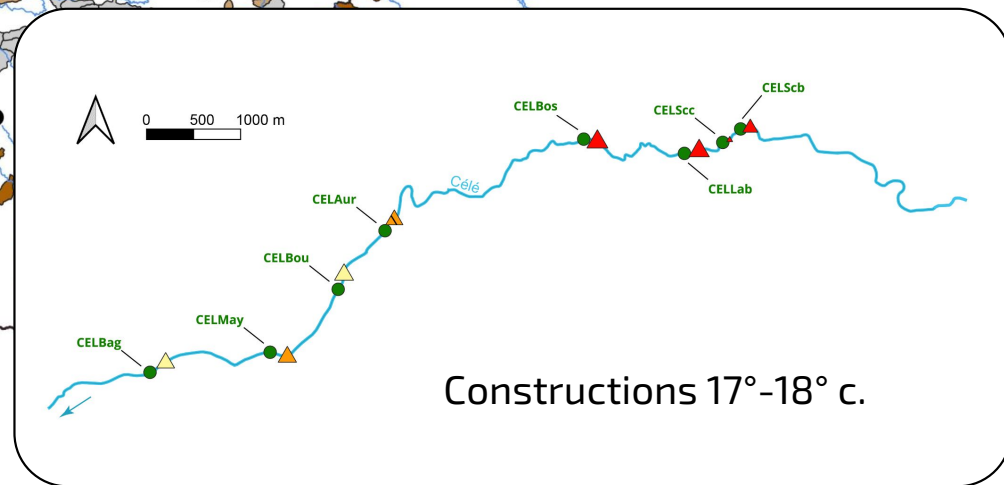
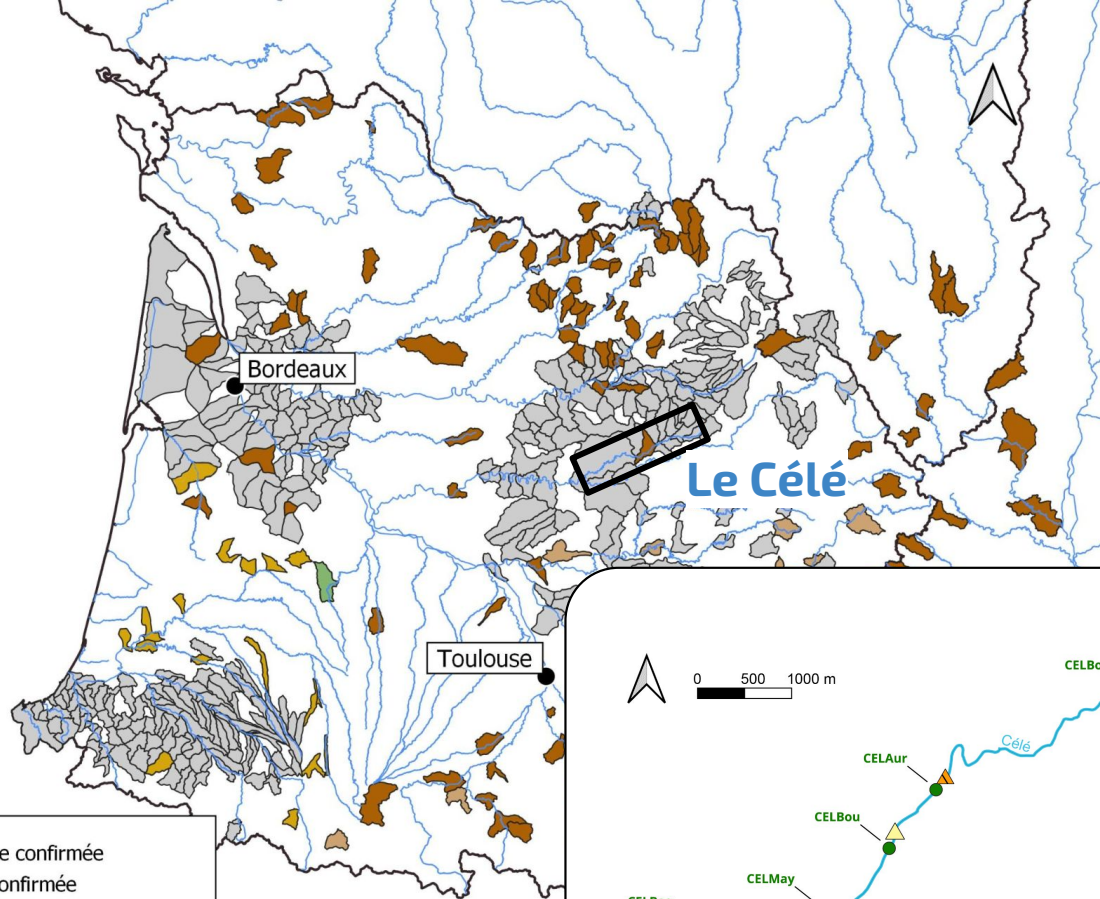


but **human activities** have
created **very recent**
possible barriers to gene
flow (< 10 generations ago)

The case of the **Languedoc gudgeon** (goujon occitan)

Gobio occitaniae



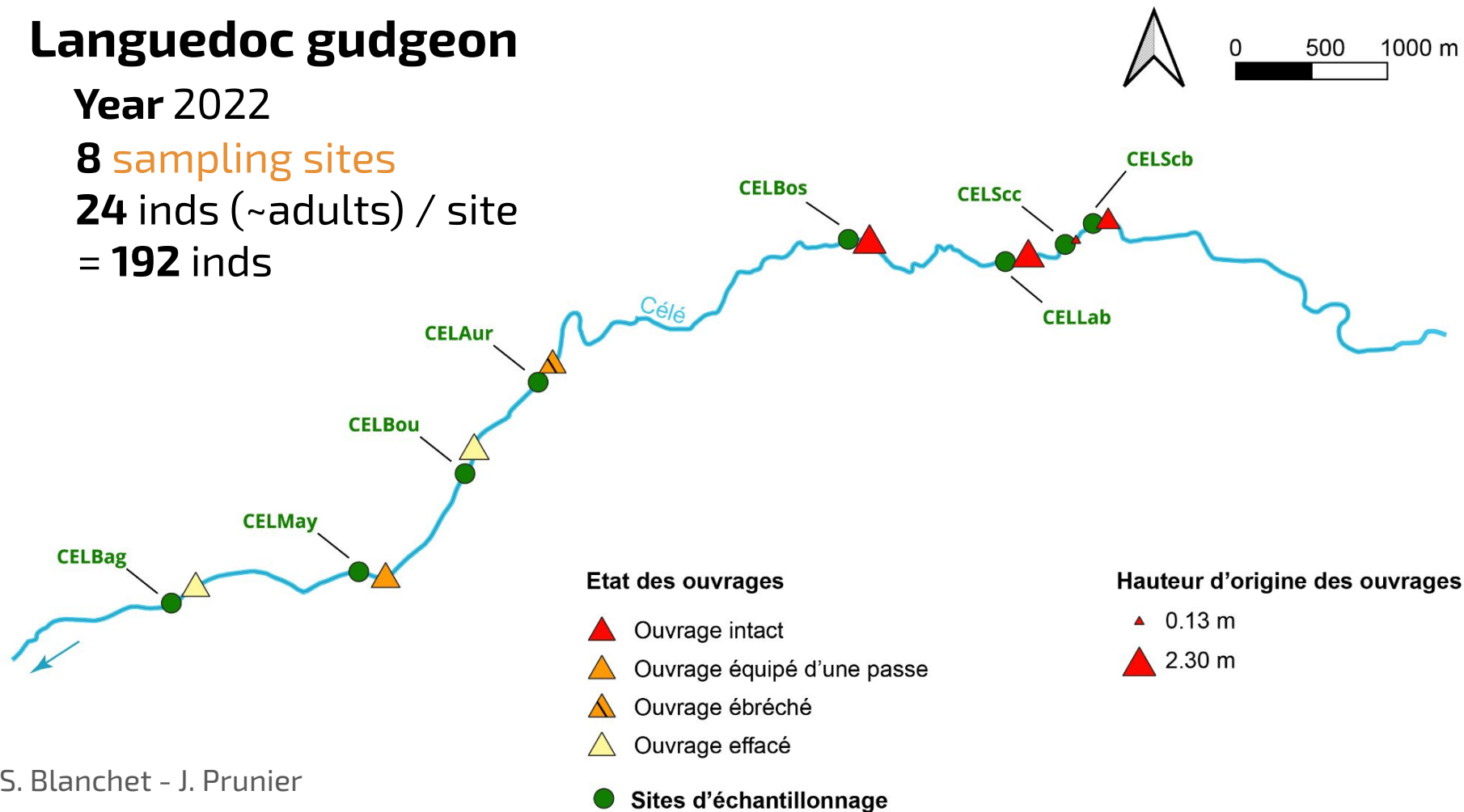


Languedoc gudgeon

Year 2022

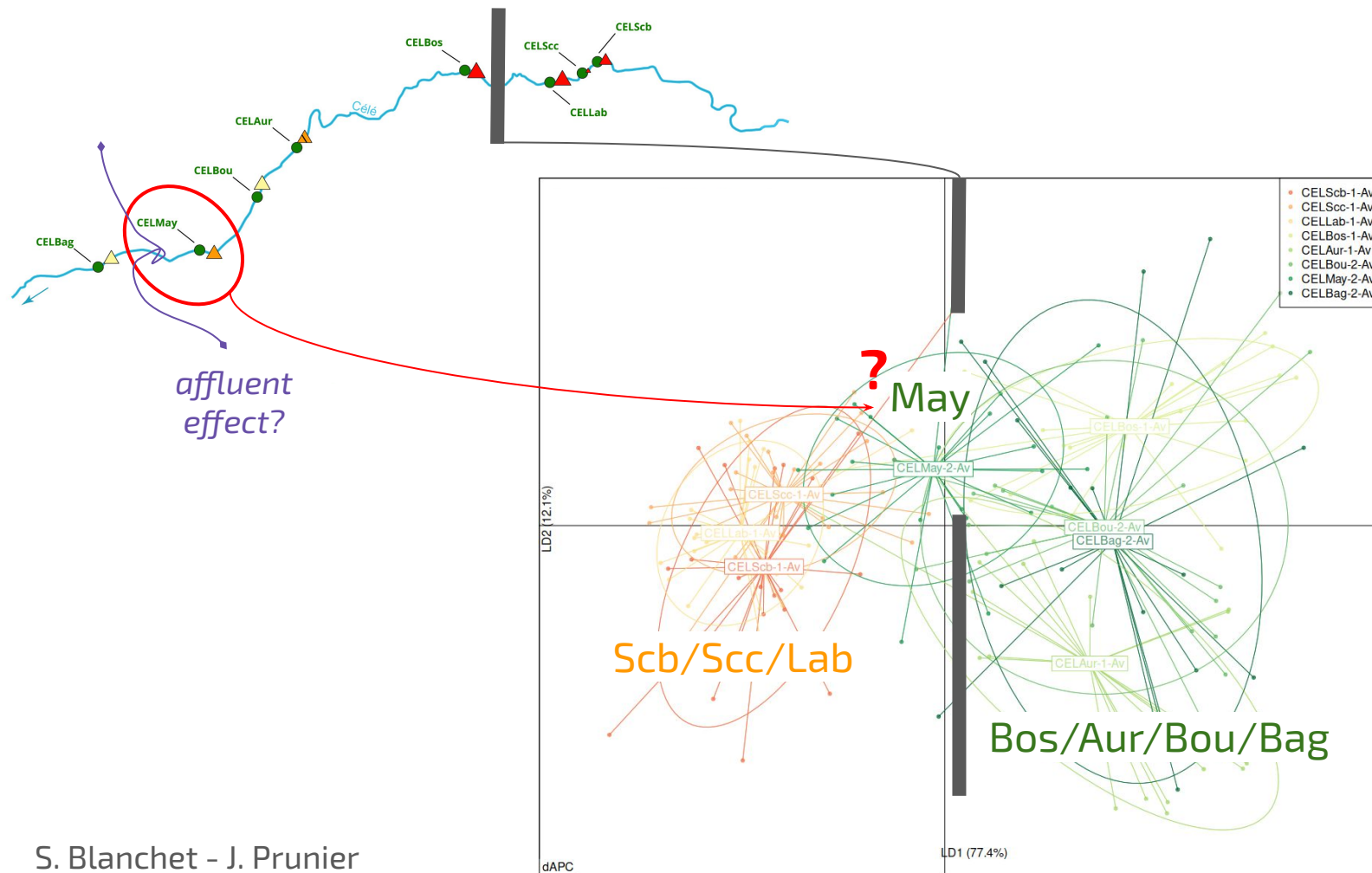
8 sampling sites

24 inds (~adults) / site
= 192 inds



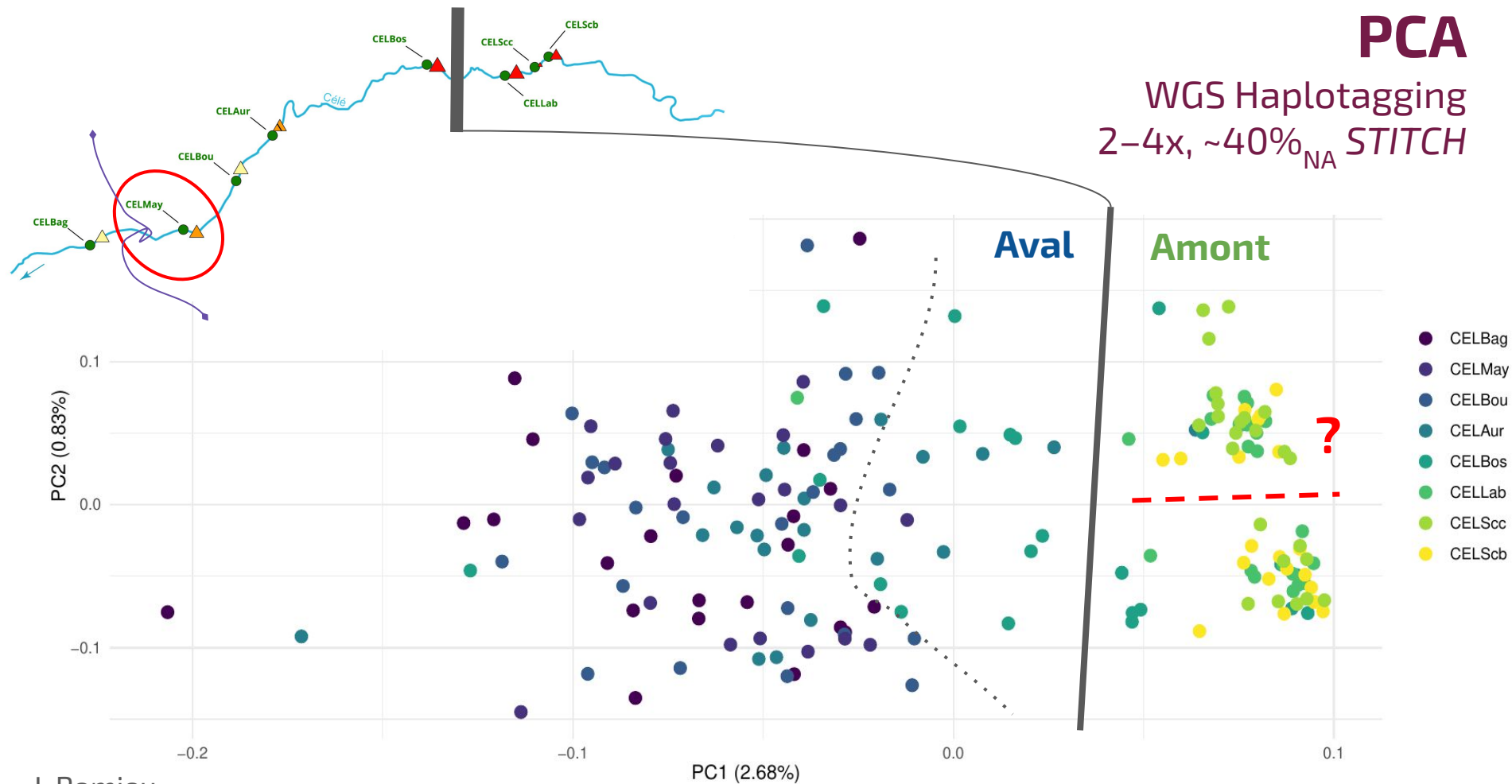
DAPC

48 SSR



PCA

WGS Haplotagging
2-4x, ~40%_{NA} *STITCH*

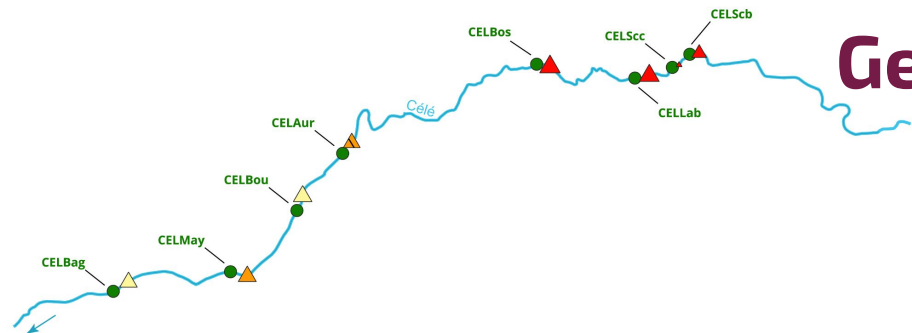


Genetic differentiation index

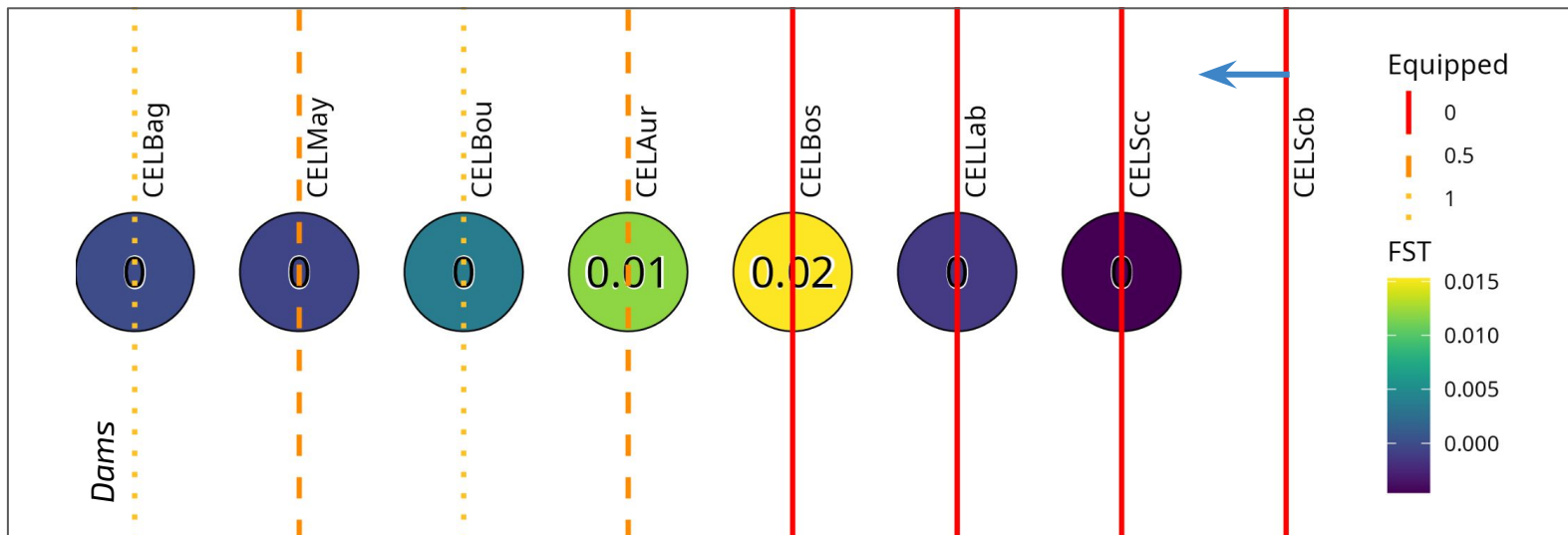
WGS Haplotagging 2–4x, ~40%_{NA} STITCH

$F_{ST}=0$: total exchange

$F_{ST}=1$: total isolation



0.07

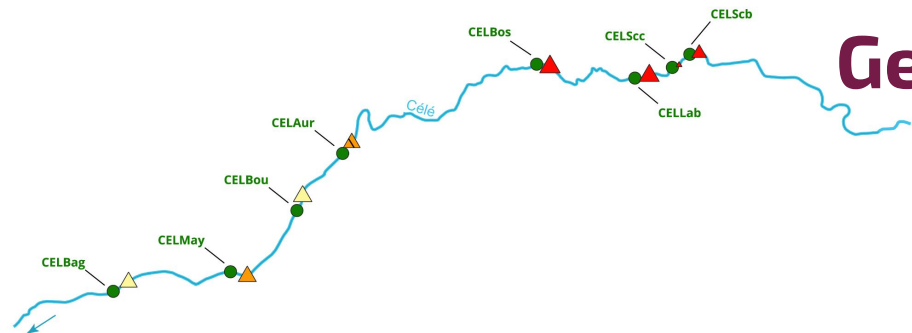


Genetic differentiation index

WGS Haplotagging 2–4x, ~40%_{NA}

$F_{ST}=0$: total exchange

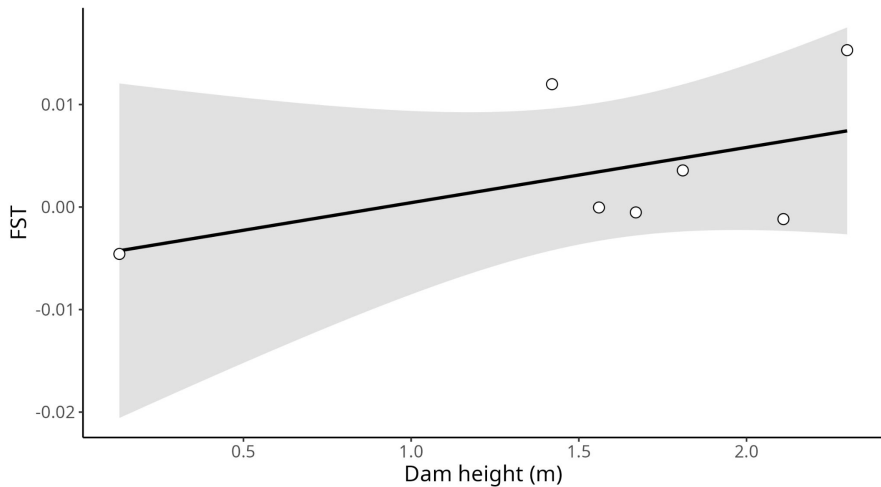
$F_{ST}=1$: total isolation



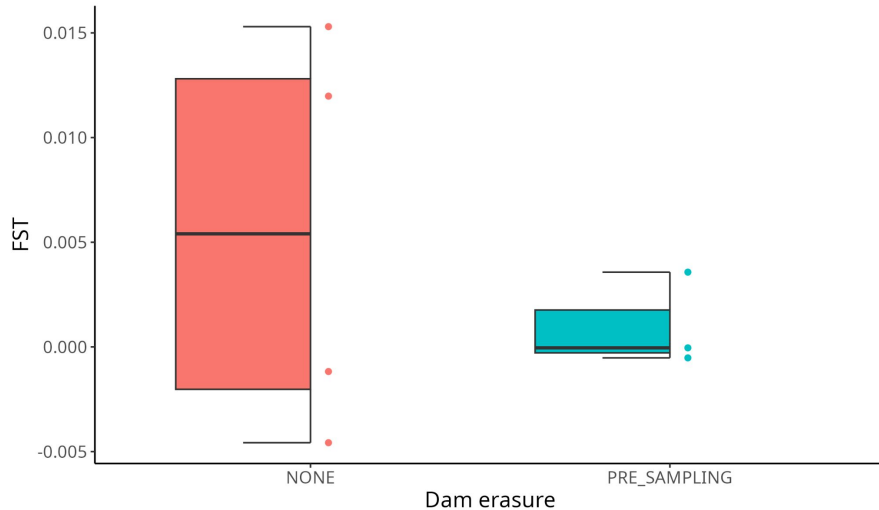
> No significant effect of dam height

> No significant effect of dam erasure

Pearson R=0.51
P=0.24



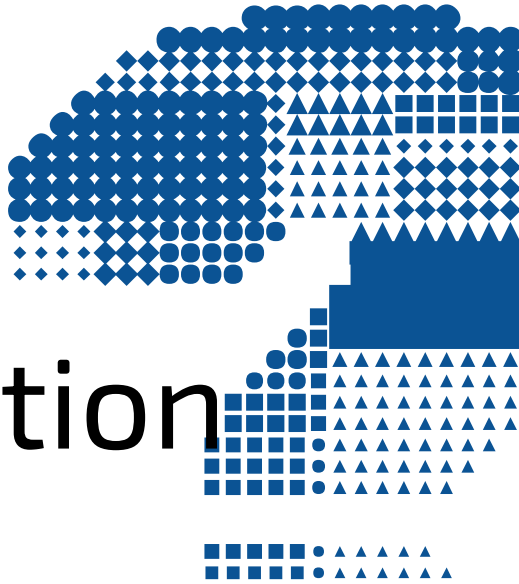
Wilcoxon test: P=1





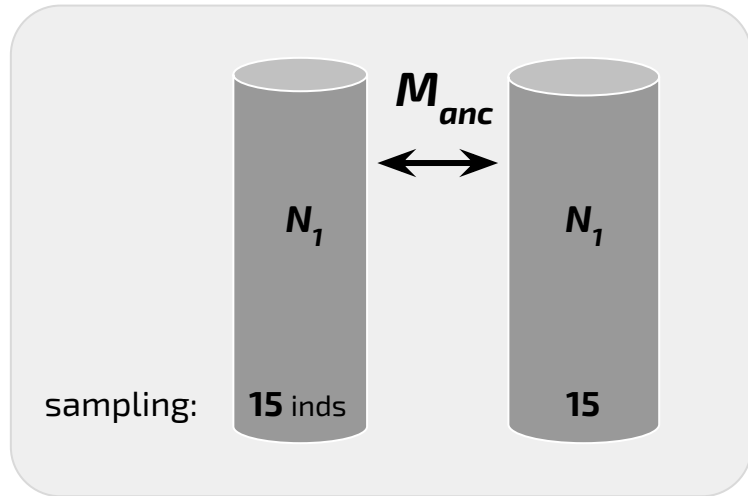
how well **DNA**
can help us

detect
very
recent
fragmentation

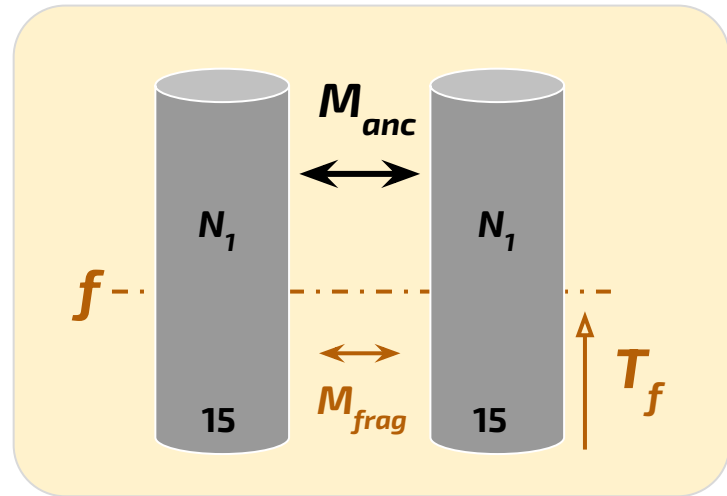


A study using **simulations**

STATIONARY
model



FRAGMENTED
model

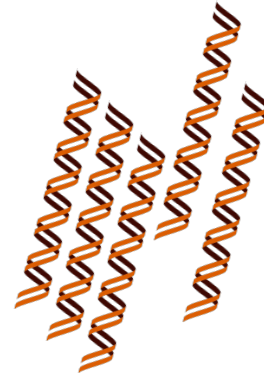


STATIONARY
model

FRAGMENTED
model

10,000 simulated
genetic data per model

msprime



$G=5 \times 50$ Mbp

Test the performance to infer underlying models
using **ABC** with **random forests (RF)**

train

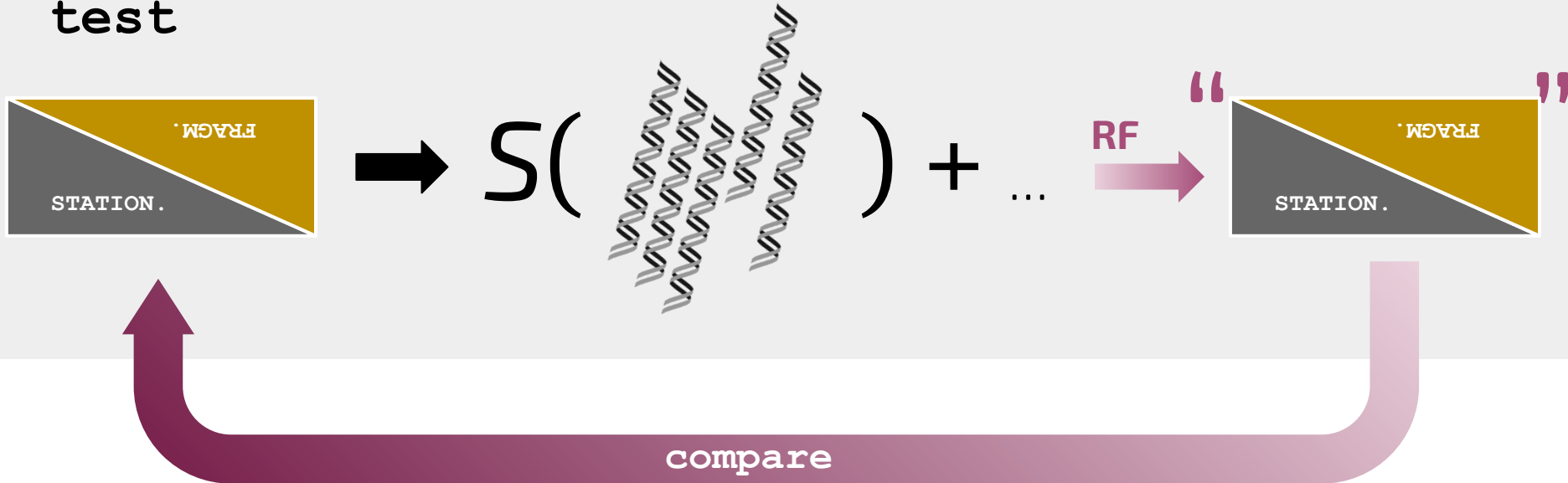


$$\sim S(\text{DNA helix bundle}) + S(\text{DNA helix bundle}) + \dots$$

summary
statistics

Test the performance to infer underlying models
using **ABC** with **random forests (RF)**

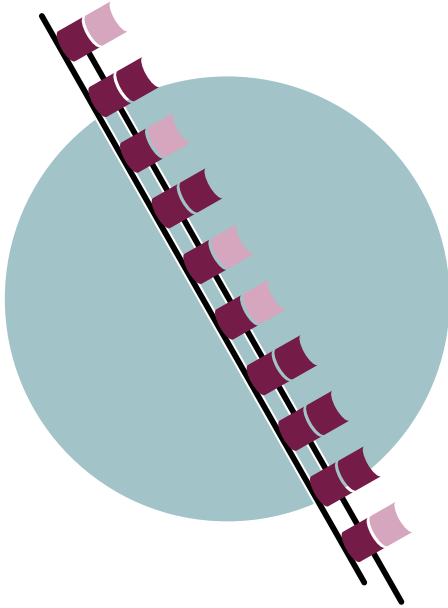
test



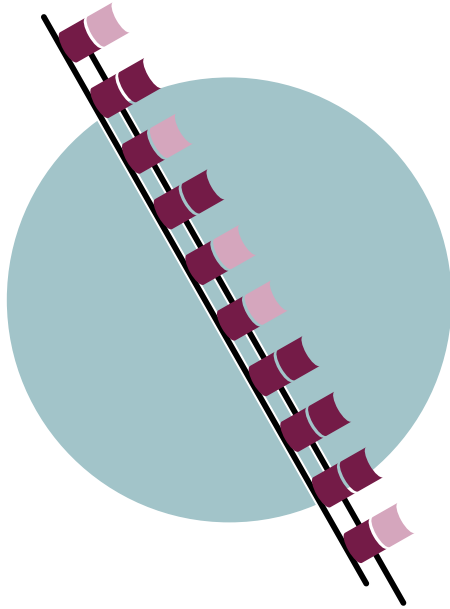
Using different
types of
genomic data

types of genomic data

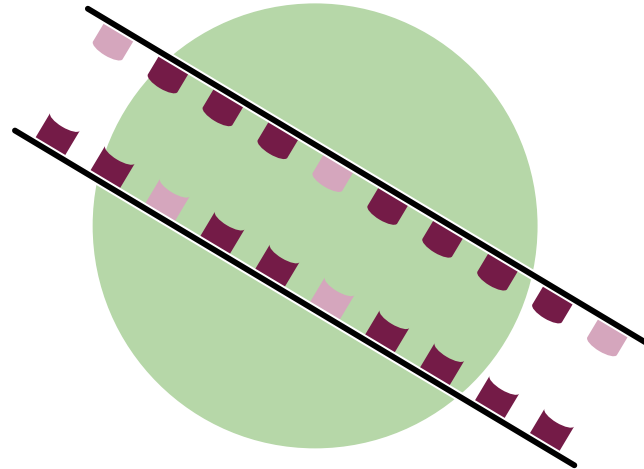
unphased



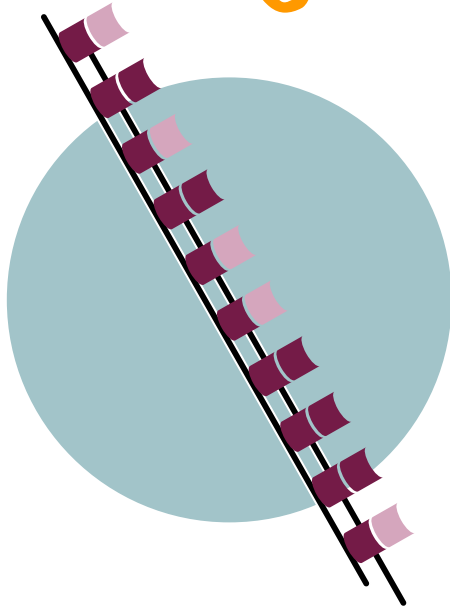
unphased



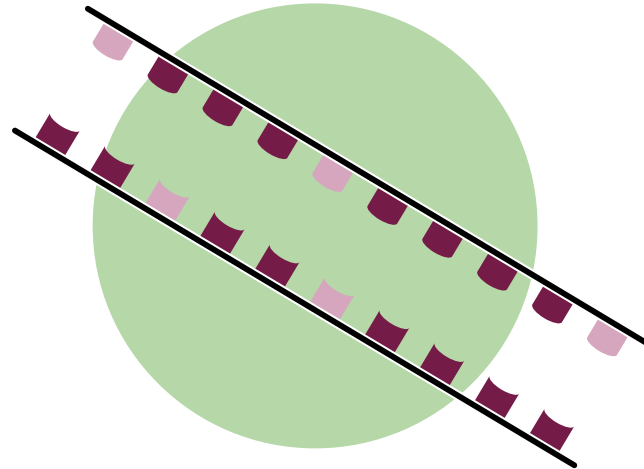
phased



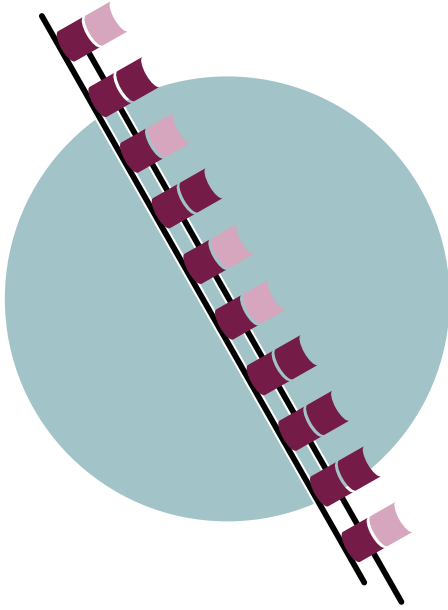
unphased



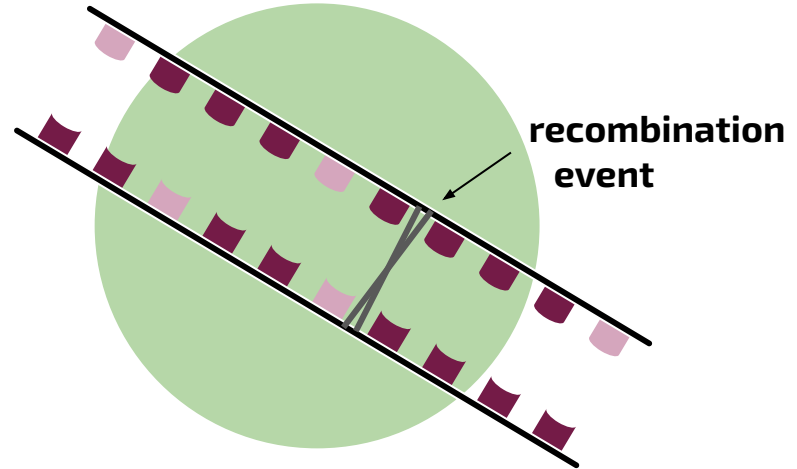
phased

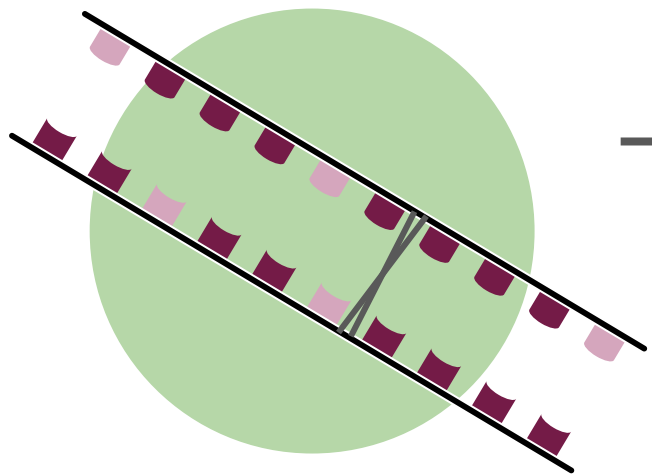


unphased

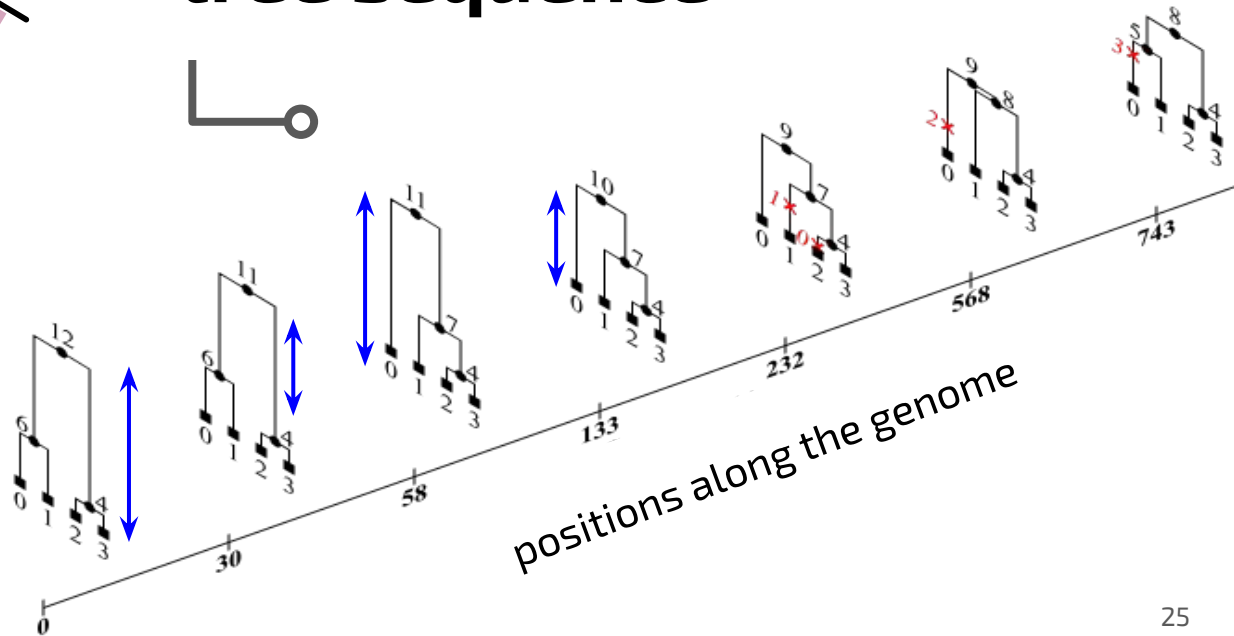


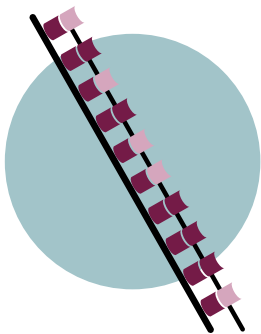
phased



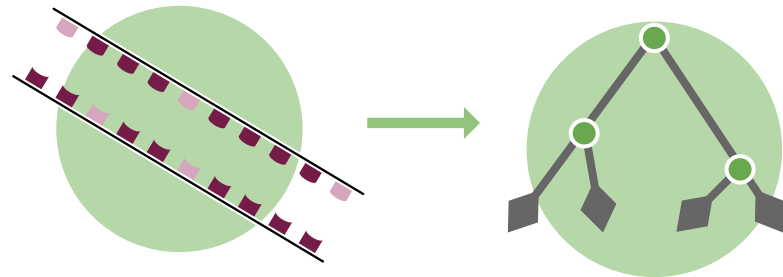


tree sequence





genotypic
statistics



genealogical
statistics

within-pop ——— between

within-pop ——— between

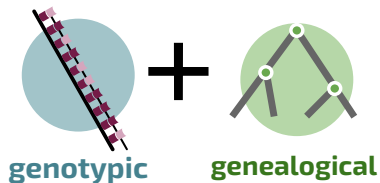
subtracted
within - between

total

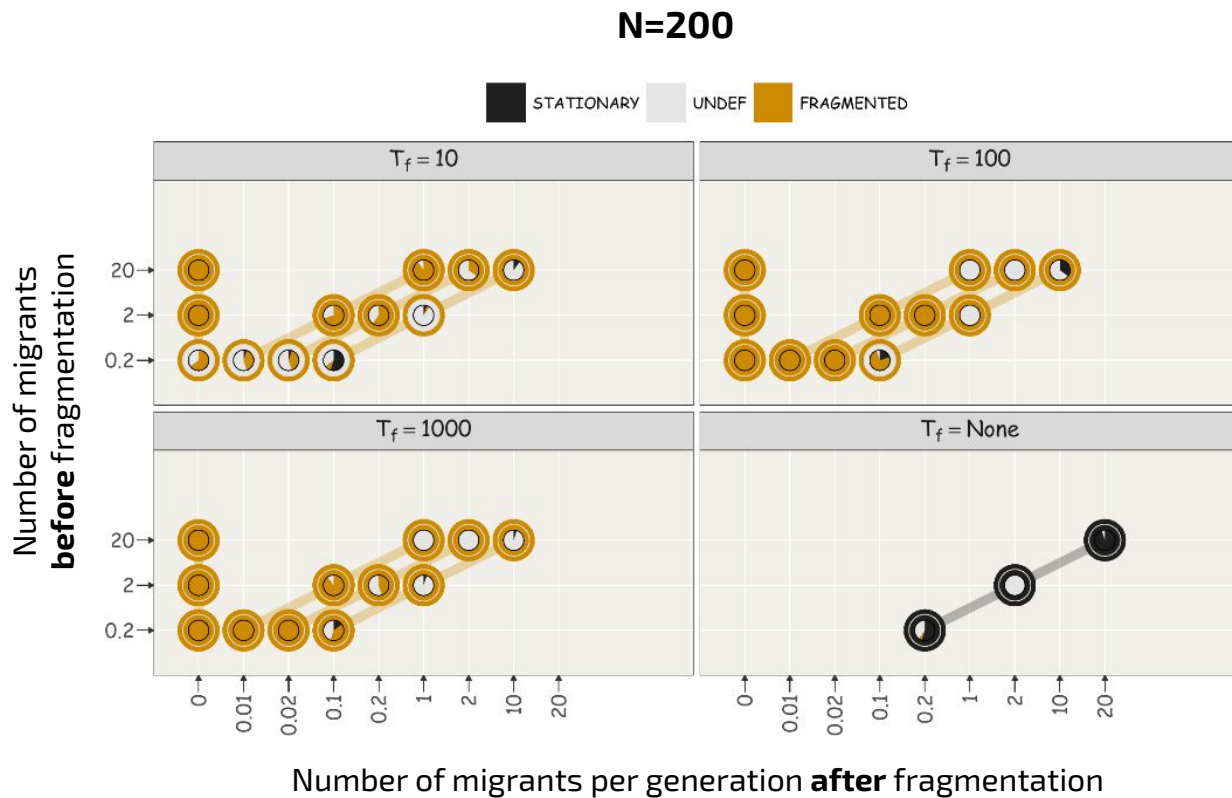
statistics:

28,971

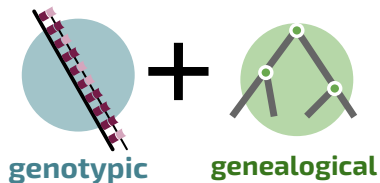
Detection power



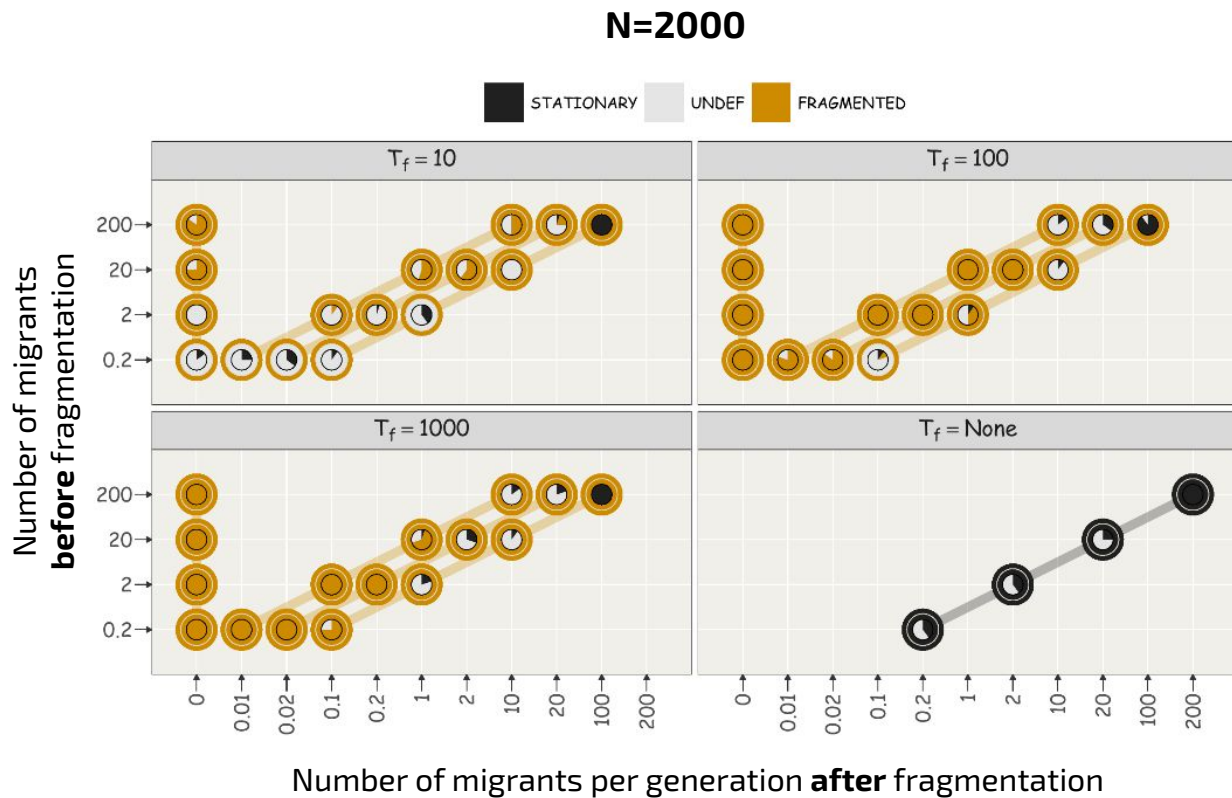
limited power to
detect **stationarity**



Detection power



limited power to
detect **weak**
reduction when pops
already weakly
connected



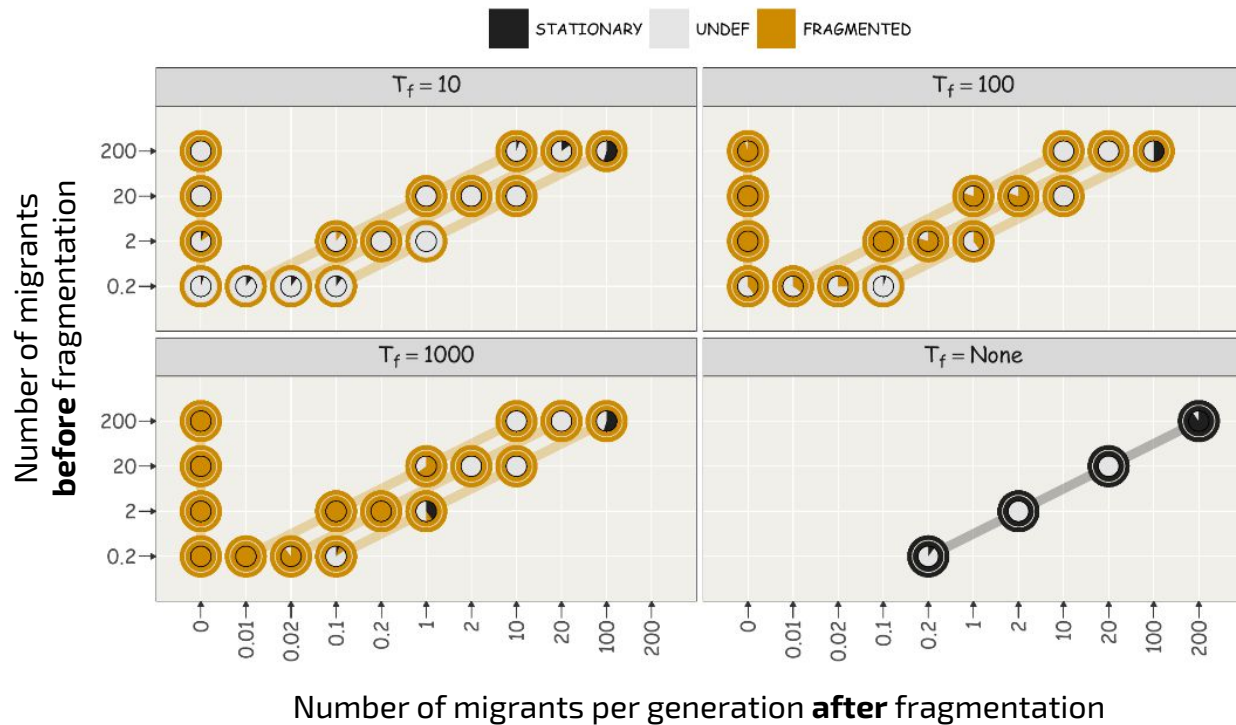
Detection power



more uncertainty,
especially to detect
stationarity

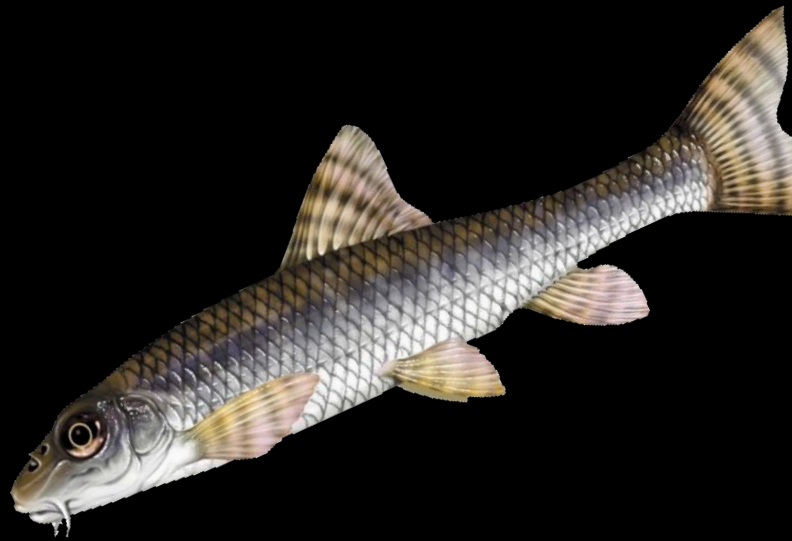


N=2000

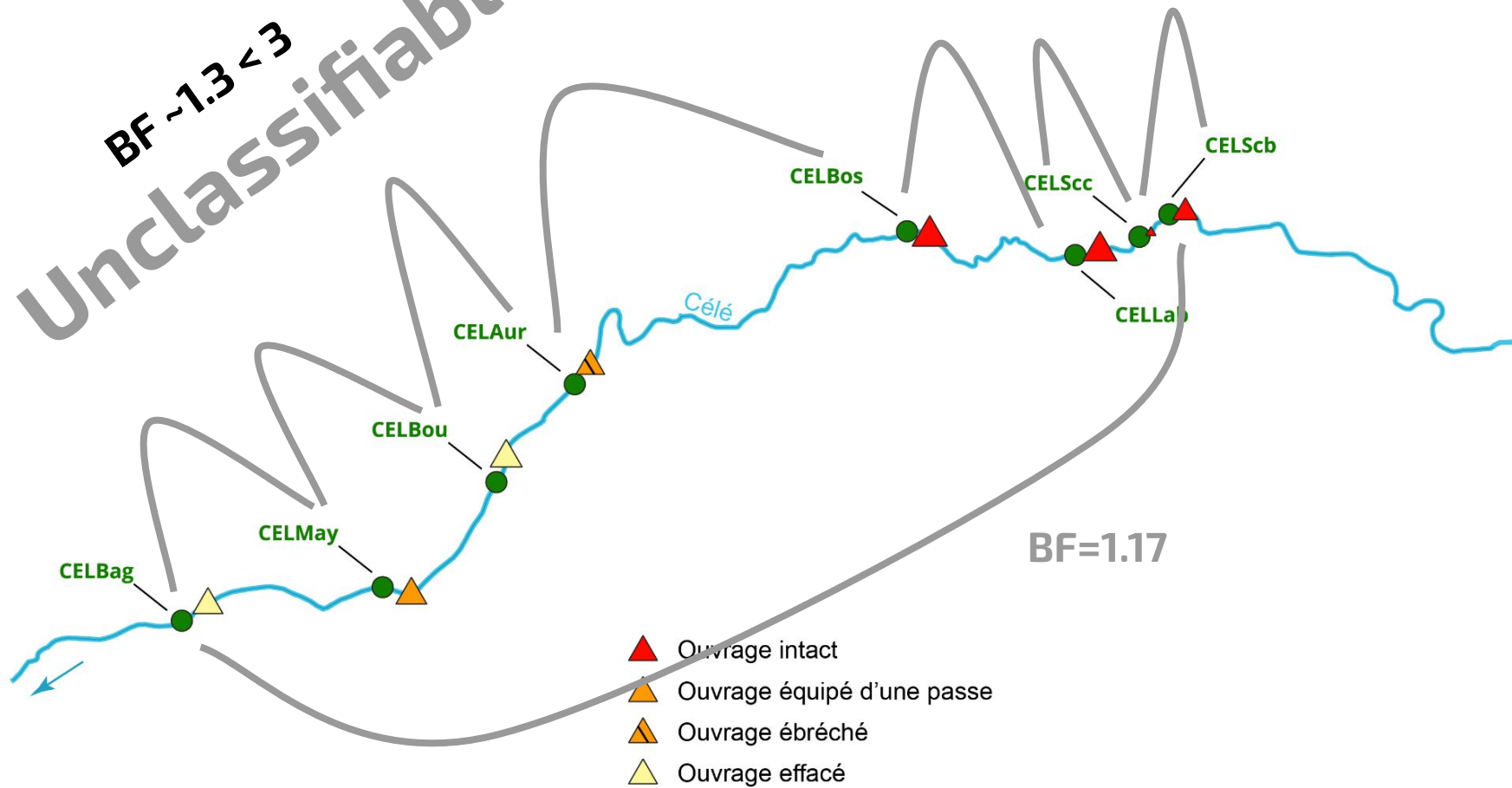


The gudgeon case

WGS Haplotagging: 2–4x, ~40%_{NA}
Single chromosome (q1)
STITCH - SHAPEIT4 - tsinfer

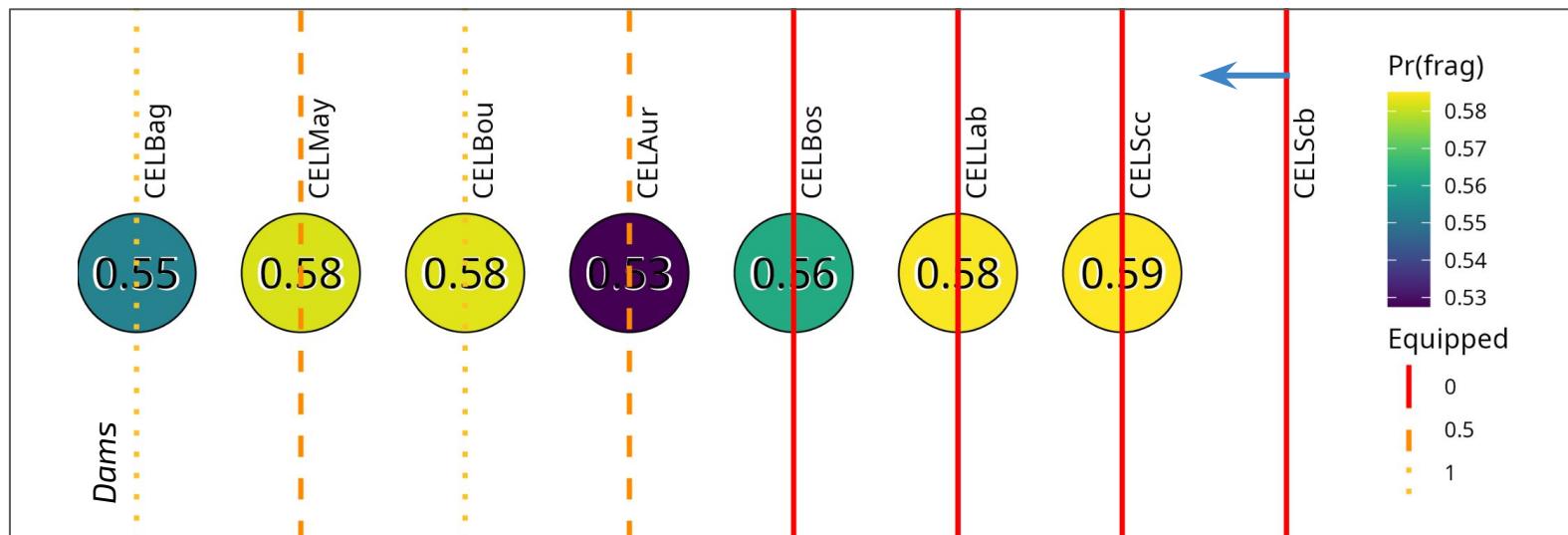
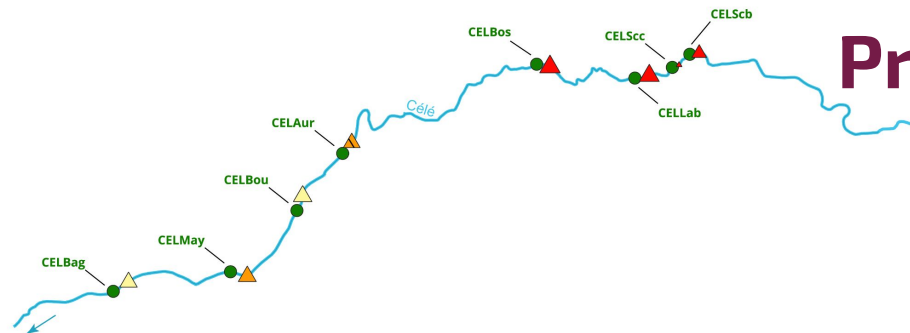


BF ~1.3 < 3
Unclassifiable



Probability of fragmentation

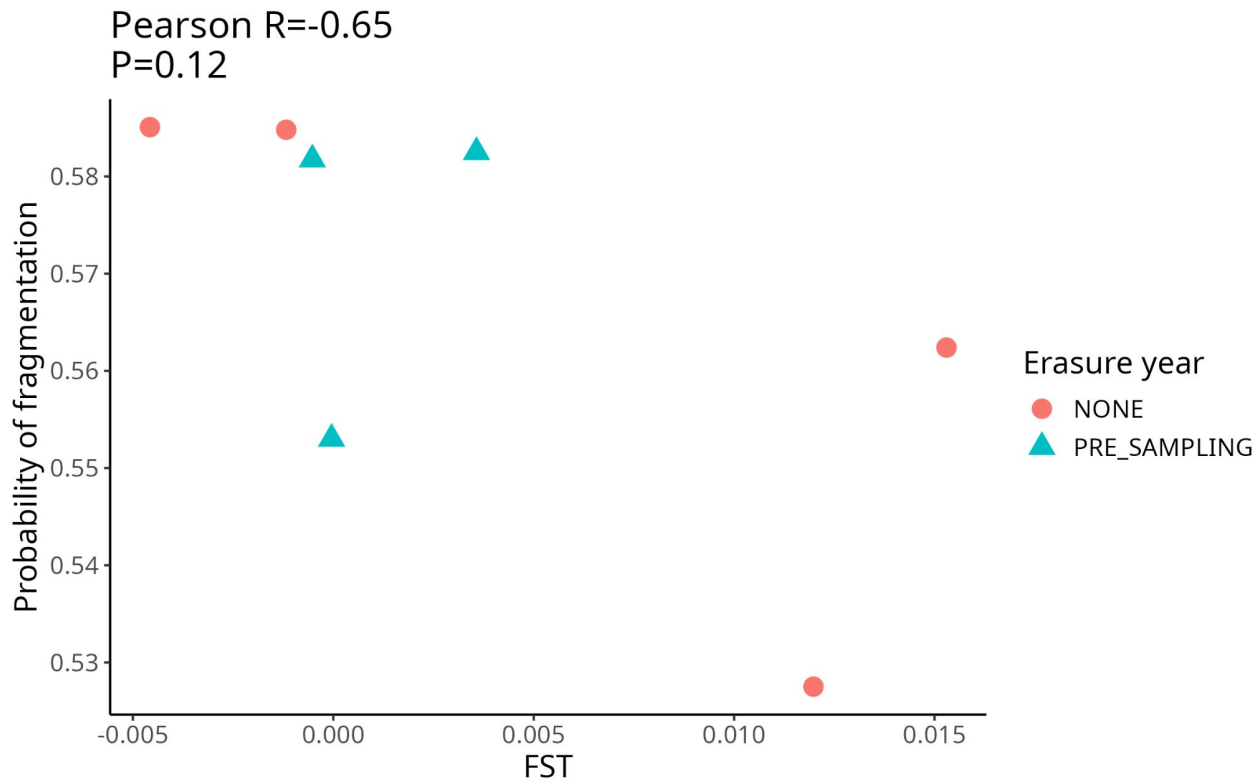
WGS Haplotagging 2–4x, ~40%_{NA}
q1 - *STITCH* - *SHAPEIT4* - *tsinfer*

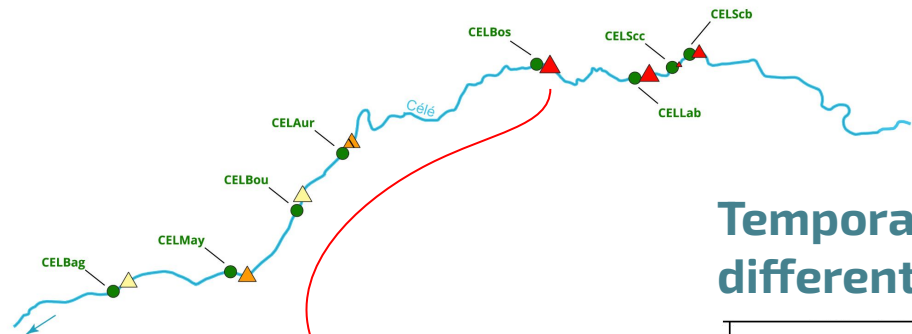


F_{ST} alone **not** a
good predictor of
the **probability** of
fragmentation

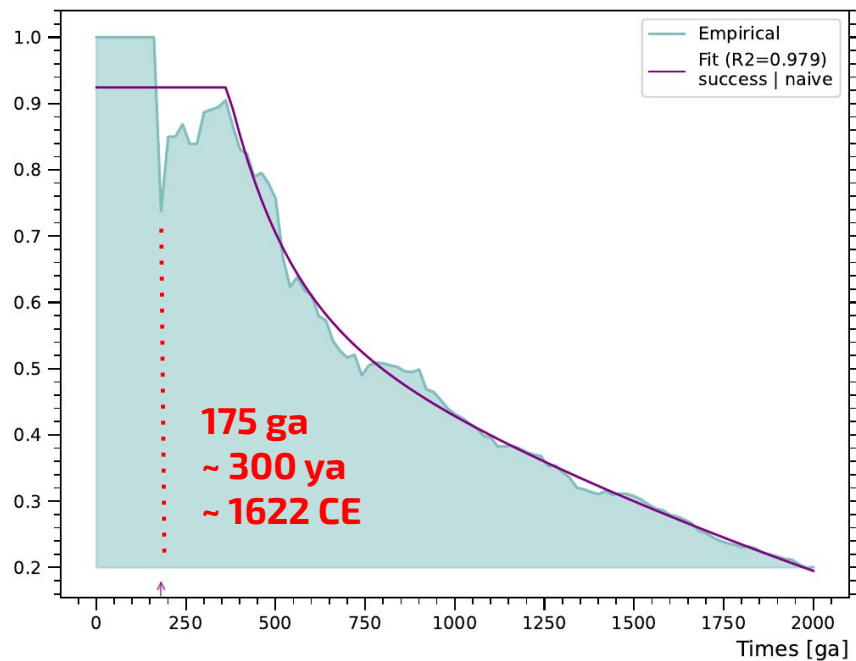
Probability of fragmentation

WGS Haplotagging 2–4x, ~40%_{NA}
q1 - *STITCH* - *SHAPEIT4* - *tsinfer*





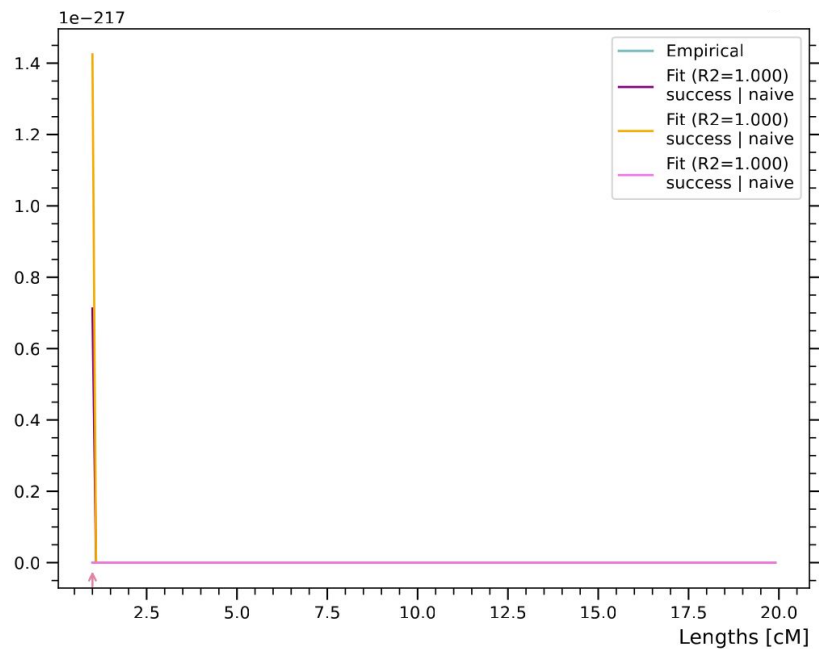
Temporal genealogical differentiation index



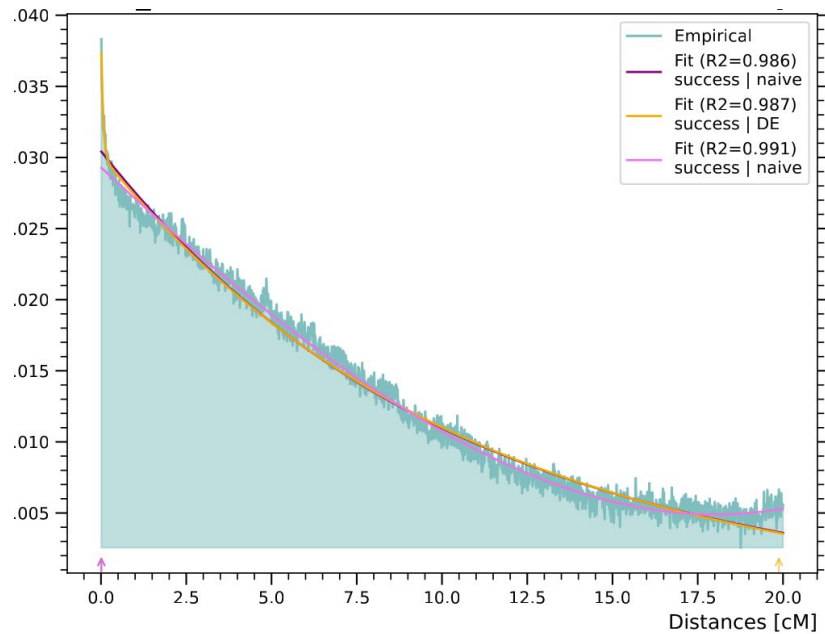
IBD length issues?

WGS Haplotagging 2–4x, ~40%_{NA}
q1 - *STITCH* - *SHAPEIT4* - *tsinfer*

IBD-based average genome sharing



Allele sharing correlation (IBD-free)



Conclusions

Genomic data **useful** to detect recent fragmentation

Genotypic stats already good

New **genealogical** stats **improve** classification



Gudgeon data are not **robustly** classifiable

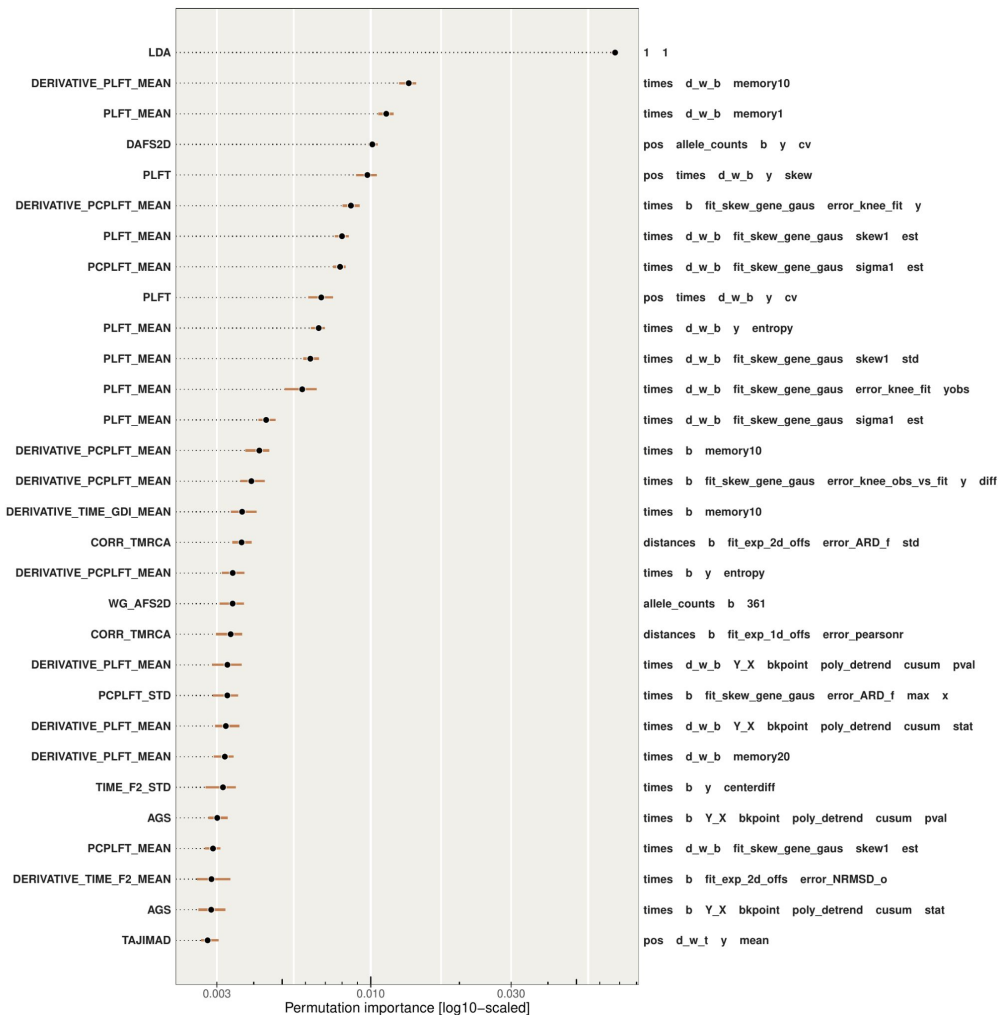


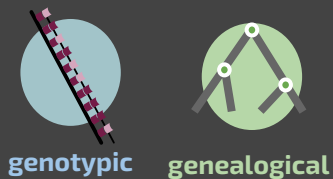
T h a n k

y o u !



Appendix

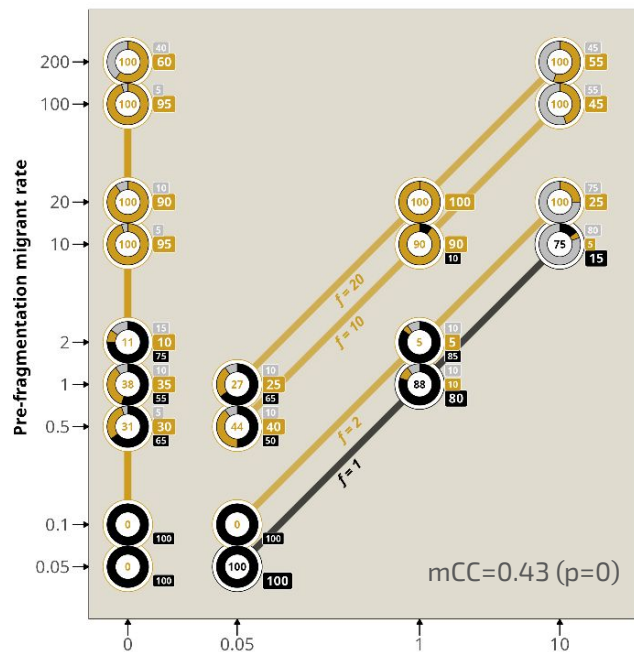




20 sim°/case
N=2,000

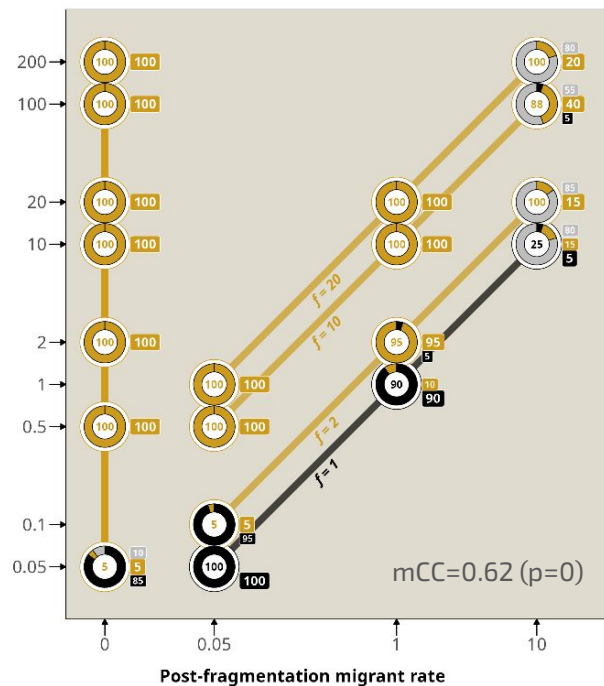
Change: 10 generations ago

CONST FRAG UNCERTAIN
a a a



Change: 100 generations ago

CONST FRAG UNCERTAIN
a a a



Change: 1000 generations ago

CONST FRAG UNCERTAIN
a a a

