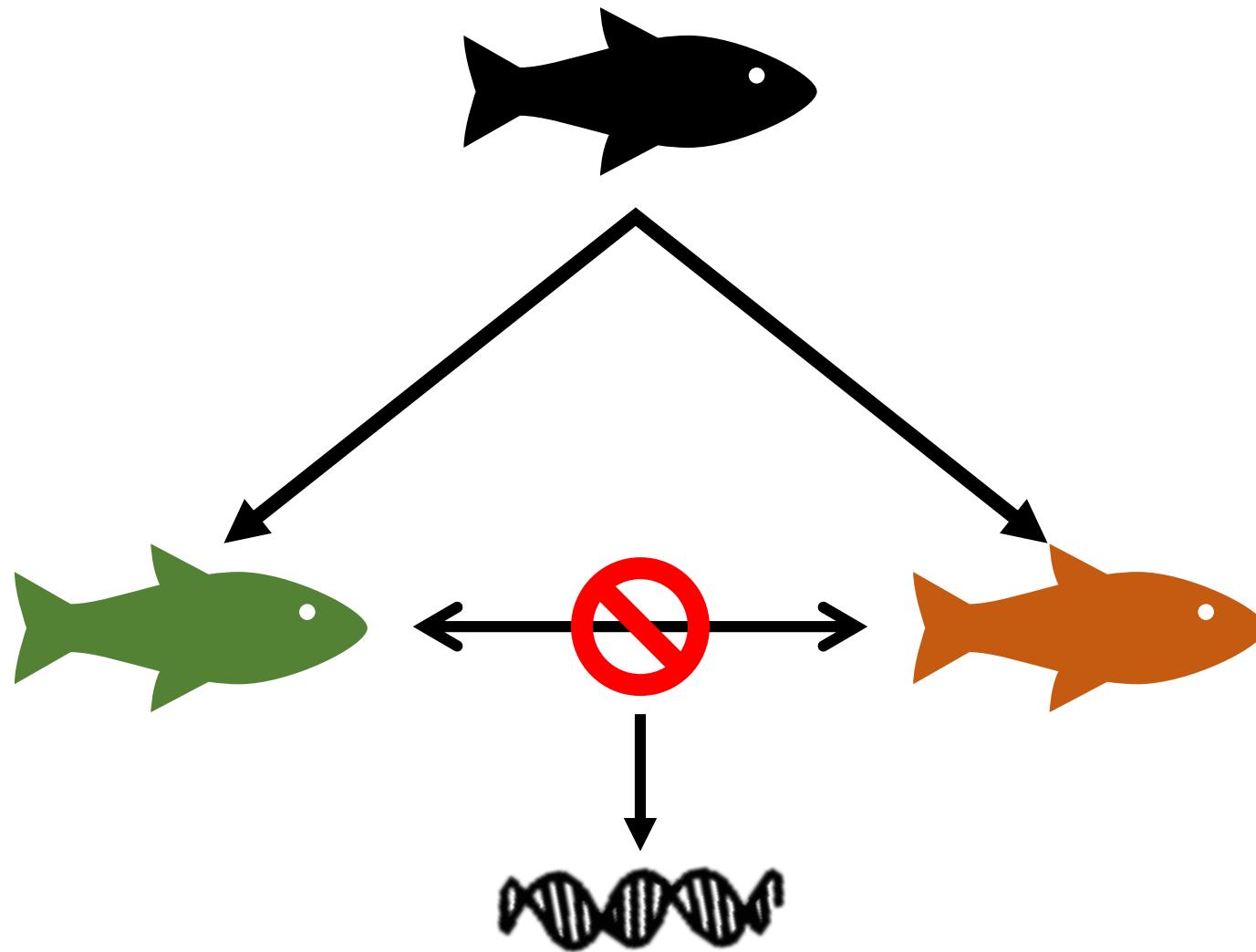


# Using HTC for genomic ancestry analysis

Megan Frayer  
Ph.D. Student, Genetics

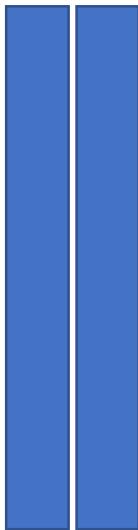
July 21, 2017

# Genetics of Speciation

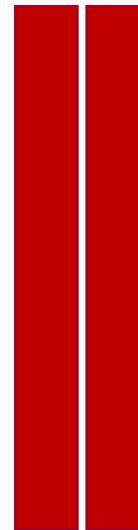


The house mouse hybrid zone can tell us about how speciation is proceeding between these subspecies

*M. m. domesticus*

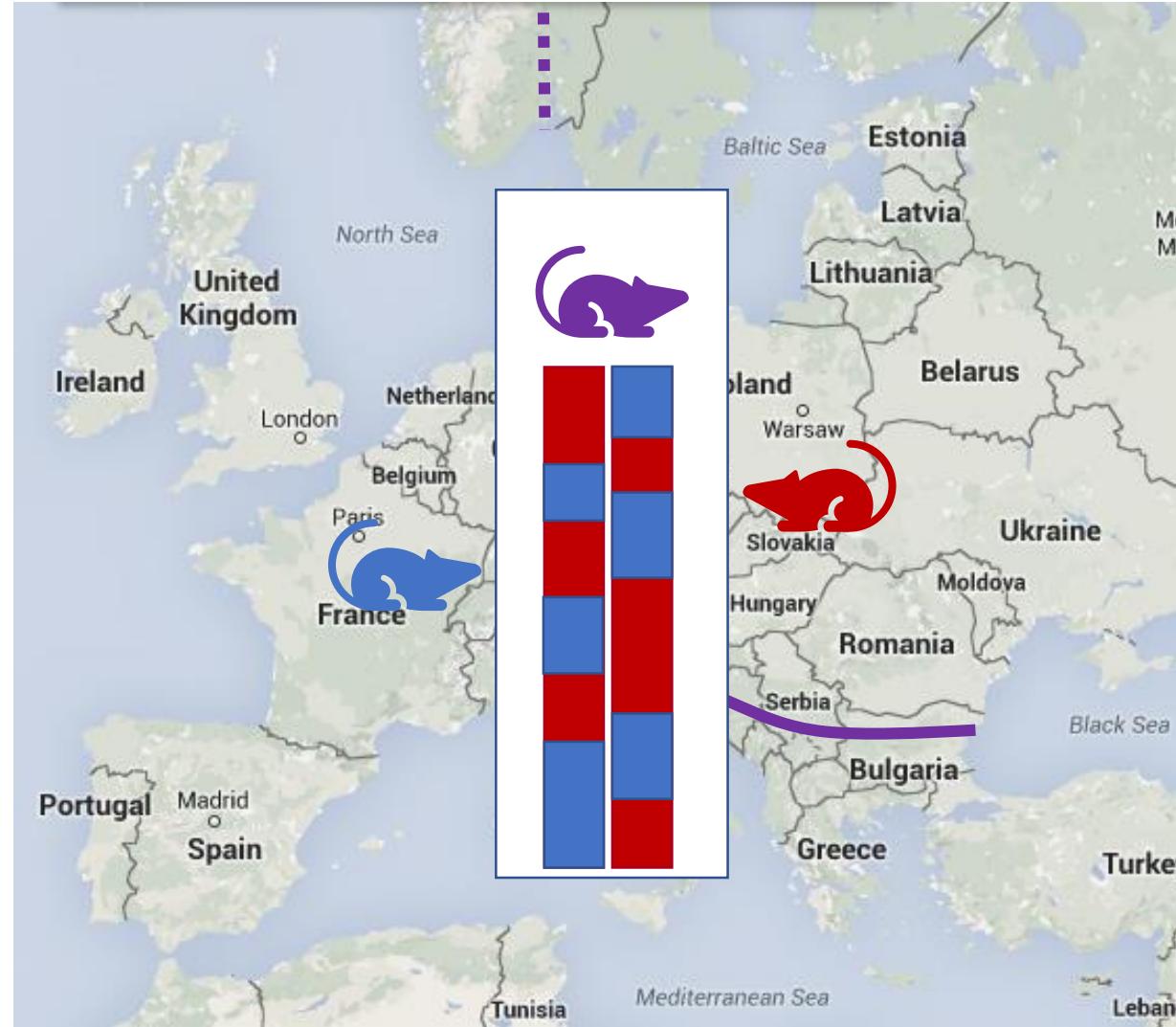
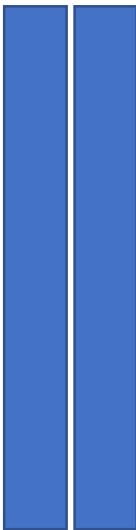


*M. m. musculus*

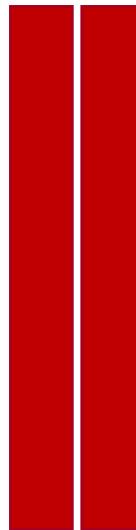


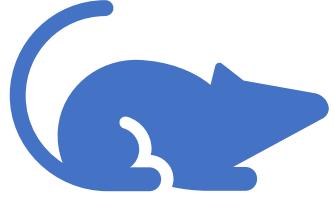
The house mouse hybrid zone can tell us about how speciation is proceeding between these subspecies

*M. m. domesticus*

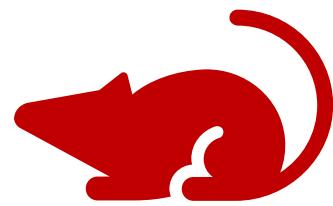


*M. m. musculus*





ATCGTCAGTCAGTCGATCGATACTAGCAGTACGATGCAGTACGATGATA  
TAGCAGTCAGACACGTAGCTATGCATCGTACGTACGCTACGTACTATGC



# DAG for Junction Inference

Phase the  
source  
population  
panels

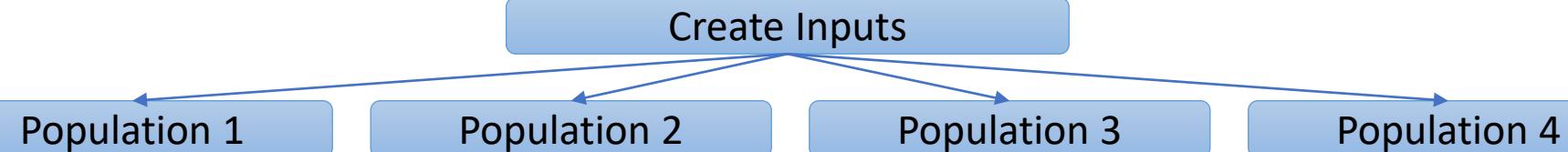
Create the  
input files

Run the  
inference  
and  
analysis

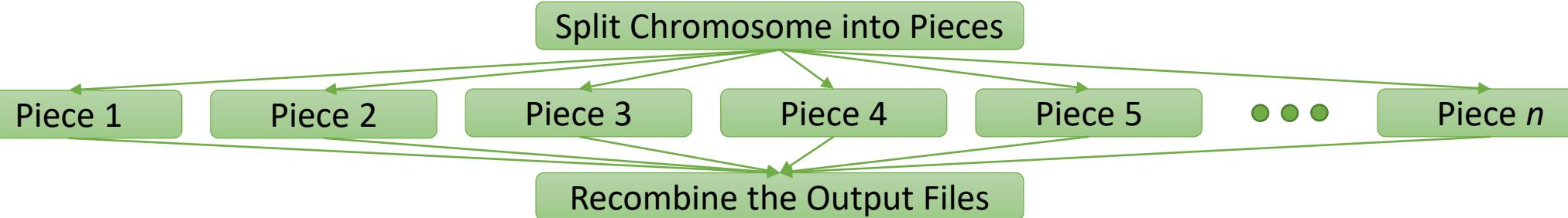


chr1.dag

SPLICE beagle.dag



SUBDAG\_EXTERNAL inputs.dag

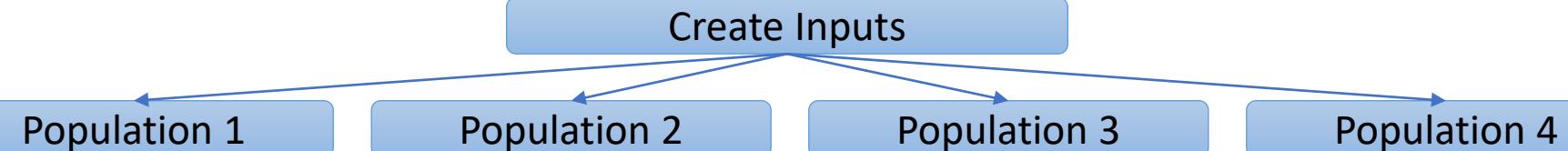


Run Inference Program

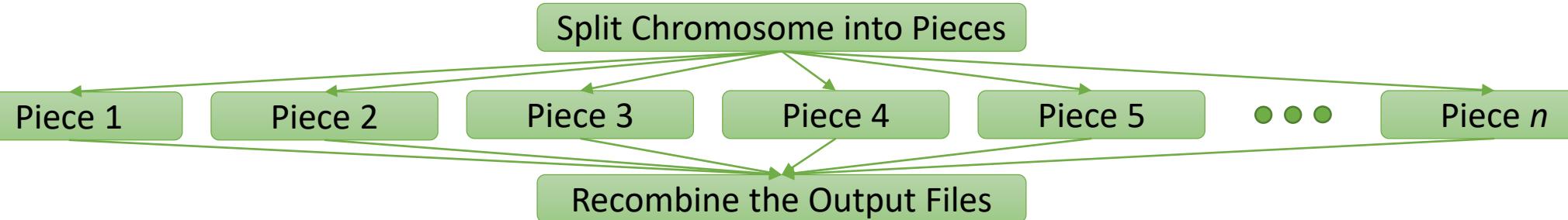
Analyze the Output

chr1.dag

SPLICE beagle.dag



SUBDAG\_EXTERNAL inputs.dag



Before HTC: 72 hours/test  
57 days/19 tests  
With HTC: 14 hours/test  
4 days/19 tests  
**57 days → 4 days**

Run Inference Program

Analyze the Output

# Parameter grid search

- What is the combination of input parameters with the highest likelihood?

# Parameter grid search

Parameter	Values to be tested				
defaultRate	0.8	0.86	0.99	1.15	
timeSince					
Admixture	1000	3750	6500	9250	12000
ancestryProp1	0.4	0.5	0.6		
ancestralRate1	41000	69250	97500		
ancestralRate2	14000	23650	33290	20815	35158
mutation1	1E-04	1E-05	1E-06	1E-07	1E-08
mutation2	3.4E-05	3.4E-06	3.4E-07	3.4E-08	3.4E-09
miscopyRate	0.01	0.001	1E-04	1E-05	1E-06
Miscopy Mutation	0.01	0.001	1E-04	1E-05	1E-06

108,000 combinations of parameters to be tested

# Parameter grid search

Create  
input files

Run  
parameter  
tests

Compile  
and  
analyze  
results

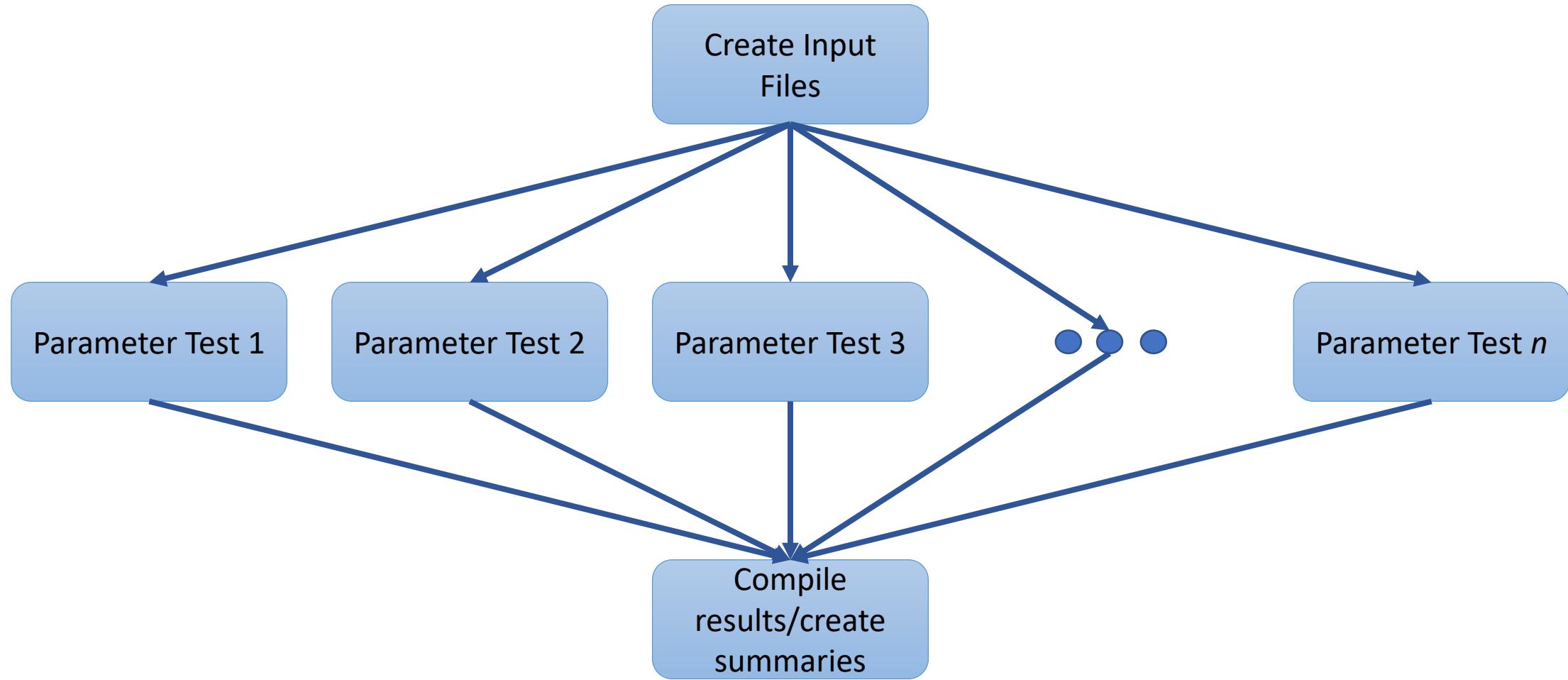
## parameter\_test.dag

Create Input  
Files

Examples of files to print:

Submit files  
Executables  
Input for programs being run  
Scripts that will need to be run

parameter\_test.dag



## parameter\_test.dag

SUBDAG\_EXTERNAL

Create Input  
Files

Parameter Test 1

Parameter Test 2

Parameter Test 3

• • •

Parameter Test  $n$

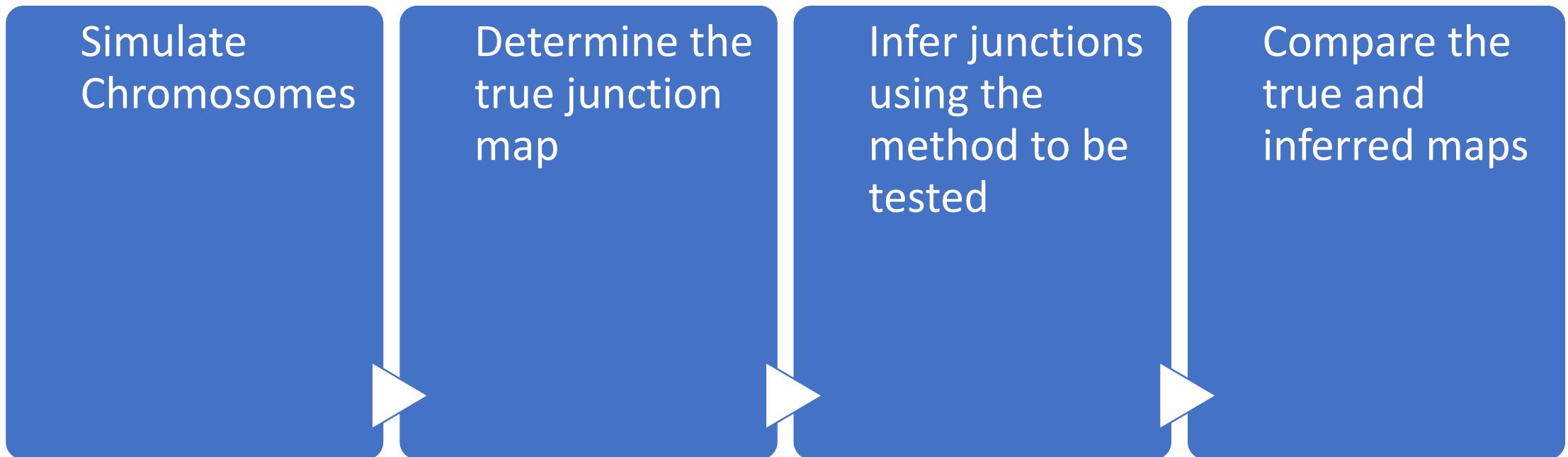
Before HTC: 2 hours/test  
24.6 years/108,000 tests  
With HTC: 2 hours/test  
10 days/108,000 tests  
**24.6 years → 10 days**

Compile  
results/create  
summaries

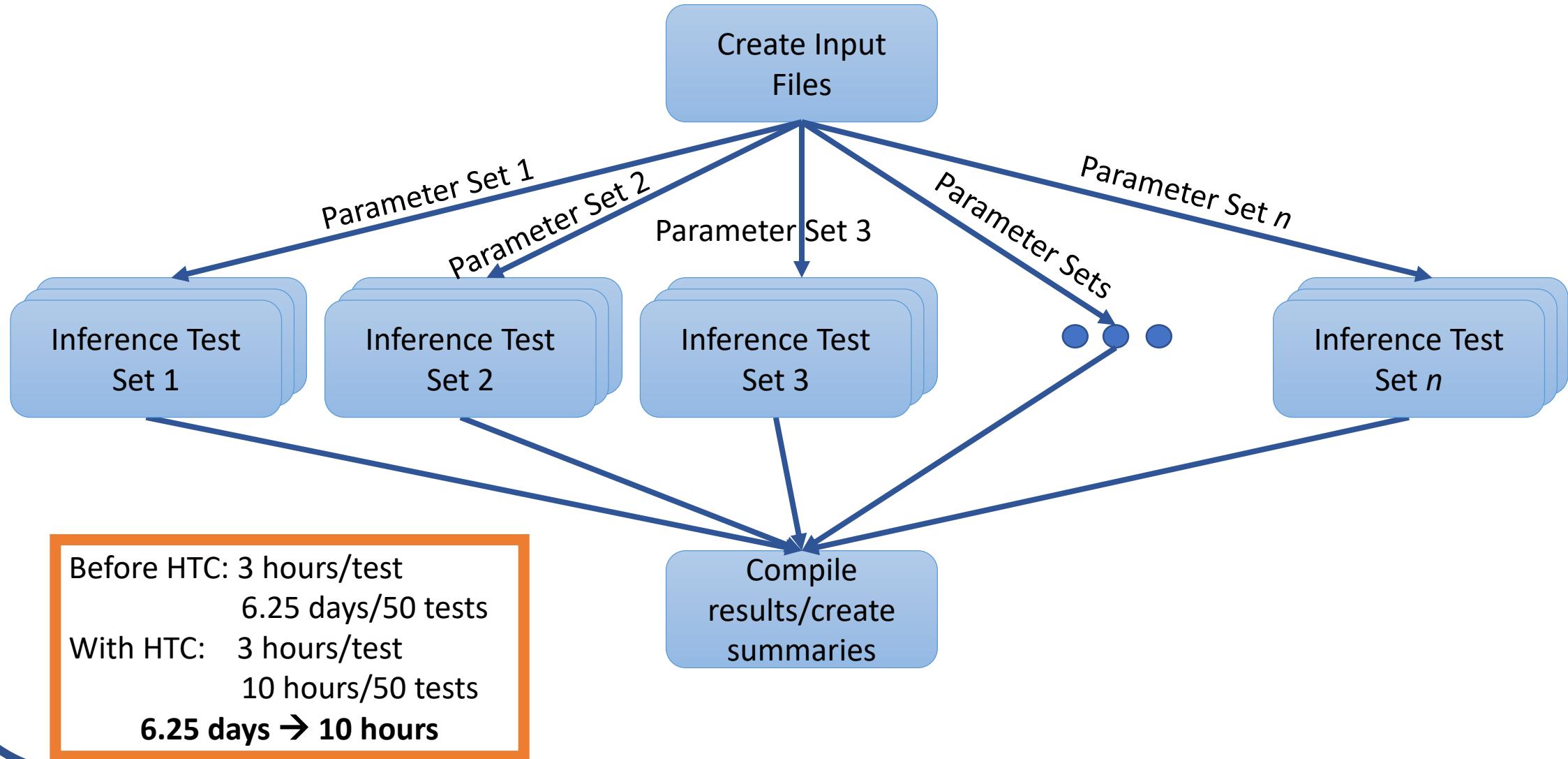
# Testing with Simulated Chromosomes

- How well is the program performing?

# Testing with Simulated Chromosomes



## `inference_testing.dag`



# Conclusion

- HTC can improve research in biological sciences
- Even simple DAGs can make a big impact on your research
- DAGs can also improve reproducibility

HTC has shortened my Ph.D. by 39.8 years so far.