

Tassel Pipeline Tutorial (*Command Line Interface*)

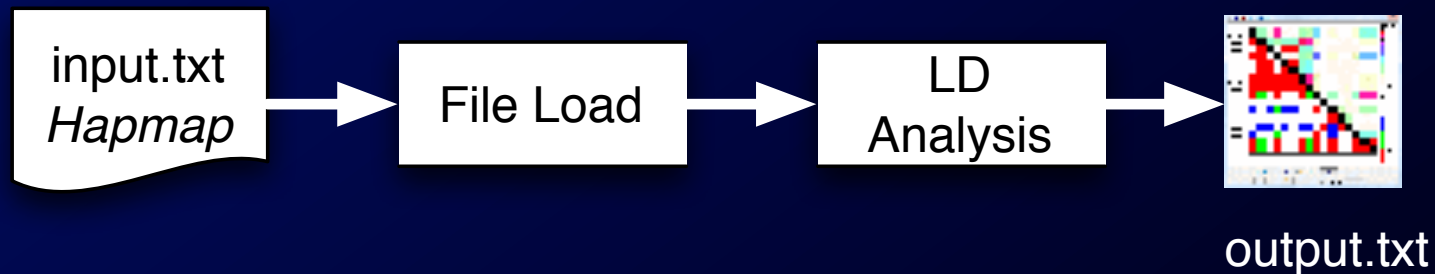
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Tassel Pipeline Basics...

- **Consists of Modules (i.e. Plugins)**
- **Output from one Module can be Input to another Module. Determined by order specified.**



```
run_pipeline.bat -fork1 -h input.txt -ld -ldd png  
-o output.png -runfork1
```

Tassel Pipeline Naming...

- Pipelines can consist of Pipeline Segments (Each executes in it's own computing process).
- Each Segment has a name (i.e. 1, A). Follows **-fork** or **-combine**.
- Output from a Pipeline Segment can be used as input to a Module by referencing with **-input**.

`run_pipeline.bat -fork1 ... -forkA ...
-forkC -module -input1`



`run_pipeline.bat -forkX ... -forkY ... -forkZ ...
-combine1 -inputX -inputY -inputZ`



Tassel Pipeline -combine...

- Combining data from multiple Segments (-combine)...
 - -input
 - -inputOnce

run_pipeline.bat  fork1  -forkA ...
-combineC -input1 -inputOnceA

Tassel Pipeline Execution...

- Pipeline Segments can start execution in two ways...
 - Using `-runfork`
 - By Receiving Input from a Module

`run_pipeline.bat fork1 -forkA ...`
`-combineC -input1 -inputA -forkZ -MODULE -inputC`
`-runfork1 -runforkA`

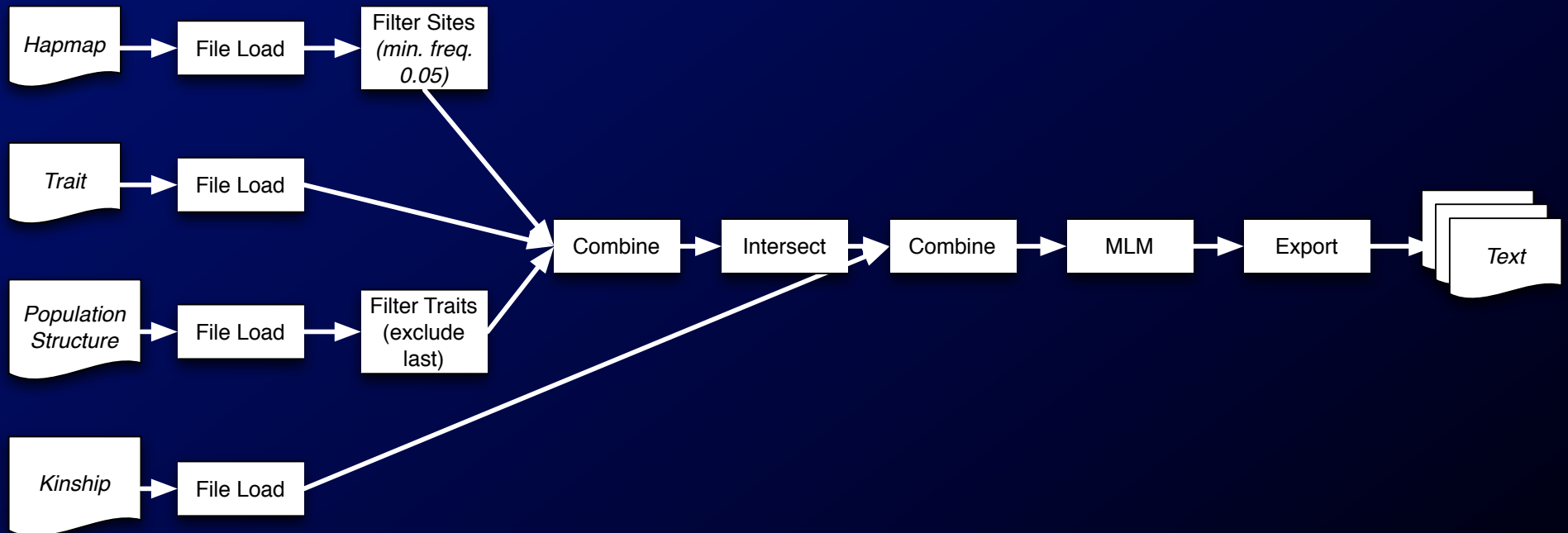


The diagram consists of five red arrows pointing from the command line to the code block. One arrow points from 'fork1' to '-runfork1', another from '-forkA' to '-runforkA', a third from '...' to '-inputC', a fourth from '-input1' to '-input1', and a fifth from '-inputA' to '-inputA'.

Tassel Pipeline MLM Example...

```
Run_pipeline.bat -fork1 -h mdp_genotype.hmp.txt -  
filterAlign -filterAlignMinFreq 0.05 -fork2 -r  
mdp_traits.txt -fork3 -q mdp_population_structure.txt -  
excludeLastTrait -fork4 -k mdp_kinship.txt -combine5 -  
input1 -input2 -input3 -intersect -combine6 -input5 -  
input4 -mlm -export mlm_output_tutorial -runfork1 -  
runfork2 -runfork3 -runfork4
```

Tassel Pipeline MLM Example...



Tassel Pipeline Documentation...

<http://www.maizegenetics.net/tassel/docs/TasselPipelineCLI.pdf>