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# TASSEL: MLM/GLM Pipeline: *Guide to using Tassel Pipeline*

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## Prerequisites

- Java SDK 5.0 or later (<http://java.sun.com/javase/downloads/index.jsp>).
- Tassel Standalone Build ([http://www.maizegenetics.net/tassel/tassel2.1\\_standalone.zip](http://www.maizegenetics.net/tassel/tassel2.1_standalone.zip))

## Source Code

- <http://tassel.cvs.sourceforge.net/tassel/maizegenetics>

## Install

Unzip the Tassel Standalone Build onto your file system. Change into the root directory:  
tassel2.1\_standalone.

## Execute

On Windows, see `run_file_input.bat` for an example how to execute the pipeline.

In Bash Shell, see `run_file_input.pl` for an example how to execute the pipeline. If you are using a UNIX operating system, you may need to change the following line to use a `:` instead of a `;`.

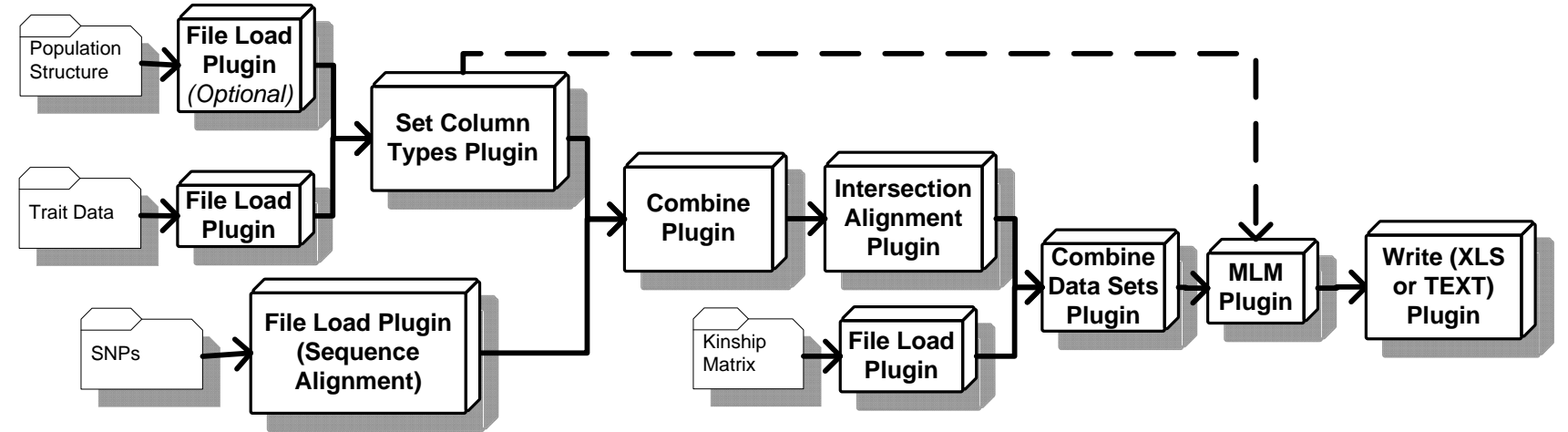
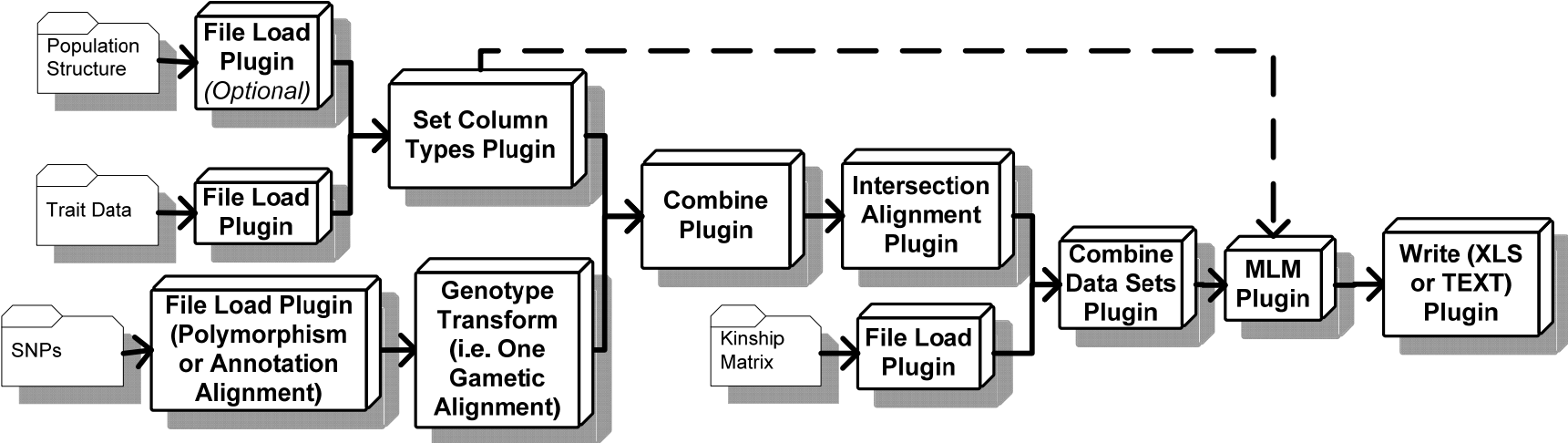
```
my $CP = join(";", @fl);
```

## Usage

```
java net.maizegenetics.pipeline.MLMGLMFileInputPipeline -t <trait
file> [-ct trait1,trait2,...] (-s <SNP file> | -p <Poly file> | -a
<Anno file>) [-gt Split|GenState|Dosage|OneGamete] [-q <population
file>] -o <output file> [-glm] [-mlm -k <kinship file>] [-xls | -txt]
[-abc true | false] [-mni <iterations>] [-mim true | false] [-fim true
| false]
```

-t <trait file>	trait data
-ct trait1,trait2	Optionally specify traits to be used as covariates. By default all traits are considered data. NOTE: Do not put spaces between trait names (only one comma).
Must specify either -s, -p or -a	
-s <SNP file>	SNP data (Loads as sequence alignment
-p <Poly file>	SNP data (Loads as polymorphism alignment
-a <Anno file>	Load annotated alignment.
-gt <transform>	Optionally specify genotype transform if loading polymorphism alignment or annotated alignment
Split	Multiple alignments by gamete
GenState	Alignment based on genotypic state (e.g. A:a > Aa) (DEFAULT)
Dosage	Dosage state (additive & dominant)
OneGamete	One gametic alignment
-q <population file>	optional population data
-k <kinship file>	kinship data needed for mlm analysis
-o <output file>	output file
-xls   -txt	kinship data needed for mlm analysis
-glm	optionally specifies to run glm analysis
-mlm	optionally specifies to run mlm analysis
-abc true   false	optionally specifies whether to Analyze by Column (default: false)
-mni <iterations>	optionally specifies Maximum Number of Iterations (only for MLM, default: 200)
-mim true   false	optionally specifies whether Markers used in Model (only for GLM, default: true)
-fim true   false	optionally specifies whether to use full model (reduced model if false) (only for MLM, default: false)

# Appendix A: MLM Pipeline Diagrams



## Appendix B: GLM Pipeline Diagrams

