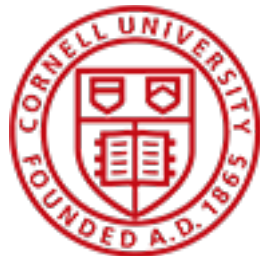


Tassel 5 Pipeline Tutorial (*Command Line Interface*)

Terry Casstevens

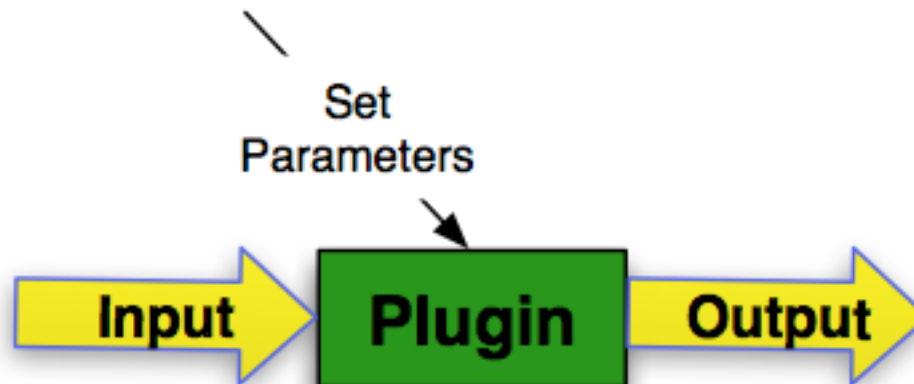
Institute for Genomic Diversity, Cornell University

March 30, 2016



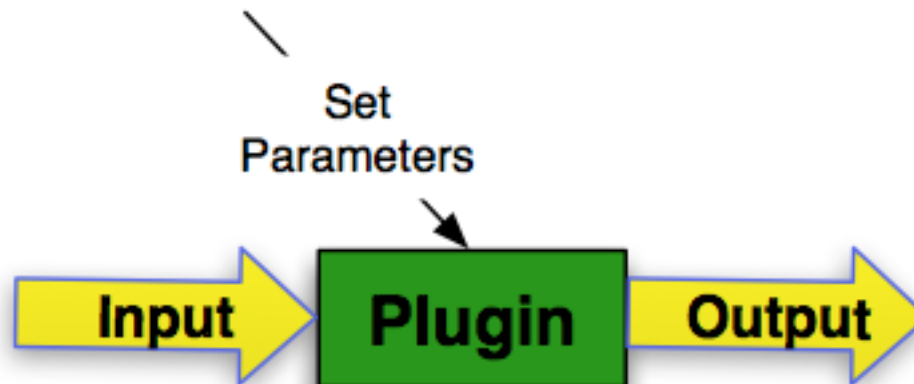
Tassel Plugin...

- Plugins are **Modularized Functionality** (i.e. import, export, GLM, MLM, Kinship, LD, etc.)
- First step is to **set parameters**. Although this could be optional as, defaults may be provided or there are none.
- **Input** may come from the Output of another Plugin.
- The Plugin may produce **Output**.



Setting Plugin Parameters...

- **-flag (true or false)**
 - **-includeSites**
 - **-includeSites false**
- **-flag <value>**
 - **-siteMinAlleleFreq 0.01**



Tassel Pipeline...

- Plugins can be chained together.

```
./run_pipeline.pl <plugin> <plugin> <plugin>
```



Tassel Plugin Usage...

- Some are **Legacy Flags (i.e. doesn't use -endPlugin)**

<https://bitbucket.org/tasseladmin/tassel-5-source/wiki/docs/Tassel5PipelineCLI.pdf>

-importGuess

-intersect

- Others follow our **Preferred Plugin Design**

<https://bitbucket.org/tasseladmin/tassel-5-source/wiki/docs/TasselSelfDescribingPlugin.pdf>

<Plugin Name> <Parameters> -endPlugin

-KinshipPlugin -method Centered_IBS -endPlugin

Tassel Available Plugins...

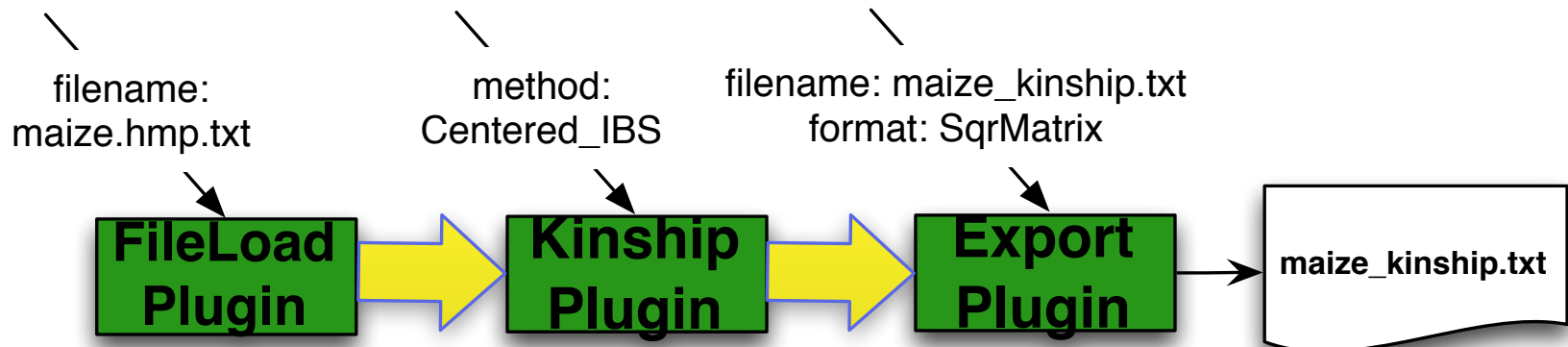
(Plugins following preferred design)

`./run_pipeline.pl -ListPlugins`

`./run_pipeline.pl -ListPlugins -usage true`

Example Tassel Pipeline...

```
./run_pipeline.pl -importGuess maize.hmp.txt  
-KinshipPlugin -method Centered_IBS -endPlugin  
-export maize_kinship.txt -exportType SqrMatrix
```

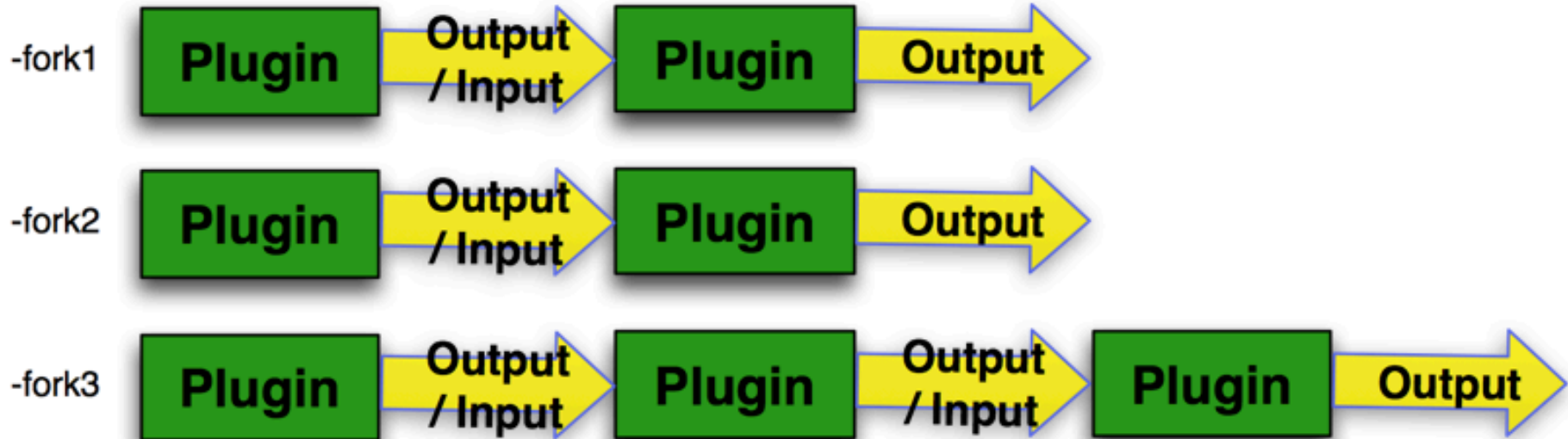


Tassel Pipeline Forks...

- Pipelines can consist of **multiple** Pipeline Forks (i.e. **Sub-Pipelines**).
- Defined by **-fork** or **-combine** flags. (Not needed if only one fork).
- **-combine** only used when combining output from multiple Plugins, as input to a single Plugin.
- Each Fork has a **name** (i.e. **-fork1**, **-combineA**).
- **Output** from a Sub-Pipeline can be used as **Input** to a another Sub-Pipeline by referencing with the flag **-input**. (i.e. **-input1**)
- Each Sub-Pipeline (i.e. **-fork**) runs in it's **own CPU Process** (i.e. Thread)

Tassel Pipeline Forks...

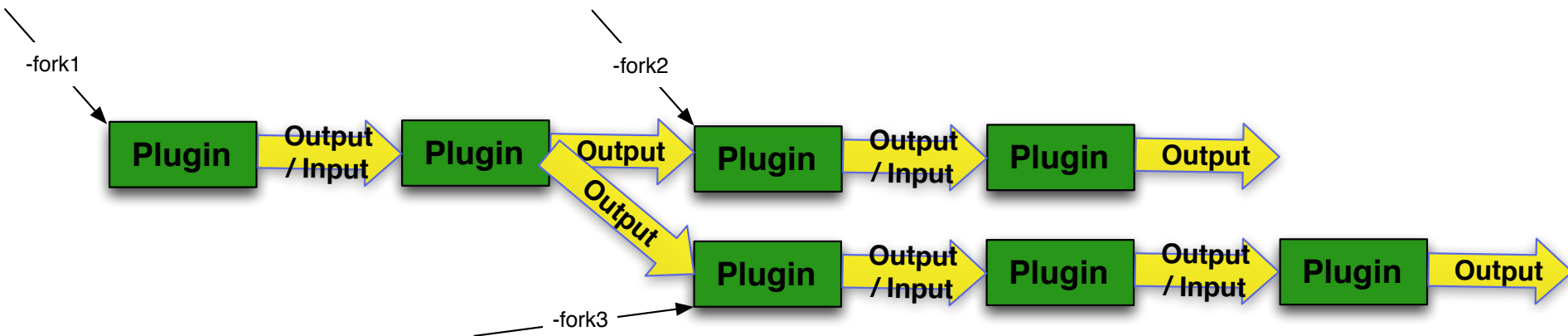
```
./run_pipeline.pl -fork1 <plugin> <plugin> -fork2  
<plugin> <plugin> -fork3 <plugin> <plugin> <plugin>
```



Tassel Pipeline Inputs...

(Output Used as Input Twice)

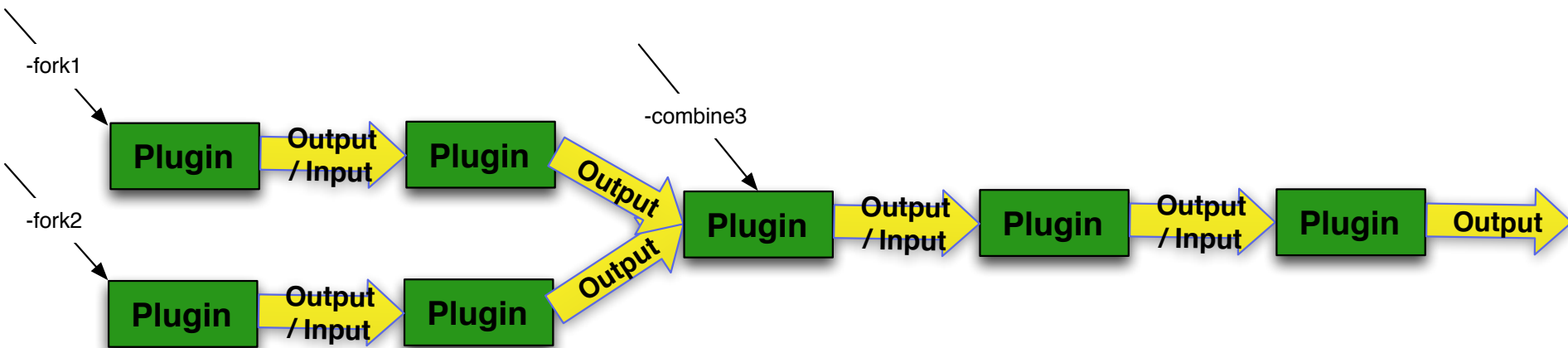
```
./run_pipeline.pl -fork1 <plugin> <plugin> -fork2  
<plugin> -input1 <plugin> -fork3 <plugin> -input1  
<plugin> <plugin>
```



Tassel Pipeline Inputs...

(Two Outputs Combined into One Input)

```
./run_pipeline.pl -fork1 <plugin> <plugin> -fork2  
<plugin> <plugin> -combine3 -input1 -input2 <plugin>  
<plugin> <plugin>
```



Tassel Pipeline Inputs...

(Incorrect Usages!)

This -input1 doesn't follow a Plugin or a -combine flag.

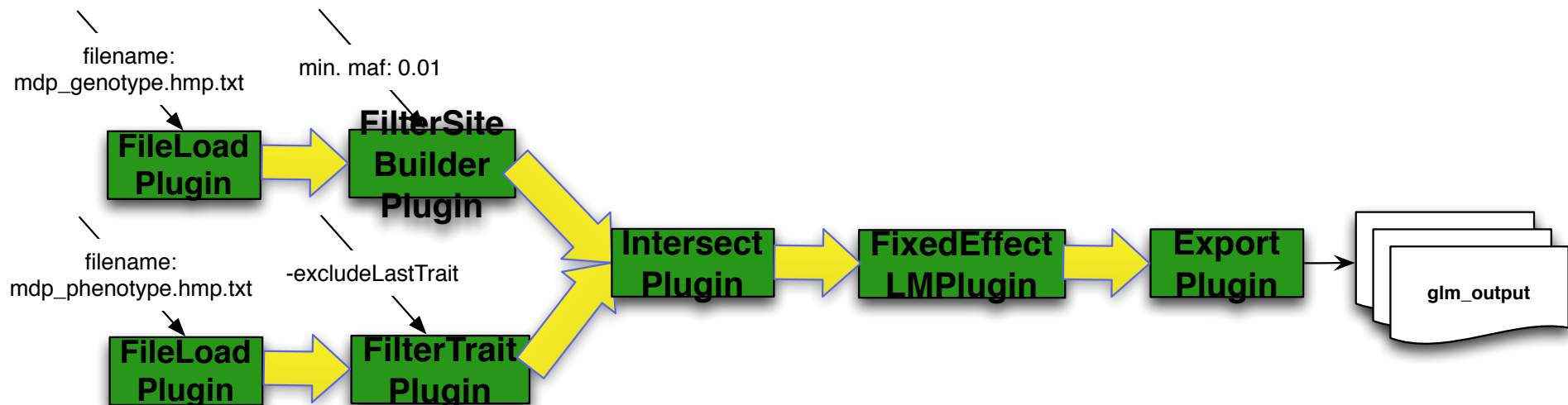
```
./run_pipeline.pl -fork1 <plugin> <plugin> -fork2  
-input1 <plugin> <plugin>
```

pluginB getting input from pluginA and -input1

```
./run_pipeline.pl -fork1 <plugin> <plugin> -fork2  
<pluginA> <pluginB> -input1
```

Tassel Pipeline GLM Example...

```
./run_pipeline.pl -fork1 -importGuess  
mdp_genotype.hmp.txt -FilterSiteBuilderPlugin  
-siteMinAlleleFreq 0.01 -endPlugin -fork2  
-importGuess mdp_phenotype.txt -excludeLastTrait  
-combine3 -input1 -input2 -intersect  
-FixedEffectLMPlugin -endPlugin -export glm_output
```



Tassel Pipeline Options...

*Run in **debug mode***

`./run_pipeline.pl -debug [<filename>] ...`

*Set **maximum heap size***

`./run_pipeline.pl -Xmx10g ...`

*Get **usage** for a plugin*

`./run_pipeline.pl <Plugin Name> -help`