SpoonFedNanopore

Just Works™

Goals

➔ Super simple
➔ Educational
➔ Reads -> Assembly + taxa info
➔ Use cases
  ◆ Undergrad/HS teaching
  ◆ Remote areas with limited access to resources

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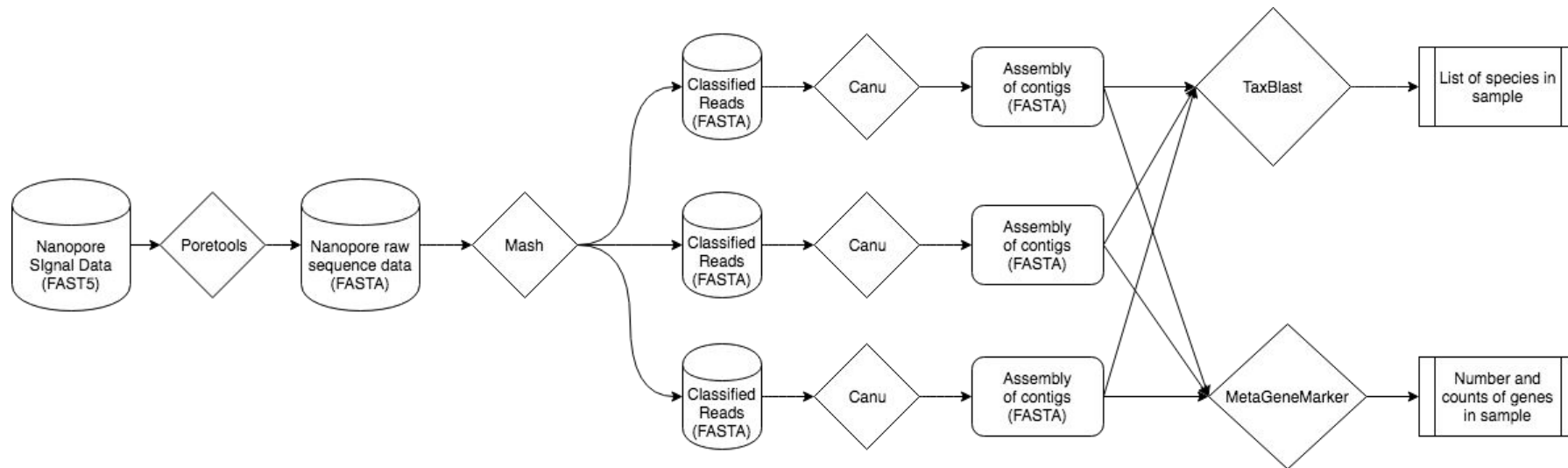   ◆ Undergrad/HS teaching
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Workflow diagram

How to Jupyter will look

In [18]: `directory='/mnt/borage/nick/nanopore/data/Flowcell6/downloads'`

In [65]: `!find $directory -maxdepth 1 -name "*.fast5" | wc -l`

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There are 60,196 FAST5 files in the directory.

poretools has a number of different command line options. Running **poretools** with no parameters gives us a brief list (and complies with Torsten's first rule)

In [21]: `!poretools`

```
usage: poretools [-h] [-v]

                  {combine,fastq,fasta,stats,hist,events,readstats,tabular,nucdist,qualdist,winner,squiggle,times,yield_p
                  ...
poretools: error: too few arguments
```

We can get more information if we run **poretools** with the -h (help) option.

In [22]: `!poretools -h`

```
usage: poretools [-h] [-v]

                  {combine,fastq,fasta,stats,hist,events,readstats,tabular,nucdist,qualdist,winner,squiggle,times,yield_p
                  ...

optional arguments:
  -h, --help            show this help message and exit
  -v, --version         Installed poretools version
```

Difficulties so far

➔ Canu has been difficult to get running, debugging + alternatives
➔ BLAST-ing contigs is slow/doesn't work (CPU Limit errors)?
➔ Offline BLAST databases
➔ How to package everything so it Just Works™