

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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Aaron Pomerantz

@AaronPomerantz

Follow

Welcome to my laboratory :)

Sequencing long ribosomal cluster from plants, insects & fungi in real-time in the Amazon rainforest. Within a few mins of [@nanopore](#) data generated, performed BLAST & got correct hits! Dual indexing looks great for pooling many samples [#junglegenomics](#)



0:20 6,505 views

11:23 AM - 2 Apr 2018

147 Retweets 434 Likes



10



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Aaron Pomerantz @AaronPomerantz · 24h

Will be so much fun when pipelines automatically generate consensus sequences & align to database (like WIMP but for all of life). Lyophilized reagents & cheaper flow cells (flongle) will be fantastic for remote areas, perform rapid biodiversity & conservation assessments

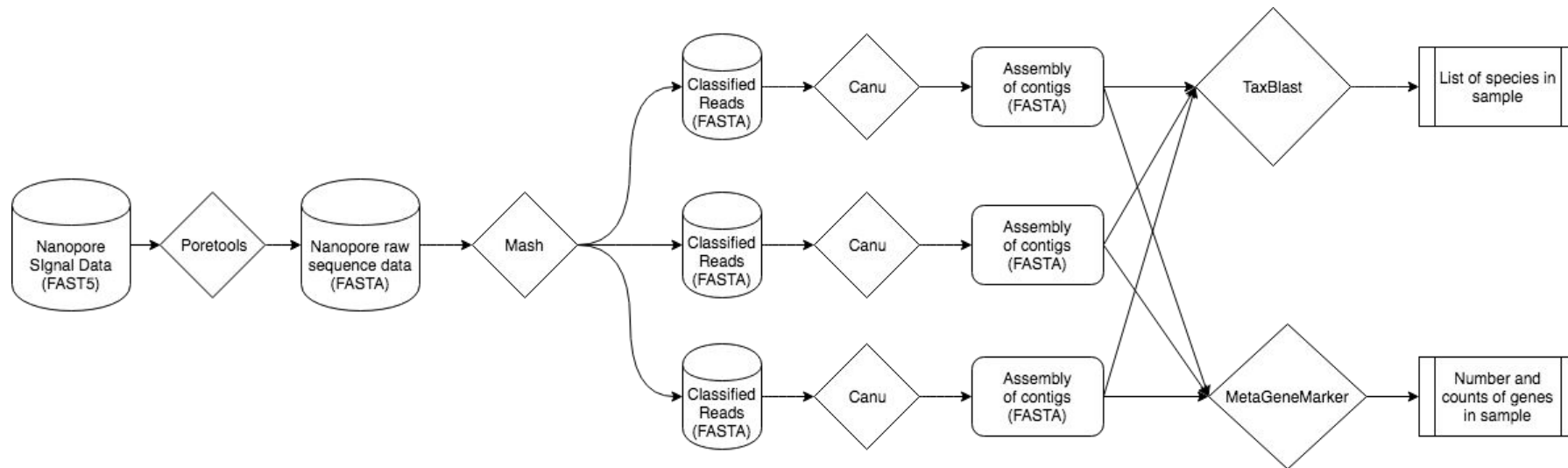
2

3

10



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
```

```
60196
```

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™