

# GopherPipelines

## ArgHandling

```
args.py
usage()
pipeline_args()
```

import

```
bulk_rnaseq_args.py
add_args(parser)
```

```
sc_rnaseq_args.py
add_args(parser)
```

import

```
set_verbosity.py
verb(level, name)
```

import

## Pipelines

```
Pipeline.py
class Pipeline(object)
```

import

```
BulkRNASeq.py
class BulkRNASeqPipeline(Pipeline)
```

## FileOps

```
default_dirs.py
default_output(pipeline)
```

import

import

```
dir_funcs.py
```

```
dir_exists(d)
dir_writeable(d)
dir_empty(d)
```

import

## SampleSheet

```
Samplesheet.py
class SampleSheet(object)
```

import

```
Sample.py
class Sample(object)
```

User Bash Shell

python3

```
gopher_pipelines.py
brnaseq(args)
main()
```

import

import

pipeline.sh

subprocess.call()

qsub

```
single_sample.template.pbs
```

qsub

```
run_summary_stats.pbs
```

R CMD Batch

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subread.r

tpm.r

prep.r