

GopherPipelines

ArgHandling

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

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

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

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

FileOps

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

```
dir_funcs.py
```

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

SampleSheet

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

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

Pipelines

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

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

User Bash Shell

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

```
pipeline.sh
```

```
single_sample.template.pbs
```

```
run_summary_stats.pbs
```

```
subread.r
```

```
tpm.r
```

```
prep.r
```

python3

import

import

import

import

import

import

import

import

subprocess.call()

import

import

qsub

qsub

R CMD Batch

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