## Pipeline fq dir: pathlib.Path outdir: pathlib.Path required mods: list sample sheet: list init (self, args) check dirs(self) prepare\_samplesheet(self, ss=None) setup workdir(self) prepare\_qsub(self) BulkRNASeqPipeline pipe\_name: str init (self, args) summarize\_counts(self) SCRNASeqPipeline pipe name: str init (self, args)

## SampleSheet Sample samples: list name: str r1: str r2: str tech: str trim\_opt: str hisat\_opt: str init (self, args) write sheet(self) \_init\_\_(self, args) parse\_umgc(self, u) resolve\_options(self) build\_from\_dir(self, d) sanitize\_paths(self)