## Pipeline sample\_sheet: list programs: list useropts: dict defaultopts: dict finalopts: dict logger: Logging.Logger \_init\_\_(self, args) check\_dirs(self) resolve\_options(self) prepare\_samplesheet(self, ss=None) setup\_workdir(self) prepare\_qsub(self) BulkRNASeqPipeline pipe name: str pipe\_logger: Logging.Logger init (self, args) validate\_hisat\_idx(self) SCRNASeqPipeline

## scrnaseqPipeline pipe\_name: str \_\_init\_\_(self, args)

