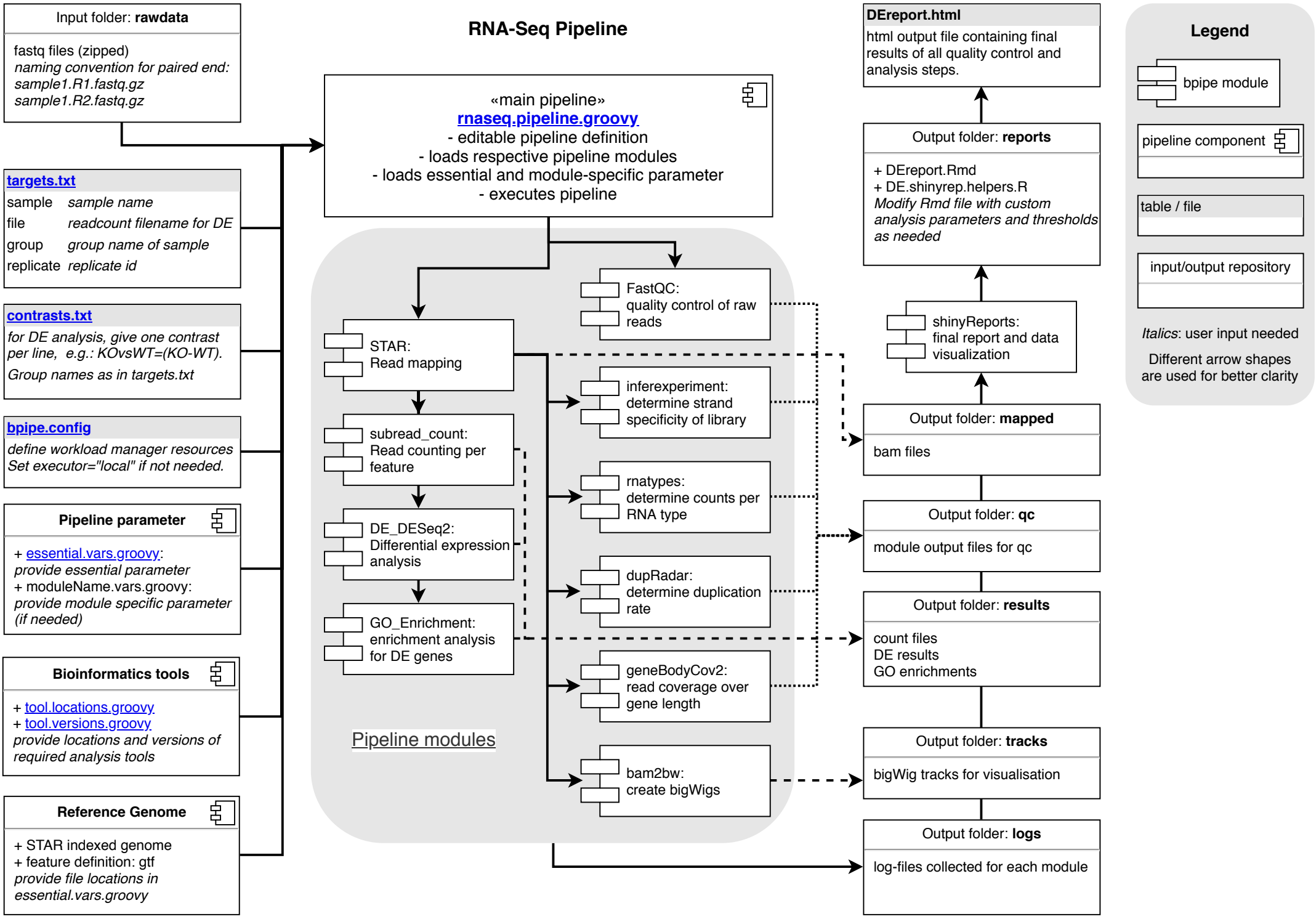
RNA-Seq Pipeline
Input folder: rawdata
fastq files (zipped)
naming convention for paired end:
sample1.R1.fastq.gz
sample1.R2.fastq.gz
«main pipeline»
rnaseq.pipeline.groovy
- editable pipeline definition
- loads respective pipeline modules
- loads essential and module-specific parameter
- executes pipeline
targets.txt
sample sample name
file readcount filename for DE
group group name of sample
replicate replicate id
contrasts.txt
for DE analysis, give one contrast per line, e.g.: KOvsWT=(KO-WT).
Group names as in targets.txt
bpipe.config
define workload manager resources
Set executor="local" if not needed.
Pipeline parameter
+ essential.vars.groovy:
provide essential parameter
+ moduleName.vars.groovy:
provide module specific parameter (if needed)
Bioinformatics tools
+ tool.locations.groovy
+ tool.versions.groovy
provide locations and versions of required analysis tools
Reference Genome
+ STAR indexed genome
+ feature definition: gtf
provide file locations in essential.vars.groovy
STAR: Read mapping
subread_count: Read counting per feature
DE_DESeq2: Differential expression analysis
GO_Enrichment: enrichment analysis for DE genes
FastQC: quality control of raw reads
inferexperiment: determine strand specificity of library
rnatypes: determine counts per RNA type
dupRadar: determine duplication rate
geneBodyCov2: read coverage over gene length
bam2bw: create bigWigs
Pipeline modules
DEreport.html
html output file containing final results of all quality control and analysis steps.
Output folder: reports
+ DEreport.Rmd
+ DE.shinyrep.helpers.R
Modify Rmd file with custom analysis parameters and thresholds as needed
shinyReports: final report and data visualization
Output folder: mapped
bam files
Output folder: qc
module output files for qc
Output folder: results
count files
DE results
GO enrichments
Output folder: tracks
bigWig tracks for visualisation
Output folder: logs
log-files collected for each module
Legend
bpipe module
pipeline component
table / file
input/output repository
Italics: user input needed
Different arrow shapes are used for better clarity