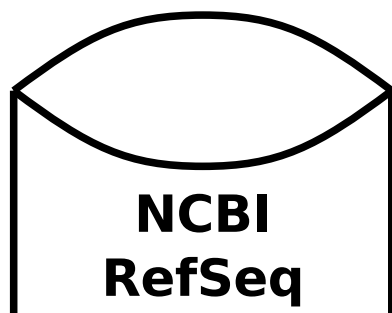


**internal
standards
.fna**





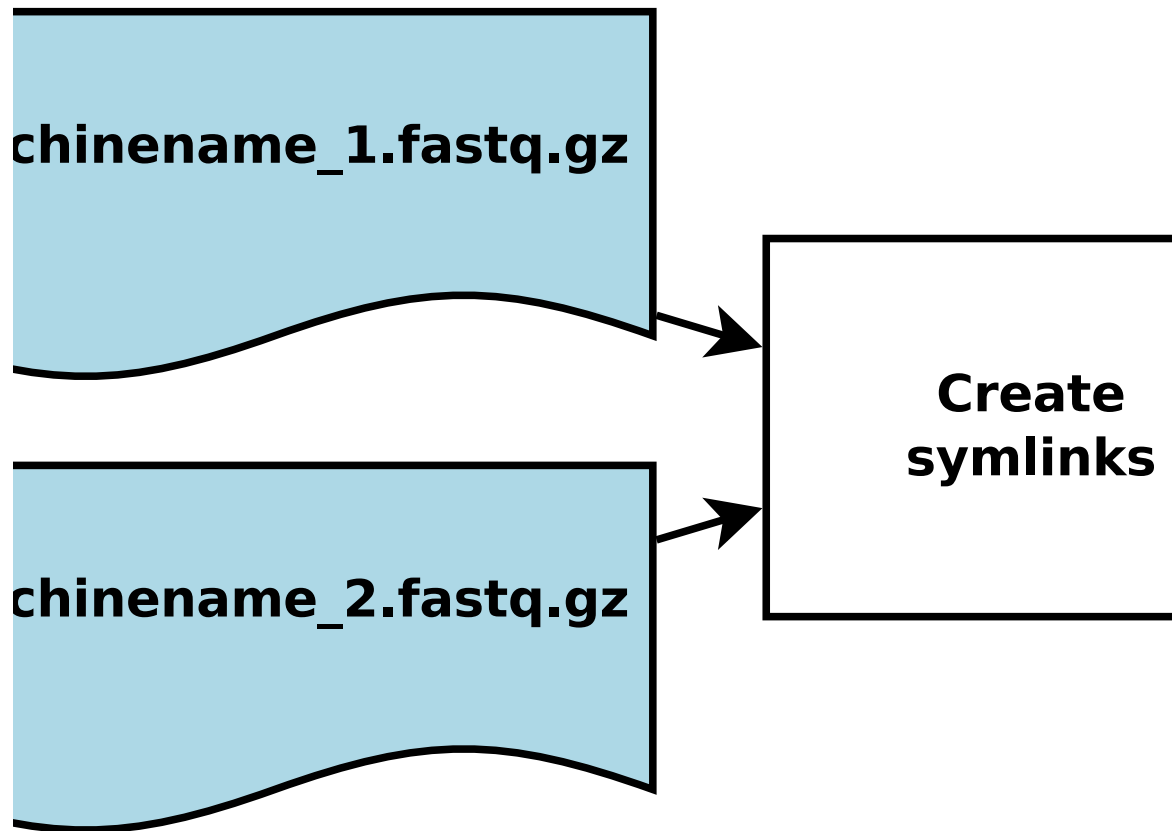
refseq2taxonomy

refseq2go

refseq2interpro

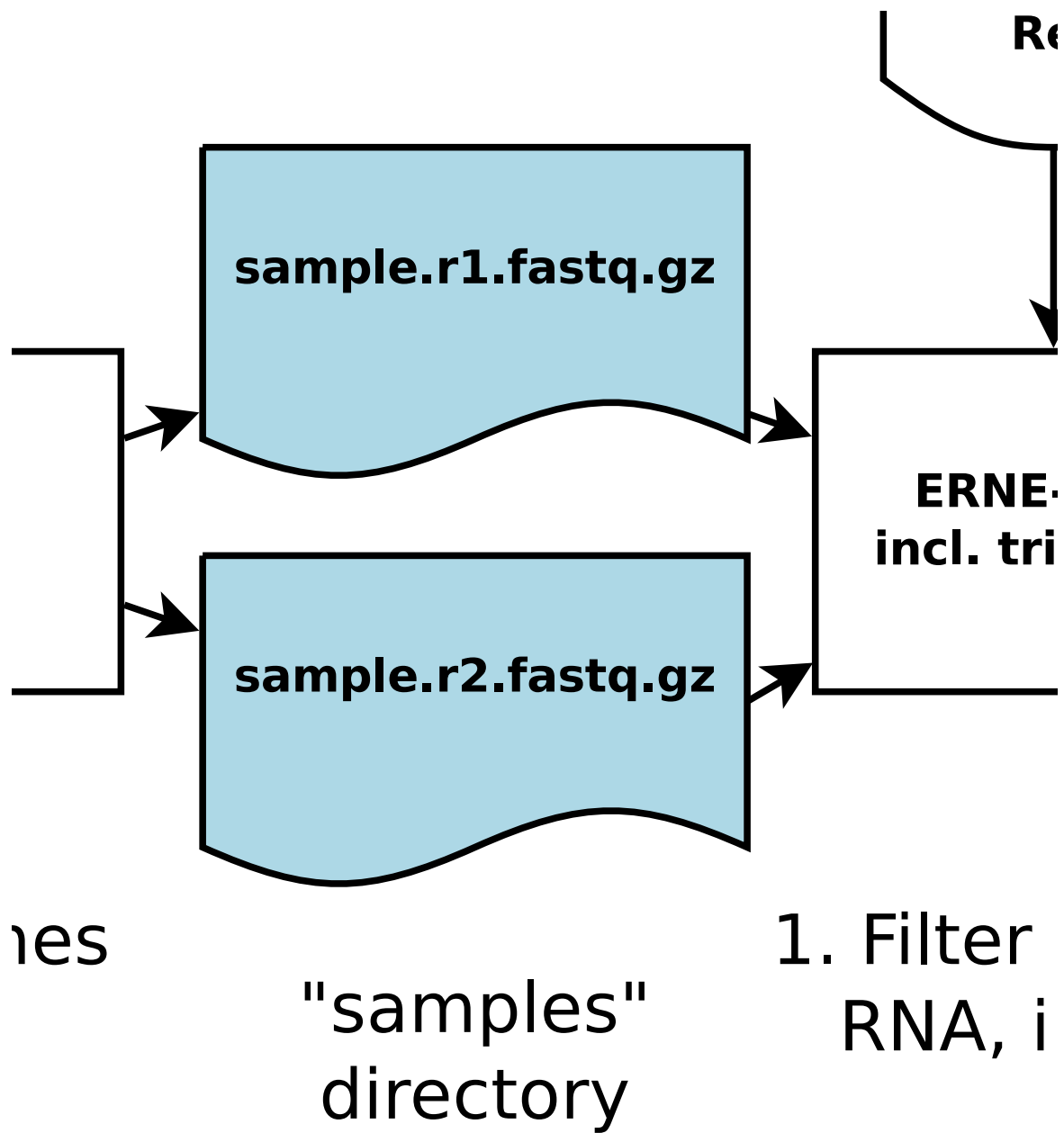
refseq2seed





project root
directory

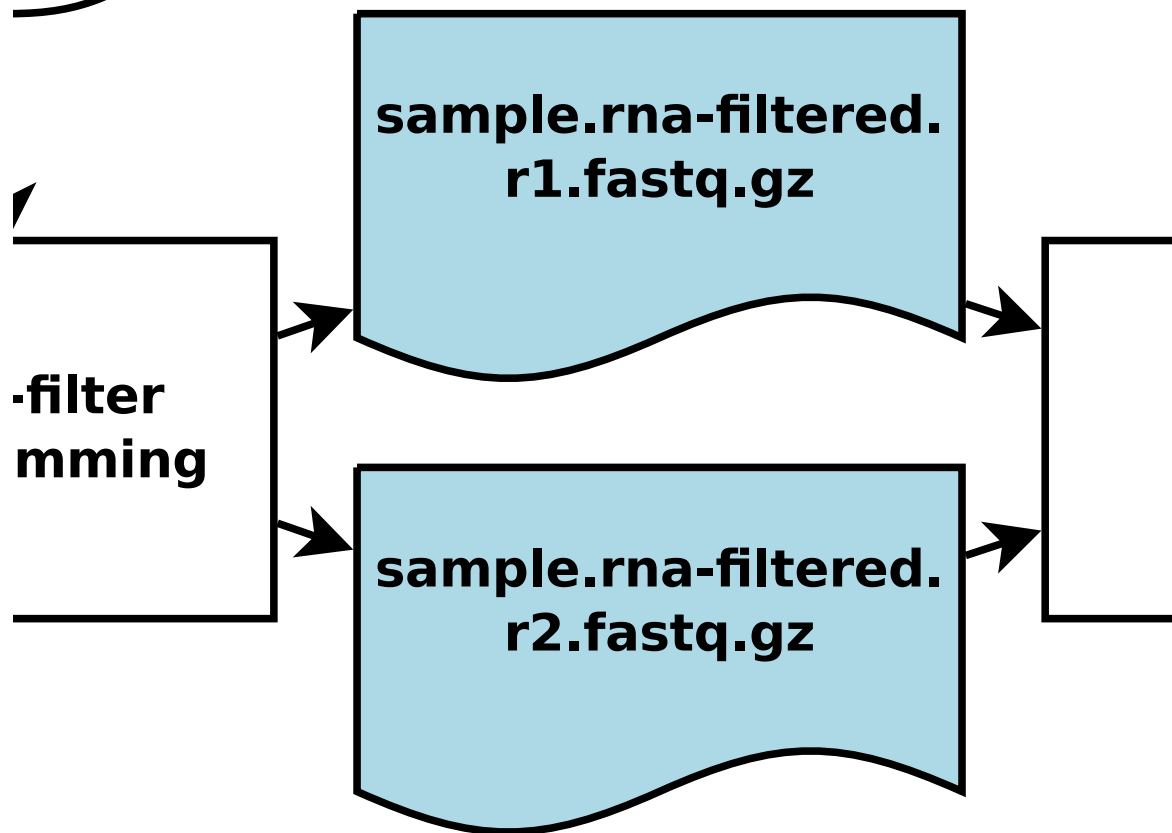
0. Translate name
of files from
sequencing to
sample names



ies

5

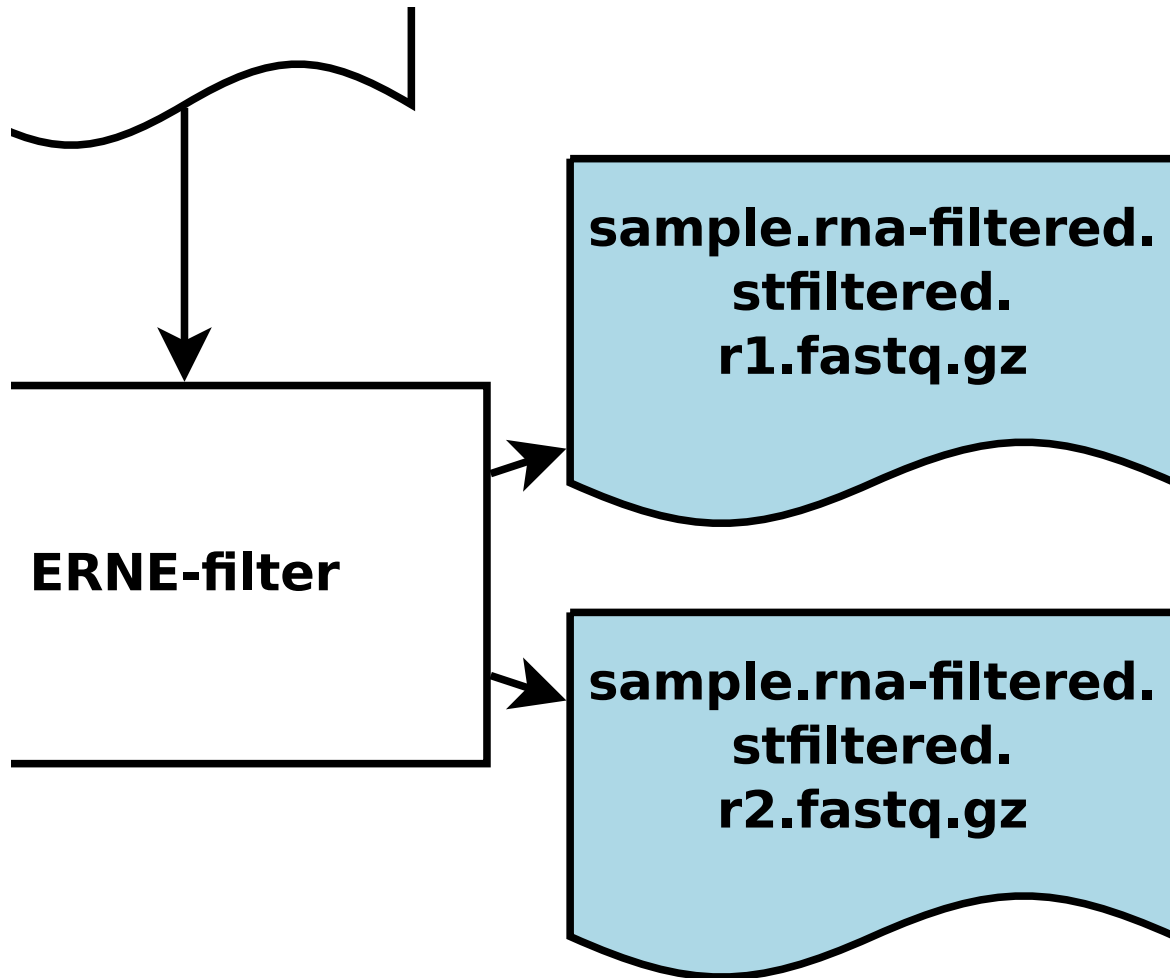
ef



out stable
.e. rRNA

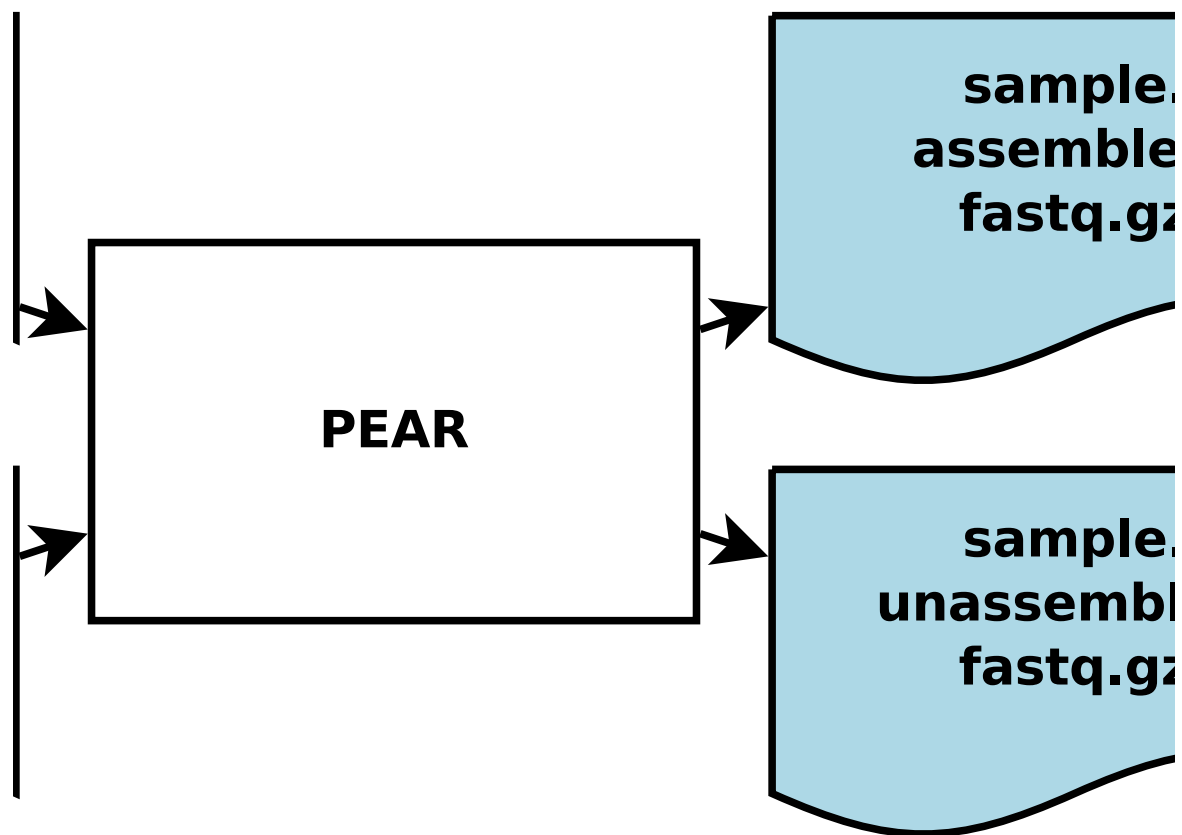
"erne-rrna"
directory

2. Opt
out
intern
sec



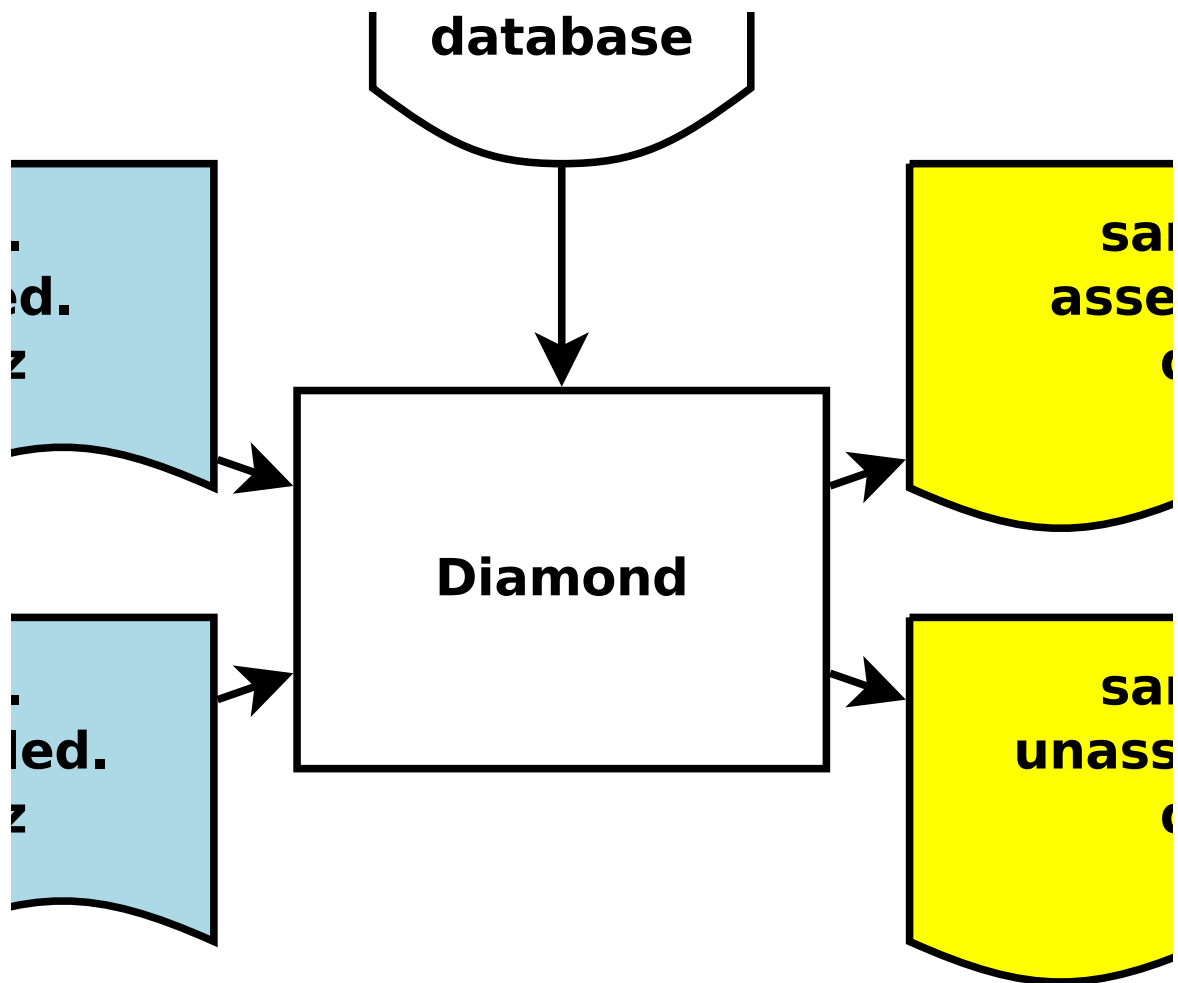
ditional: Filter
: added
al standard
quences

"erne-standards
directory



3. "Assemble"
pairs into one
sequence

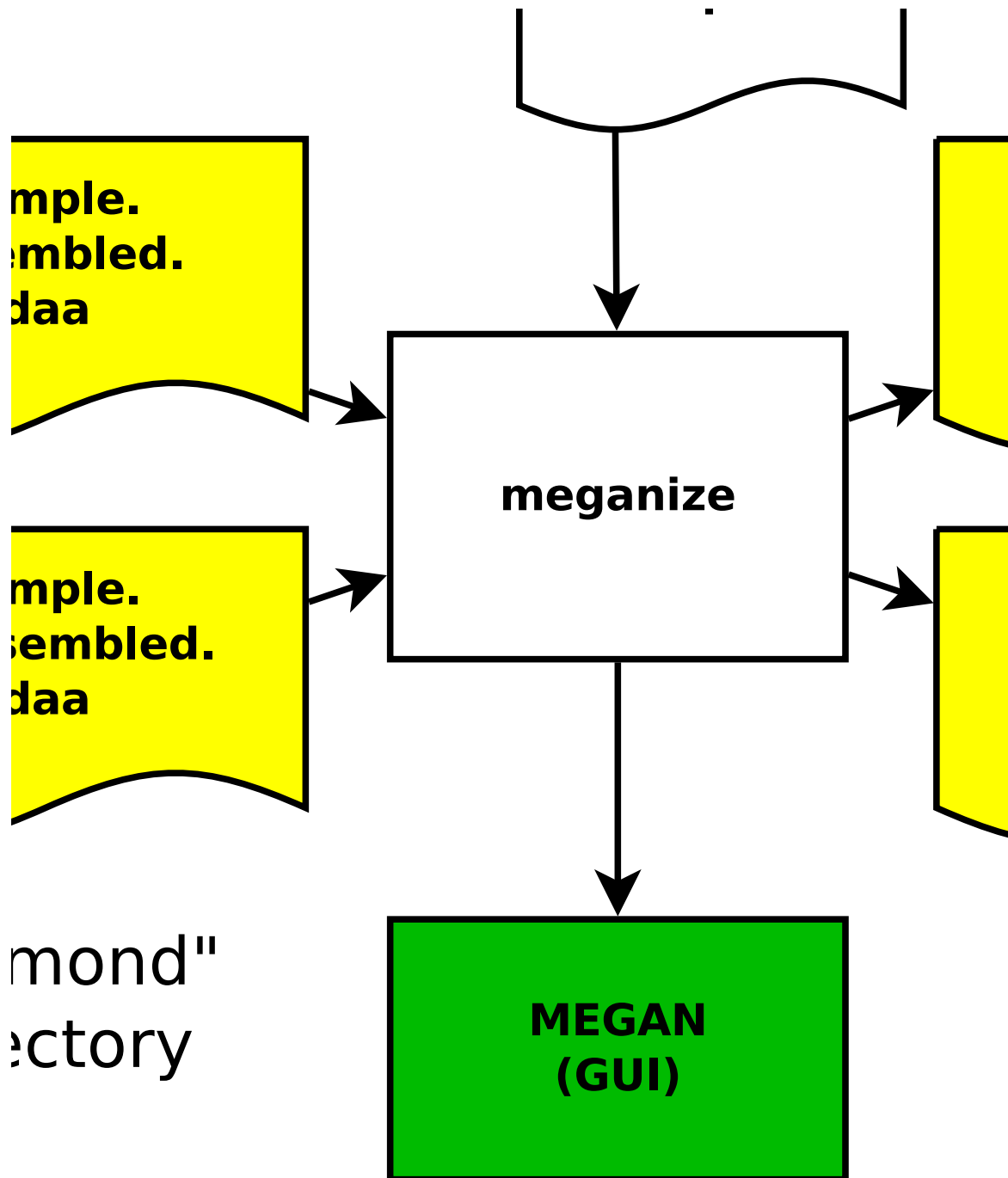
"pear"
directo



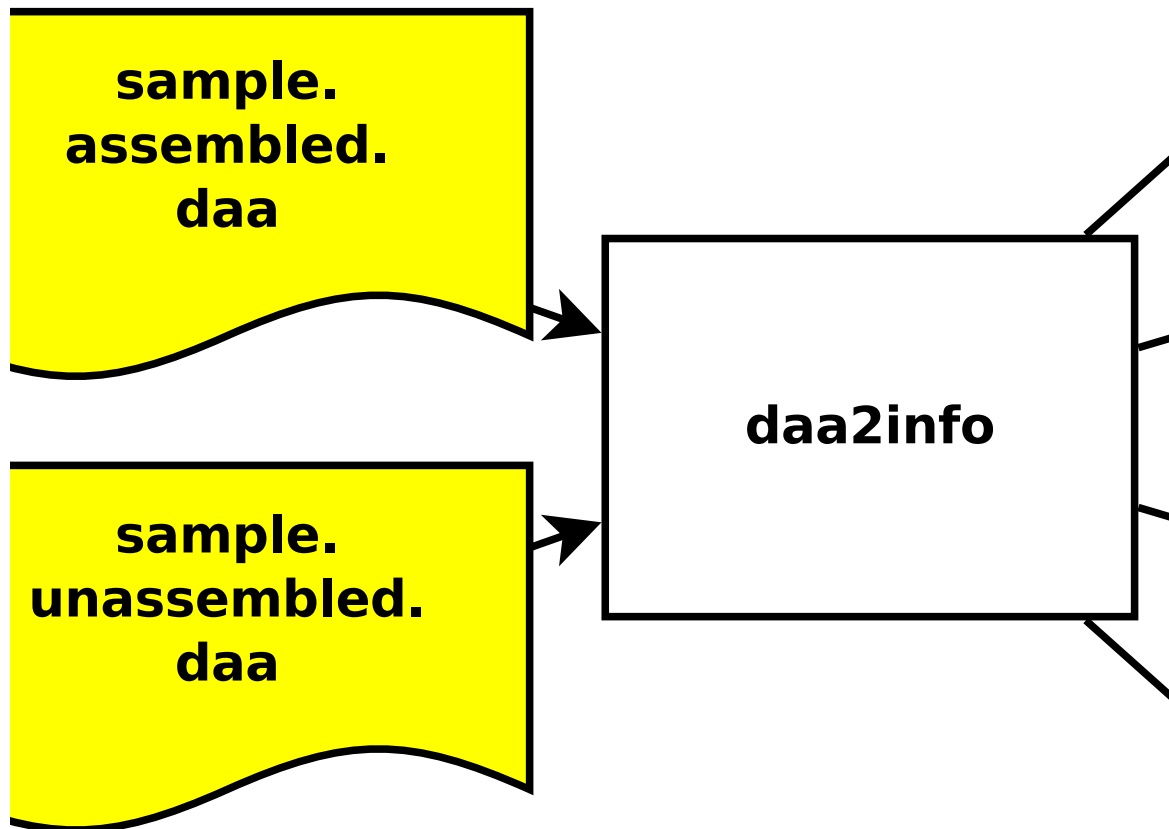
4. Align all reads
to the RefSeq
database

"
ry

"dial
dire



5. Transform
output from
diamond into
MEGAN files



"diamond"
directory

6. Export tab
separated
files for use in
e.g. R