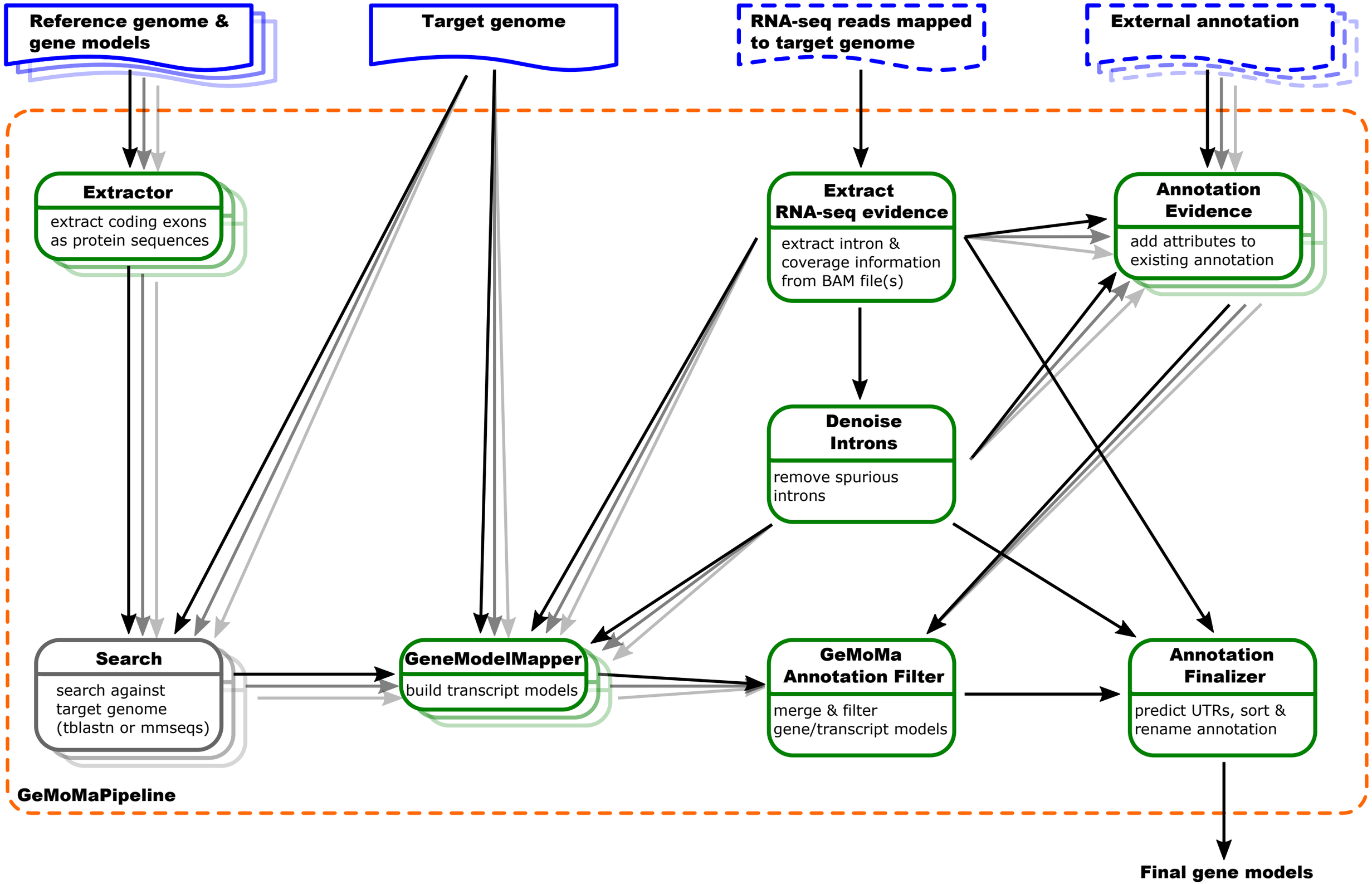
Reference genome & gene models
Target genome
RNA-seq reads mapped to target genome
External annotation
Extractor
extract coding exons as protein sequences
Extract RNA-seq evidence
extract intron & coverage information from BAM file(s)
Annotation Evidence
add attributes to existing annotation
Denoise Introns
remove spurious introns
Search
search against target genome (tblastn or mmseqs)
GeneModelMapper
build transcript models
GeMoMa Annotation Filter
merge & filter gene/transcript models
Annotation Finalizer
predict UTRs, sort & rename annotation
GeMoMaPipeline
Final gene models