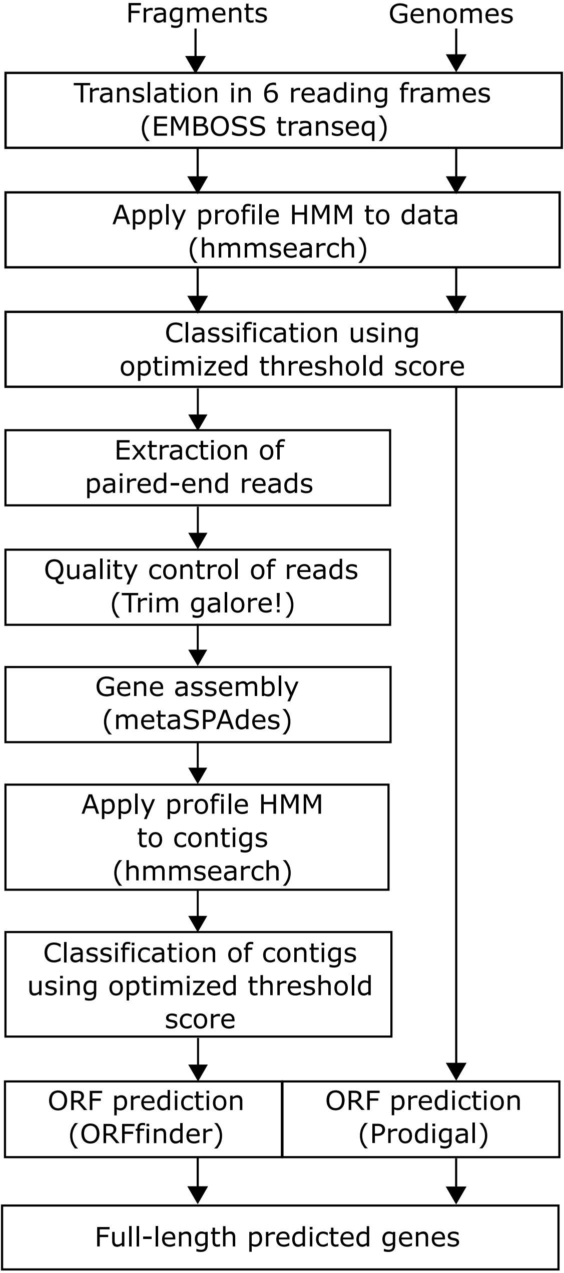
Fragments
Genomes
Translation in 6 reading frames (EMBOSS transeq)
Apply profile HMM to data (hmmsearch)
Classification using optimized threshold score
Extraction of paired-end reads
Quality control of reads (Trim galore!)
Gene assembly (metaSPAdes)
Apply profile HMM to contigs (hmmsearch)
Classification of contigs using optimized threshold score
ORF prediction (ORFfinder)
ORF prediction (Prodigal)
Full-length predicted genes