Module	Description
transMap	Uses the cactus alignment to project the reference annotation onto each target genome. Transcript projections are then filtered based on alignment metrics to resolve paralogous alignments. Produces an unfiltered and filtered alignment and transcript set.
Alignment classification	Populates the database with transMap metrics, including alignment metrics, valid start/stop codons, and analysis of synteny and gap spanning.
AugustusTMR	Takes each individual transMap transcript projection and passes it through AUGUSTUS, cleaning up transcript projections. If RNA-seq is provided, repeats the process allowing the RNA-seq to influence the results. Produces a transcript set for each mode.
AugustusPB	Takes long read RNA-seq and produces an annotation set suitable for discovering novel isoforms.
AugustusCGP	Performs simultaneous comparative gene prediction across all species in the alignment, using all extrinsic evidence. Produces an annotation set for each genome.
Gene assignment	Takes transcripts from AugustusPB/AugustusCGP and compares them to the output of transMap, determining if predictions overlap projection transcripts in the filtered and unfiltered sets to determine if they are novel, paralogous or a known gene
Transcript alignment	Performs pairwise BLAT between each transMap projection as well as the output of AugustusTMR with the source transcript.
homGeneMapping	Runs the homGeneMapping tool, which transfers annotations and extrinsic evidence across all pairwise combinations in the alignment, providing evidence for cross-species support.
Transcript classification	Uses the output of transcript alignment to evaluate the structure of transcripts, including indels and splice site shifts.
Consensus finding	Uses the output of each transcript prediction mode as well as transcript classification and alignment classification to determine which transcript prediction best matches the source transcript. Filters transcript sets based on user parameters. Combines AugustusPB and AugustusCGP predictions, finding novel loci and isoforms.