# general params
ASSEMBLY_VERSION = assembly3.0
PREDICTION_VERSION = prediction4.0
EASYGENE_RESULTS_FILE = easygene_results_assembly3.0.txt
ISFINDER_RESULTS_FILE = tabular_results_assembly3.0.txt

# output file names and preferences
FASTA_NUM_CHARS_PER_LINE = 60
RAW_GENE_PREDICTIONS_OUTFILE = raw_gene_predictions.gff
CONSENSUS_GFF_OUTFILE = consensus.genes.gff
CONSENSUS_FASTA_OUTFILE = consensus.genes.fna
TRNA_GFF_OUTFILE = tRNAs.gff
TRNA_FASTA_OUTFILE = tRNAs.fna
RRNA_GFF_OUTFILE = rRNAs.gff
RRNA_FASTA_OUTFILE = rRNAs.fna
IS_GFF_OUTFILE = is_elements.gff
IS_FASTA_OUTFILE = is_elements.fna
IS_GFF_HIGH_QUAL_OUTFILE = is_elements_high_qual.gff
IS_FASTA_HIGH_QUAL_OUTFILE = is_elements_high_qual.fna

# BLAST options
BLAST_ANNOTATED_CDS_SEQS_FILE = /compgenomics2009/prediction/src/Neisseria_meningitidis_Z2491.fnn
# the blast variants used to run search, parameter should be tested
BLAST_PROGRAM = blastn
# evaluate threshold, parameter should be tested
BLAST_EVALUE_FILTER = 1e-05
# Blast hits' length threshold, parameter should be tested
BLAST_MIN_LENGTH_FILTER = 90
# Blast hits' length divided by the query sequence length, parameter should be tested
BLAST_MIN_RATIO_FILTER = 0.5

# GeneMark.hmm model file
GM_MODEL_FILE = /compgenomics2009/prediction/gememark/models/hmm/Neisseria_meningitidis_Z2491.mod

# tRNAscanSE genetic code
TRNASCANASE_ALT_GENETIC_CODE = /compgenomics2009/prediction/tRNAscan/gcode.txt

# RNAmmer installation location
RNAMMER_PROGRAM = /compgenomics2009/prediction/rnammer-1.2/rnammer

# IS Finder options
ISFINDER_EVALUE_FILTER = 1e-10
ISFINDER_PERC_COVERAGE_FILTER = 0.5
ISFINDER_HIGH_QUAL_EVALUE_FILTER = 1e-10
ISFINDER_HIGH_QUAL_PERC_COVERAGE_FILTER = 0.9
ISFINDER_INFO_FILE = /compgenomics2009/prediction/is_finder_results/is_finder_info_table.txt