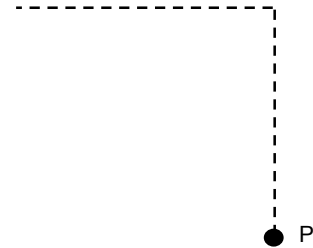
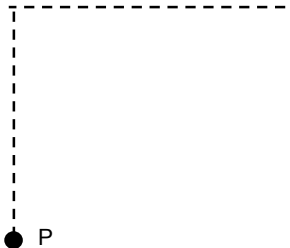


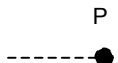
### genome\_versions

genome_vers_id
unix_name
tax_id
lineage
source_id_list
num_proteins
num_scaffolds
completion
source_db
site_id
rev_date
minGC
maxGC
meanGC
stdevGC



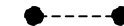
### searches

search_id
genome_vers_id
query_filename
blast_tab_filename
min_coverage
threshold
num_matches
raw_lpi_max
search_date
dh_version
excl_keywords
excl_level



### matches

match_num
search_id
query_id
bestmatch_id
raw_lpi
norm_lpi
num_db_matches
cand_set_size
align_length
pct_query_coverage
bitscore
evaluate



### queries

query_id
genome_vers_id
locus_tag
refseq_id
gi_num
scaffold_id
start
stop
strand
annot
pct_GC
zscore_GC