

Chromid
<u>_record</u>
<u>_genome</u>
<u>_operons</u>
<u>_init__</u>
genome
record
accession_number
description
sequence
random_seq
random_seqs
promoter_regions
random_seq_from_promoters
length
subsequence
genes
protein_coding_genes
operons
genes_to_fasta
directons
operon_prediction
find_closest_gene
<u>_repr__</u>

BLAST
<u>_in_file</u>
<u>_db_file</u>
<u>_log_file</u>
<u>_seq_fasta</u>
<u>_db_type</u>
<u>_init__</u>
makeblastdb
search
tblastx
blastx
tblastn
get_best_hit
get_e_value

OrthologousGroup
<u>_genes</u>
<u>_regulation_states</u>
<u>_init__</u>
genes
description
member_from_genome
all_genes_from_genome
blast_eggnog_database
discretize_regulation_states
bootstrap_traits
get_terminal_states
ancestral_state_reconstruction
regulation_states
prob_regulation_at_root
most_likely_state_at
ancestral_state_reconstruction_svg_view
<u>_repr__</u>

BlastNoHitFoundException
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Exception
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OneStateException
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SiteCollection
<u>_TF</u>
<u>_name</u>
<u>_motif</u>
<u>_init__</u>
TF
name
pwm
IC
sites
site_count
length
to_jaspar

Protein
<u>_record</u>
<u>_init__</u>
record
accession_number
description
sequence
to_fasta
<u>_repr__</u>

TFBindingModel
<u>_metaclass</u>
<u>_background</u>
<u>_collection_set</u>
<u>_mu_m</u>
<u>_mu_bg</u>
<u>_init__</u>
background
site_collections
bayesian_estimator
build_bayesian_estimator
binding_probability
threshold
score_seq
length

PSSMModel
<u>_pwm</u>
<u>_init__</u>
pwm
length
psmm
rev_comp_psmm
alphabet
IC
patser_threshold
threshold
sites
score_self
<u>_calculate</u>
score_seq
weblogo_from_pwm
<u>_combine_pwmms</u>

Genome
<u>_strain_name</u>
<u>_chromids</u>
<u>_TF_instance</u>
<u>_TF_binding_model</u>
<u>_putative_sites</u>
<u>_init__</u>
strain_name
chromids
num_chromids
directons
intergenic_distance_threshold
operons
operon_prediction
length
num_operons
operons_to_csv
genes
protein_coding_genes
genes_to_fasta
blast_client
TF_instance
TF_instance
TF_binding_model
build_PSSM_model
random_seqs
get_gene_by_locus_tag
find_gene_homolog
find_protein_homolog
identify_TF_instance
calculate_regulation_probabilities
infer_regulons
<u>_output_posterior_probabilities</u>
<u>_putative_sites</u>
<u>_weblogo_from_putative_sites</u>
<u>_identify_sites</u>
<u>_output_identified_sites</u>
<u>_output_TF_binding_model</u>
<u>_PSSM_model_to_jaspar</u>
<u>_repr__</u>

Gene
<u>_index</u>
<u>_seq_feature</u>
<u>_product_feature</u>
<u>_chromid</u>
<u>_regulation_probability</u>
<u>_init__</u>
start
end
strand
sequence
length
is_forward_strand
operon
upstream_gene
upstream_noncoding_region_location
upstream_forward_strand_gene
upstream_reverse_strand_gene
upstream_noncoding_region_sequence
promoter_region
calculate_regulation_probability
regulation_probability
chromid
genome
db_xrefs
name
locus_tag
product_type
product
is_protein_coding_gene
protein_accession_number
to_protein
find_homolog_in_genome
reciprocal_blast_hit
distance
distance_to_region
to_fasta
<u>_repr__</u>

NotProteinCodingGeneException
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Operon
<u>_genes</u>
<u>_operon_id</u>
<u>_init__</u>
chromid
genes
operon_id
genome
strand
is_forward_strand
start
end
first_gene
regulation_probability
is_probably_regulated
<u>_repr__</u>

Phylo
<u>_proteins</u>
<u>_names</u>
<u>_distance_model</u>
<u>_tree_algorithm</u>
<u>_init__</u>
proteins
alignment
proteins_to_fasta_file
<u>_clustalo</u>
tree
tree_lookup
distance
draw_ascii
to_newick
to_nexus
draw
svg_view

UserInput
<u>_input</u>
<u>_init__</u>
genome_name_and_accessions
genome_names
protein_accessions
protein_names
sites_list
protein_accessions_and_sites
prior_regulation_probability
has_prior_probability_set
probability_threshold
phylogenetic_weighting
site_count_weighting
operon_prediction_probability_threshold
operon_prediction_distance_tuning_parameter
ancestral_state_reconstruction