

R-COMPLETE Documentation

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ToC

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(TODO : Add Omit list which negates from the total gene list of all organisms)

R - COMPLETE

Pipeline for extracting localization elements/motifs using a comparative approach. Library can be installed and tested on R(>=4.1). For a list of genes, the pipeline downloads full transcript sequences for all organisms (or selected organisms) from ENSEMBL or NCBI, Formats the headers and stores them according to the clusters (optionally taken from [OrthoDB](#) or clustered otherwise). Sequences without cluster information are clustered based on sequence identity/sequence coverage of Reciprocal Bidirectional BLAST Hits (RBH) of CDS regions. Next step would be to stitch the transcript regions into full length transcripts and align them. Pipeline is format agnostic(to my knowledge - TMK), packaged with a multi-threaded BLAST framework, to BLAST directly from R ([QuickBLAST](#) - available a precompiled library) coupled with Arrow IPC, can load and convert BLAST formats (internally - to GRanges) and sports functions for performing Reciprocal Bidirectional Hits. The multithreaded BLAST framework can handle many-many BLAST Hits across organisms. The package is interfaced with bash, R transforms the data & calls the shots and bash handles files & BLASTing. Check requirements and installation instructions before proceeding.

Ironically this repo is incomplete but the functionality in it works. Under Construction Indefinitely. Documentation can be found within the package, Play around with the functions for the rest

Installation (on R - Linux or RStudio Docker with WSL in Windows) :

•

```
sudo apt-get update && sudo apt-get install curl bzip2 parallel liblmbd-dev ncbi-blast+ santools bedtools
```

•

```

BiocManager::install(c("Rhtslib", "devtools", "BiocManager", "Biostrings", "biomaRt", "S4Vectors", "IRa
remotes::install_git("https://github.com/vizkidd/R-COMPLETE.git")

```

REQUIRES :

- Linux with BASH (\$SHELL must be set or /bin/bash must exist) (export SHELL="/bin/bash")
- **Config Files**
- Lot of space in `genomes_path`, `fasta_path` and `annos_path` path locations (in parameters file)
- GNU parallel (in \$PATH - BASH functions)
- [AGAT](#)
- [GffRead](#)
- [Samtools](#) (in \$PATH - BASH functions)
- [Bedtools](#) (in \$PATH - BASH functions)
- [ncbi-blast+](#) (Compile from .src.tar.gz with ./configure && make all_r && sudo make install) (or sudo alien -i ncbi-blast-X.XX.X+-2.src.rpm) (or download binaries) ([Docs](#) & [Compilation](#))
 - Check if you have the binaries for `blastdb_path` and `makeblastdb`
- [Zlib](#) - (Compile from sources) (or) (sudo apt install libz-dev or yum install zlib-devel)
- LZMA SDK - (sudo apt-get install liblzma-dev or yum install xz-devel)
- BZLIB - (sudo apt-get install libbz2-dev libclang-dev or yum install bzip2-devel.x86_64)

OrthoDB : (Optional)

- [OrthoDB \(ODB\) Flat Files \(>= v10.1\)](#) (Pipeline is tested with ODB v12.2)
 - [odb12v2_species.tab.gz](#) - Ortho DB organism ids based on NCBI taxonomy ids (mostly species level)
 - [odb12v2_genes.tab.gz](#) -Ortho DB genes with some info
 - [odb12v2_OG2genes.tab.gz](#) - OGs to genes correspondence (**OR**)
 - [odb12v2_OGgenes_fixed.tab.gz](#) - Merged & Transformed ODB file (Done within pipeline - Only once)
 - [odb12v2_OGgenes_fixed_user.tab.gz](#) - Merged & Transformed ODB file BASED on user gene list (Done within pipeline - For different gene sets)

NOTE : Set `orthodb_path_prefix` in parameters file if you use OrthoDB files

Tools - (Paths in parameters file)

- [MACSE](#) (Path to the .jar)
- [MAFFT](#) (Compile from sources with extensions because *mafft-qinsi* is required)
- [TRANSAT](#) (Download preferred tarball and check INSTALL file)
- [RNADECODER](#) (Compiled program is in the bin/ of the repo) (Give path to the folder containing the binary)
- [FastTree](#)

Files (Config)

- [Parameters](#)
- [User Data](#) (Optional)
- [Reference Organisms](#) (COMPLETE_env\$org.meta has the list of organisms available)

Install Requirements :

```
git clone https://github.com/NBISweden/AGAT.git # Clone AGAT
cd AGAT # move into AGAT folder
perl Makefile.PL # Check all the dependencies*
make # Compile
make test # Test
sudo make install # Install
```

Install AGAT :

```
git clone https://github.com/gperteia/gffread
cd gffread
make release
sudo cp gffread /usr/bin/
```

Install GffRead :

```
curl -OJL https://github.com/samtools/samtools/releases/download/1.23/samtools-1.23.tar.bz2
tar xvf samtools-1.23.tar.bz2
cd samtools-1.23
./configure
make
sudo make install
```

Install Samtools :

```
curl -OJL https://github.com/arq5x/bedtools2/releases/download/v2.31.1/bedtools-2.31.1.tar.gz
tar xvzf bedtools-2.31.1.tar.gz
cd bedtools2
make
sudo make install
```

Install Bedtools :

```
curl -OJL https://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/LATEST/ncbi-blast-2.17.0+-src.tar.gz
tar xvzf ncbi-blast-2.17.0+-src.tar.gz
cd ncbi-blast-2.17.0+-src/c++
./configure --with-openmp
make all
sudo make install
```

Install ncbi-blast+ :

Run Example :

To run the example, from the context of your current working directory,

- Download OrthoDB(ODB) files (optional) and Tools
- Check config files
- Provide paths and options in the parameters file
- **NOTE : Default parameters file ([parameters.txt](#)) is at `fs::path_package("COMPLETE", "pkg_data", "parameters.txt")`**

```
params_list <- COMPLETE::load_params(fs::path_package("COMPLETE", "pkg_data", "parameters.txt"))
gene_list = fs::path_package("COMPLETE", "pkg_data", "genelist.txt")
user_data = fs::path_package("COMPLETE", "pkg_data", "user_data.txt")
COMPLETE::EXTRACT_DATA(db="user", params_list = params_list, gene_list = gene_list, user_data = user_data)
COMPLETE::EXTRACT_DATA(db="ensembl", params_list = params_list, gene_list = gene_list, keep_data=T)
COMPLETE::EXTRACT_DATA(db="genbank", params_list = params_list, gene_list = gene_list, user_data = user_data)
COMPLETE::FIND_TRANSCRIPT_ORTHOLOGS(params_list = params_list, gene_list = gene_list, blast_program = "blastn")
```

[!CAUTION] **NOTE : First run will take some time due to conversion of ODB file structure (if OrthoDB is used)**

Documentation :

```
?COMPLETE_PIPELINE_DESIGN (in R docs)
```

PARAMETERS

The pipeline takes a single [parameter](#) file. This design was chosen,

- To expose as many options as possible to the end user.
- The pipeline uses BASH to BLAST and handle files (significantly faster than R) and the parameter file is shared between R and BASH.
- Parameters tagged as output in comment column are outputs from COMPLETE.

```
* Delimited by '=='  
* Inputs and Outputs are specified in the comments  
* The file is of the format [param_id==value==comment] where param_id and value columns are CASE-SENSITIVE  
* A default/example file is in fs::path_package("COMPLETE","pkg_data","parameters.txt")
```

USER DATA : (Optional)

```
* Columns Org,Version, genome, gtf  
* Can accept empty or '-' in genome and/or gtf column. If empty or '-', the genome/gtf is looked up in  
* A default/example file is in fs::path_package("COMPLETE","pkg_data","user_data.txt")
```

COMPLETE.format.ids

- Order of FASTA ID labels are stored in `COMPLETE_env$FORMAT_ID_INDEX`
- Sequences are labelled with the following long ID format of R-COMPLETE (specific to this pipeline and referred to as COMPLETE.format.ids) (seqID_delimiter & transcriptID_delimiter set in parameters, :: & || respectively in this context)
- COMPLETE.format.ids are indexed(internally) with `COMPLETE::index_BLAST_tables()` for compatibility

```
>$transcript_id $transcriptID_delimiter $transcript_region ($strand) $seqID_delimiter $org_name/$DB/$org  
>SOME_TRANSCRIPT||cds(+):SOMEORG/DB/VERSION::RANDOMGENE::ORTHOLOG_CLUSTERS  
>ENSDART00000193157||cds(+):danio_rerio/ensembl/115::sulfi::18335at7898,51668at7742,360590at33208
```

BLAST Functions

- [QuickBLAST](#)

QuickBLAST Options Same as BLAST but OUTPUT Format is not available. List of available options can be checked with `QuickBLAST::GetAvailableBLASTOptions()` (Empty elements from the list are removed and BLAST defaults are set on the c++ side). Enums used by QuickBLAST in C++ are not exposed in R and only integers are used, check `COMPLETE::GetQuickBLASTEnums()`.

FLOW

- 1) **EXTRACT_DATA()**: Extracts the transcript regions for Protein Coding Transcripts (provided in parameters, pipeline requires `cds,5utr,3utr`) from BIOMART(ensembl),genbank(ncbi) and/or User provided genomes & GTFs. This functions uses biomaRt/biomartR for extracting data from BIOMART and BASH function `extract_transcript_regions()` for user provided data. Extraction priority/flow : User Data > biomaRt > biomartR
 - ODB Files are merged and transformed with BASH function `merge_OG2genes_OrthoDB()`
 - Orthologous genes are found for genes which are not present in the organism with BASH function `check_OrthoDB()`
 - Flank lengths are calculated from GTF data for missing UTRs (with variance correction, check `?calculate_gtf_stats`)
 - FASTA Nucleotide Sequences for given TRANSCRIPT_REGIONS are fetched from BIOMART/Genome
 - 2) **FIND_TRANSCRIPT_ORTHOLOGS()** - Finds transcript-level orthologs based on minimum coverage and/or maximum sequence identity (check `?extract_transcript_orthologs`). Has a grouping mode(`group.mode`) and run mode(`run.mode`), to group transcript orthologs at the level of organisms, genes or Ortholog Clusters, sequences are grouped into any level of `COMPLETE_env$FORMAT_ID_INDEX` (Default - `COMPLETE_env$FORMAT_ID_INDEX$CLUSTERS`) and select transcript orthologs. Gene level grouping has more tight orthology and fewer transcript orthologs. Ortholog Cluster level grouping is a level higher than Genes (Because an Ortholog Cluster can have more than one gene) and have highest number of transcript orthologs with a lot of dissimilarity. Different run modes determine how transcript-level orthologs are selected by their HSP coverages after grouping. After grouping, non-overlapping BLAST hits which maximize coverage for each transcript are chosen with [WISARD](#). Transcripts which do not have bi-directional hits are discarded with `COMPLETE::RBH()`. Finally, HSP coverage is calculated with `COMPLETE::calculate_HSP_coverage()` and transcripts are processed according to `run.mode` option which can be one of,
 - “coverage_distance” - Hits are filtered based on distance between bi-directional minimum HSP coverages (`coverage_distance <= min_coverage_filter`). This option selects more BLAST hits and should be used when the coverage values are very low (and the BLAST Hits/sequences are distant). `coverage_distance = 1 - (2 * aligned_length) / (query_length + subject_length)`. (`coverage_distance >= min_coverage_filter`)
 - “coverage_filter” - Filters Hits based on minimum coverage of HSPs from either direction. Use this option when the coverage values are high (and the BLAST Hits/sequences are closely related). (`cov_q >= min_coverage_filter && cov_s >= min_coverage_filter`)
 - “both” - Uses both “coverage_distance” and “coverage_filter” and is very strict. (Default) . (`coverage_distance >= min_coverage_filter && cov_q >= min_coverage_filter && cov_s >= min_coverage_filter`)
 - “no_filter” - Only calculates HSP coverages and does not filter any Hits .
- NOTE : ONLY USE THIS FUNCTION WHEN RUNNING THE PIPELINE OF R-COMPLETE.** Use other helper function to work with custom BLAST files not generated by this R package.

3)

Example Data

Parameters :

Parameter ID	Value (CASE SENSITIVE)	Comment
gene_search_mode	EASY	EASY/HARD, Mode to search for genes, EASY is default and HARD matches the whole gene name (with grep -w flag wherever necessary) (ONLY FOR biomart genomes/GTFs and USER DATA) (Input, Optional)
e_value_thresh	1e-05	E-value threshold (Input)
minIdent_thresh	25	Minimum % identity threshold for BLAST RESULTS (Input)
blast_options	-strand plus -outfmt "6 qseqid sseqid pident length mismatch gapopen qstart qend sstart send evalue bitscore score gaps frames qcovhsp sstrand qlen slen qseq sseq nident positive"	Extra options to pass to BLAST (Input)
transcript_delimiter		Delimiter which splits transcript IDs (do not use equal sign or underscore!) (Input)
strand	+	Either +/-/' '(), Select genes from the strand (Input)
transcript_regions	cds,3utr,5utr	Regions to extract sequences from, cds,3utr,5utr,transcript,gene,exon,start_c (Input)
seqID_delimiter	::	Delimiter which splits sections in sequence IDs (Input)
transcript_regions_delimiter		Delimiter which splits RNA regions into CDS and UTR (Input)
fasta_path	files/fasta	Path to save transcript FASTA (Output)
out_path	files	Path to save meta output (Output)
temp_path	files/temp	Path to save temporary files (Temp)
groups_path	files/groups	Path to save FASTA sequences as orthologous groups (Output)
ref_orgs	files/reference_ORGS.txt	Subset of orgs from FASTA PATH(each line should be a folder name of an org) (Input)
max_concurrent_jobs	10	Number of concurrent jobs/threads to be executed at any given time (threads) (Input, Optional)
genomes_path	/mnt/data/storage/genomes	Path to save GENOMES (Input/Output)
annos_path	/mnt/data/storage/annos	path to save GTF annotations (Input/Output)
bed_path	files/bed	Path to save the extracted BED files (to avoid re-extraction each time) (Input/Output)

Parameter ID	Value (CASE SENSITIVE)	Comment
clean_extract	FALSE	Remove old files and Re-extract transcript regions? (Input)
select_all_genes_from_cluster	FALSE	Select all genes from each cluster for each organism? (otherwise only the user specified genes are selected from each ODB cluster) (Default-FALSE) (Input, Optional)
select_groups_with_ref_orgs	TRUE	Select only clusters which contain the sequences from the reference organisms? (Default-TRUE) (Input, Optional)
select_groups_with_ref_orgs_method	ALL	Select only groups which contain the sequences from ANY/ALL of the reference organisms? (Default-ALL) (Input, Optional)
plot_path	files/plots	Path to save plot images (Output)
gene_drop_thresh	0	Threshold to filter genes (Input)
orthodb_path_prefix	/mnt/data/storage/orthodb/odb12v2	Path and prefix to OrthoDB files, check docs to know which files you need (merge_OG2genes_OrthoDB.R) (Input/Output)
macse_path	tools/macse_v2.jar	Path to MACSE jar file or the installed executable (for coding sequence alignment) (Input)
mafft_path	/usr/local/bin/mafft-qinsi	Path to MAFFT executable (for UTR alignment) (Input)
transat_path	tools/Transat	Path to TRANSAT executable (for predicting helices) (Input)
rnadecoder_path	tools/	#/data/meyer/viz/tools/Transat_latest/TransatC FOLDER (only folder path,executable must be named RNA-decoder) (for predicting base-pair probabilities) (Input)
msys2_path		Path to MSYS2 (ONLY FOR WINDOWS) (Input)
fasttree_path	tools/FastTree	Path to FastTree executable (for generating trees) (Input)
alignments_path	files/alns	Path to save alignments (Output)
aln_gap_thres	0.50	The proportion of gaps to delete the column in an alignment (higher values will give more gaps and discards less sequences) (Input)
min_coverage_thres	0.5	Threshold for minimum coverage(higher values give highly conserved sequences) (Input)

User Data :

Organism	Accession	TaxID	Version	Genome URL/Path	GTF URL/Path
xenopus_tropicalis	acc1	taxid1	0	URL	URL
xenopus_laevis	acc2	taxid2	1	URL	URL
danio_rerio	GCA_000002035.4	taxid3	GRCz11	-	-

[!NOTE] **NOTE:** When Genome/GTF is '-' or empty, the query database given by db parameter is searched.