

# biogo Command Line Applications User Manual

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biogo (<https://github.com/\`biogo/examples/>) is a bioinformatics library for the Go language. biogo/krishna and biogo/igor are de-novo repeat family identifying and annotation packages, which employ computational methods for identifying repeat element boundaries and family relationships from sequence data. biogo assists the runs of krishna and igor given a genomic database and uses the output to build, refine and classify consensus models of putative interspersed repeats.

## Prerequisites

### 1. Download Go

Available at (<https://golang.org/dl>). Developed and tested with version 1.5.2.

#### Install on Linux:

Unpack the Go language in your home directory or in a location where it may be shared with other users of your system ( ie. /usr/local/).

- \* cp go#.#.linux-amd64.tar.gz /usr/local/
- \* tar -C /usr/local -xzf go#.#.linux-amd64.tar.gz
- \* export PATH=\$PATH:/usr/local/go/bin

If you installed Go to your home directory you should add the following commands to \$HOME/.profile. For example, put your go path into a directory called "work":

- \* export GOROOT=\$HOME/go
- \* export GOPATH=\$HOME/work
- \* export PATH=\$PATH:\$GOROOT/bin

For more installation details, follow the instructions on the [Go installation](#) page.

### 2. Git

To perform the next step you may have Git installed. (Check that you have a git command before proceeding.)

If you do not have a working Git installation, follow the instructions on the [Git download](#) page.

### 3. Download **biogo** Packages

Download krishna and igor packages from github.

- \* `go get github.com/biogo/examples/krishna`
- \* `go get github.com/biogo/examples/igor`
- \* `go get github.com/biogo/examples/external`

### 4. Install **biogo** Packages

Install packages from **biogo** in you home directory, for example directory called "work".

- \* `cd work/src/github.com/biogo/examples/krishna`
- \* `go build -o $HOME/work/bin/krishna-matrix matrix.go`
- \* `go build -o $HOME/work/bin/krishna krishna.go`
- \* `cd work/src/github.com/biogo/examples/igor`
- \* `go build -o $HOME/work/bin/igor igor.go`
- \* `go build -o $HOME/work/bin/sequer sequer.go`

### 5. Install CENSOR

Install censor to screens target genomes against a reference collection of repeats libraries with masking symbols, as well as generating a report classifying all found repeats. CENSOR needs wu-blast and Bioperl.

The version is now available at [CENSOR download](#) page.

### Example run

In this example, human genome were downloaded by chromosomes (24 chromosomes) from UCSC into files called chr-\*.fa.

## **1. Use krishna-matrix to run alignment between human sequences as a matrix, it will run self alignment first, and then run pairwise alignment.**

The default minimum hit length for krishna (-dpid) is 400bp, and minimum hit identity (-dplen) is 94%. The smaller number of parameters you use, the longer time and bigger memory will be needed.

If you want change these parameters, just add "-dplen=\*bp" and "-dpid=0.\*" in 'matrix.go' under krishna source code: lines 102 and 132 (codes begin with "cmd := exec.Command").

Change the work directory that stores temporary files generated from krishna to you own directory (line 64 in matrix.go), Then rebuild 'matrix.go'.

**Notes: You need to rebuild the code every time when you did any changes.**

Now runs the job:

- \* cd /data/rc003/lu/human (directory contains the sequences)
- \* krishna-matrix chr-\*.fa

If the genome sequence were very big and consisted by multiple contigs or scaffolds (>200MB), split it into smaller files (using bundle.go).

- \* go build -o \$HOME/work/bin/bundle bundle.go
- \* bundle -bundle 50000000 -in seq.fa

-bundle: Specifies the sum of sequence length in a bundle. (default 20000000, 20MB).

-in: the genomes sequences need to split.

Then run krishna job.

## **2. Use igor to take pairwise alignment data produced by krishna, and reports repeat feature family groupings in JSON format.**

- \* cat \*.gff > hg\_krishna.gff
- \* igor -in hg\_krishna.gff -out hg94\_krishna.json

### 3. sequer returns multiple fasta sequences corresponding to feature intervals described in the JSON output from igor.

sequer will also produce fastq consensus sequence output from one of MUSCLE or MAFFT. gffer converts the JSON output of igor to gff.

- \* gffer < hg94\_krishna.json > hg94\_krishna.igor.json
- \* cat chr-\*.fa > hg19v37.mfa
- \* sequer -aligner=muscle -dir=consensus -fasta=true -maxFam=100 -subsample=true -minLen=0.95 -threads=12 -ref=hg19v37.mfa hg94\_krishna.igor.json

-fasta: Output consensus as fasta with quality case filtering  
-maxFam: maxFam indicates maximum family size considered (0 == no limit).  
-minLen: Minimum proportion of longest family member.  
-threads: Number of concurrent aligner instances to run.

## Benchmarks

Genome	Krishna Threads	Genome DB Size	Krishna run time (hh:mm)	Igor run time (hh:mm)	Sequer run time (hh:mm)
Human	8	3.0G	~200	128:30	2:23
Bearded Dragon	8	1.8G	~23	73:11	<4
Anolis	6	1.8G	76:52	97:32	2:40
Chicken	4	1017M	20:30	<4	<1
Opossum	8	3.5G	~83	61:48	4:52
Platypus	8	2.0G	~99	191:34	10:16
Echidna	8	1.9G	< 360	12:43	9:02

\* Analysis run on a 512GB RAM, machine running Red Hat Linux

## Repeat Library Annotation

The previous steps generate the repeat consensus sequences from the human genome, now we are going to annotated these consensus with repeat class.

## Annotate consensus sequences

**Notes: All Java scripts used here need to specify the directories where your data is and where you want your output in**

## 1. Annotate consensus sequences with repeat families.

Use `consensus` to annotated consensus sequences with Repbase library.

```
* cd consensus
* cat *.fq > ConsensusSequences.fa
* consensus -bprm cpus=8 -lib ~/Vertebrates.fa -lib ~/our_known_reps_20130520.fasta ConsensusSequences.fa
```

The `consensus` outputs usually have 5 files: `ConsensusSequences.fa.map`, `ConsensusSequences.fa.aln`, `ConsensusSequences.fa.found`, `ConsensusSequences.fa.idx`, `ConsensusSequences.fa.masked`.

## 2. Classify consensus sequences.

`ConsensusSequences.fa` and `ConsensusSequences.fa.map` were required in this step. You will also need to specify the directories where your data is and where we want your output in the java code, then compile and run it.

```
* javac ClassifyConsensusSequences.java
* java ClassifyConsensusSequences
```

You should get 5 output files: `known.txt`, `partial.txt`, `check.txt`, `notKnown.fa`, `notKnown.fa.gff`.

## 3. Filter potential protein sequences.

In this step, you will need to run the perl script `reportsJ.pl` (perl `reportsJ.pl`). This uses `wu-blast blastx`, you will also need `uniprot` database. `reportsJ.pl` will ask for a list of databases to process, "`libs.txt`". We need file `notknown.fa` and `notknown.fa.gff`, put `libs.txt` into current directory.

**Notes: `reportsJ.pl` contains three parts: used to identify uniprot, GB\_TE, or retroviruses. You can comment other two parts, and run one of each parts separately in the same time, to save the running time.**

## 4. Get proteins information from consensus sequences.

Another java program `GetProteins.java` will be used. It need two input files: `notKnown.fa`, `notKnown.fa.spwb.gff` (Generated from previous step).

```
* javac GetProteins.java
* java GetProteins
```

You will get 2 output files: `proteins.txt` (a list of families that have been identified as proteins and the proteins they have matches); `notKnownNotProtein.fa` (a fasta file of the families that have not yet been classified).

## 5. Check simple sequential repeats (SSR).

Then check any existence of SSR in the unknown sequences, using `phobos`.

```
* phobos -r 7 -outputFormat 0 -printRepeatSeqMode 0 notKnownNotProtein.fa > notKnownNotProtein.phobos
```

## 6. Identify the sequences that are SSRs from the phobos output.

The phobos output will be used to identify SSRs: notKnownNotProtein.phobos.

- \* javac IdentifySSRs.java
- \* java IdentifySSRs

You will get a file called: SSR.txt

## 7. Generate annotated repeat library.

10 input files are required to generate a repeat library:

1. ConsensusSequences.fa
2. ConsensusSequences.fa.map
3. notKnown.fa.tewb.gff
4. notKnown.fa.ervwb.gff
5. protein.txt
6. known.txt
7. GB\_TE.21032016.fa
8. all\_retrovirus.fasta
9. SSR.txt (if you do not have this, leave the definition in, it will cause error messages, but will not stop the program nor effect the results.)
10. LA4v2-satellite.fa (you do not have this, or equivalent, as you didn't have any satellites, but leave the definition in-it will cause error messages, but will not stop the program nor effect the results.)

- \* javac GenerateAnnotatedLibrary.java
- \* java GenerateAnnotatedLibrary

Then you will get a library called "\*\_Library.fasta", you can also change this to whatever you want to call your library

## Benchmarks2

Genome	Consensus sequences size	Censor first run time (hh:mm)	reportJ.pl (hh:mm)	phobos run time (hh:mm)
Human	38M	5:14	19:30	<00:05
Bearded Dragon	88M	2:41	<192	<00:05
Anolis	63M	9:42	<56	<00:05
Chicken	18M	3:01	<24	<00:05
Opossum	60M	13:17	<48	<01:00
Platypus	162M	34:34	<192	<01:00
Echidna	59M	36:40	105:12	01:54

\* Analysis run on a slurm machine with 4~16 cpus, and 8GB RAM, machine running Red Hat Linux.

**Finished! Good Luck!!!**