

# Custom Genome Databases

## Setting up a genome database and/or blast server for your new assembly

### Genome databases

It's beyond our scope in this course to show you how, but the general concept of building and hosting a genome database is not new and is not too hard if you use the [GMOD toolkit](#). GMOD is the infrastructure behind a large number of organism databases including *X. tropicalis*, *S. cerevisiae*, *E. coli*, worm, fly, etc. - it's widely used and well supported. Educational sessions are offered frequently.

As a starting point, I would recommend you only start with the Gbrowse browser and avoid Chado unless you either have or want to get some experience with LAMP stacks, php, and MySQL databases.

### Blast server

Fortunately, thanks to a clever bit of code written by Yannick Wurm and colleagues, it's very easy to serve your results out to the whole world via blast.

Recommended path to do this:

- a) Use your credit card to get an account at [Rackspace](#) (you could do this anywhere you'd like of course)
- b) Spin up a virtual machine based on the [BioLinux distribution](#) of linux, which already has a host of bioinformatics tools built-in, including blast
- c) Upload your data
- d) Start the sequencesserver
- e) Share the IP address with anyone you want!

An example of a custom genome database set up with [SequenceServer](#) can be found [here](#).

Enter in the following sequence:

```
CGGCGTAAACGCCTTATCCGGCTACAAAAATGTGCAAATTCAATAAATTGCAATTCAACTTGTAGGCCT
GATAAGCGCAGCGCATCAGGCAATTTGGCGTTGCCGTCAGTCTCAGTTAATCAGGTTACAACGATTAACC
CTGCAGCAGAGACAGAACCTGCTGCGGTACCTGGTTAGCTTTTGCCAACACGGAGTTACCGGCCTGCTGG
ATGATCTGCGCTTTCGACATATTGGACACTTCGGTCGCATAGTCGGCGTCCTGAATACGGGACTGCGCTT
```

Select *blastn* as your blast method, check *NC\_000913.2.fasta* as your nucleotide database and finally click **BLAST!**