10/23
 On Thursday we will discuss the web server design in detail. Di, Hefei and Xin are our lead web server architects.

JaroorModi will review the design of the [current online HMMER web server](#).
Please feel free to review the paper describing it before we meet (attached and on [Drive here](#)).
The current web server also has a [RESTful API described here](#).

I hope we can **draw insights from the current HMMER web server for the design of our new one**.

LOGO Accumulo + GPU + HMMER / Proteins

10/23 Meeting
Di and Xin -- will look into logo design
Jaroor on Jaenelia HMMER web server
- Lots of databases. Fit into 2 kinds
    - protein sequence databases
    - profile HMM databases
- jackhmmer does something cool, similar to hmmbuild
    - Uses a profile HMM database as the seed HMMs to build a new one
    - Multiple iterations - each one builds a better and better HMM
- Homologs-- 2 species are related
  Analogs -- 2 species are similar but not related
- Uses IP to route requests. We will let Accumulo handle load balancing and data distribution.

Multiple sequence/HMM "databases" are equivalent to multiple tables in one Accumulo Database.

Ganesan
1. MSV filter
2. Viterbi filter
3. Forward score
First stages have BIG data, not much computation per data
Last stages have small data, BIG computation per data

If we map over all the data, no need for a database. Just use MapReduce. But I think we do need a database since we have Taxonomic filtering/selection. We should outline exactly when our database will speed up operations (aka when we query specific queries).

Ganesan demoed a MapReduce job for word count.

Di introduced an Endpoint java web server thingy. Uses Antscripts.
Need to look at asynchronous return of results.