NGVV Features

These are things that NGVV doesn’t do right now, but I could make it do them. Items with numbers are independent. Letters following numbers mean they are dependant on a previous feature.

**Startup:** 1. Implement dynamic loading of sections so that section transforms are only loaded if the section is being viewed. This will make loading faster, but switching to an unloaded section slower.

2. Write a console application that computes and stores the slice-to-volume transforms onto disk so I do not need to compute them at startup. This will make loading much faster.

**Setup & First time use:**

1. I could add support for multiple volumes in a single database and the software figures out which volume you are annotating at load time. This would remove the need to setup a new database for each volume, but only having one database may be a little monolithic.

1B. It would be possible to have NGVV support viewing multiple volumes if I implemented caching to get the memory footprint under control. I don’t see a need for this.

1. There is no concept of a super-user currently. Anyone can setup or delete any information from the database. It should be possible to implement a set of rules such as only certain users can create structure classes and users can only delete their own rows from database tables. This might prevent undergrads from correcting each other’s mistakes.

**User Interface:**

1. I don’t have an automated way to populate cell CMP classification yet.
2. “Mark New Structure” and “Extend Command” are similiar commands and the union may be obvious to me once I write the code.
3. Marking synapses takes too many clicks currently. I need to find a way to make synapses simple.