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CellTracker code on github

Hi all,

I'm sending this to everyone who will potentially use the cell tracking code in the future. Please forward it on if I missed someone. As this group is expanding, it has become clear that using a shared dropbox folder for the code is a very dangerous thing, so as an alternative we are going to use github to share the code. The site has a lot of sophisticated features but for our purposes, it will allow us to safely share the code and it has version tracking which will allow us to go back if there is some horrible mistake. You can find the repository at:

<https://github.com/warmflash/CellTracker>

Detailed instructions for setting this up are here: <https://help.github.com/articles/fork-a-repo>

The way this works is that you should do the following:

- 1) sign up for github
- 2) fork the repository -- this creates a remote repository on github that is yours
- 3) clone your fork to your local machine -- this will give you a local copy of the code which you can do whatever you want with
- 4) add the original repository upstream -- this will allow you to easily update your local code with any changes that have been made

if you have code that you want to contribute back to the repository you should:

- 1) commit your changes and push them to your remote repository
- 2) submit a pull request to me and I will merge your code into the original repository

Some notes:

1. Before starting to make changes to code, it is always a good idea to fetch from the original repository. This will prevent conflicts when you try to merge your code back in.
2. There are also good features for code discussion on github -- you can create issues on the repository. This is a good place to list bugs you find in the code, or features we should have etc.
3. Right now our repository is public which means anyone can see it. I don't think I have any problem with that, but if we don't want this, we need to pay for a premium account which will allow us to create private repositories.
4. IMPORTANT: our shared dropbox folder is now obsolete and I will be deleting it to avoid confusion. If for some reason you want something from there, copy it out now or it will disappear by the end of the week. I think everything in there is in the repository anyway, but you have been warned.

Specific notes on the code:

1. There are two directories -- runFiles and paramFiles which contains the wrappers to run the core code in various ways and parameter files, respectively. These are the files that most of us use on a regular basis. I would like to clean up these directories and make sure they have everything useful in them so:
 - A. If there is a file in these directories that is yours and is obsolete, please remove it
 - B. If there is a file that is yours and is useful, please make sure it is commented properly at the top explaining what it is useful for.
 - C. If you have something that belongs in these directories but isn't there, please add it with proper commenting

In any of these cases, simply make the changes in your local copy, commit and push the changes, and submit a pull request to me.

2. Eric -- there is a directory called fromEric. Can you check whether there is anything here that we want that hasn't been incorporated into the code? If so, can you please just move the files to the correct folder in the repository and then get rid of the fromEric folder?

3. I think I have added all the files necessary to run the code but if you notice anything missing (i.e. get errors that matlab can't find a function), let me know.

Let me know if you have any questions about this.

Aryeh