Fenics - Poroelasticity Instructions

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Following FEniCS' lead, I created a docker image with everything you need to run the poroelastic models. This simplifies all of the components down to 2 pieces:

1. A Github repository with all of the codes, meshes and data
2. A Docker image that includes the latest version of FEniCS as well as all of the python packages needed to run the codes

1 Install github repository and Docker

Docker is an application that allows you to check out and run images (sort of a virtual machine) much like you check out and use files from Github. The docker **images** are downloaded locally and run in your own **container**. The following shows you how to put the appropriate image and files (from github) into a Docker container. From there you can change the files and run the models, saving the output to your local machine. A container can be closed and opened like a regular application.

1. Download Github repository
2. Install the Docker application
3. Open terminal and go to directory where the github repository is located (make sure the Docker application is running)

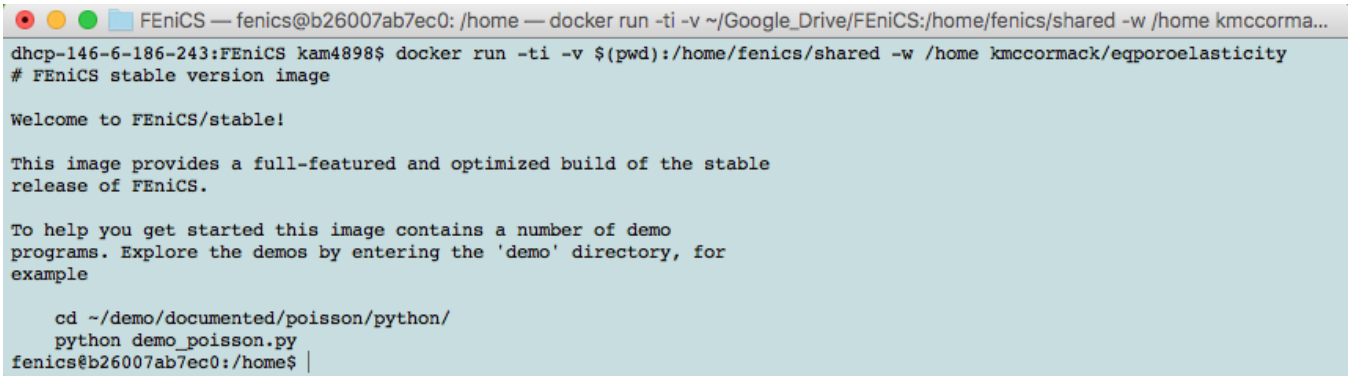
2 Run the docker image

Now you can either run the image on your local machine or run the image as a python notebook

1. Run the image on your machine in a new container and share the current folder with the container. In terminal run:

   docker run -ti -v $(pwd):/home/fenics/shared -w /home/fenics kmccormack/eqporoelasticity

   The **run** command will pull the image from the docker website the first time you run it. The image will be saved on your local machine and can be run from there until you delete it. The **-ti** option tells the image to run in interactive mode. The **-v** option tells docker to share your current local folder **$(pwd)** with the **/home/fenics/shared** folder in the docker container. This allows you to keep editing on your machine as you are running the codes in the docker container. The **-w** option tells docker where to go initially in the docker container. **kmccormack/eqporoelasticity** is the image that is being pulled from docker and run in your container. After running the above command, you should get something that looks like this in your terminal window:



From here you can navigate to the /shared folder (command: **cd shared**) where your files are located and run the model with:

python ./model_run_file.py

There is no graphics output running it this way. You can either view the generated .pvd files (saved to /results/paraview) in Paraview (download) or plot your own figures using the plotting script with the results saved as numpy arrays to /results/numpy.

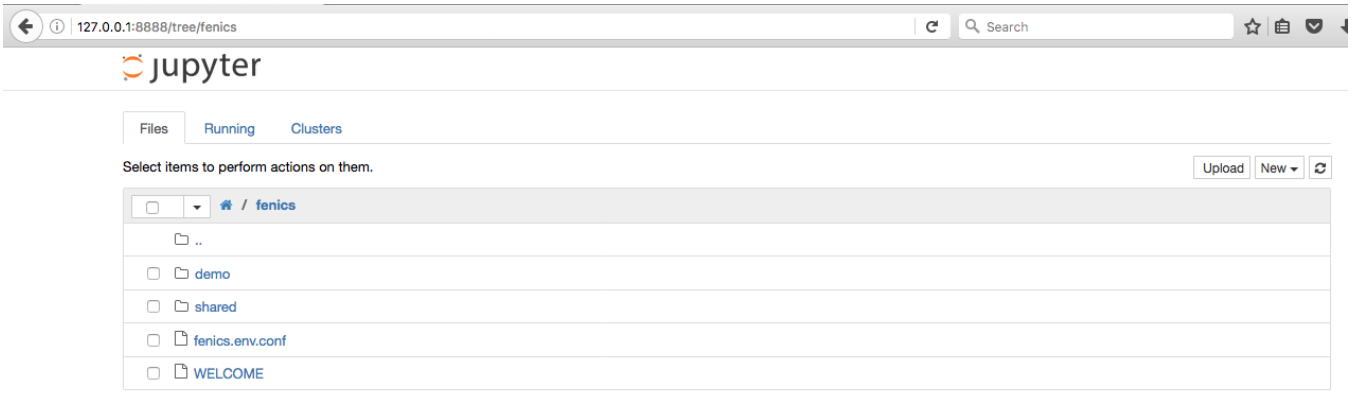
2. Run the image as a jupyter notebook

docker run -v $(pwd):/home/fenics/shared -w /home/fenics -d -p 127.0.0.1:8888:8888 kmccormack/eqporoelasticity 'jupyter-notebook –ip=0.0.0.0'

The options are similar to running the image on your machine, except now instead of running in interactive mode we use the port option **(-p)** to open up a jupyter notebook. Open up the notebook by going to:

http://localhost:8888

in any browser. It should look like this:



You can then open up any of the ipython notebook (.ipynb) versions of the codes (in /shared). I haven't written them in true notebook style that solves small pieces of code and outputs solutions and figures throughout, but it is a more interactive interface that has inline plotting capabilities - which is really nice when you are fiddling with boundary and initial conditions. *Note: Any changes you make to files in the jupyter notebook will be saved to the files in your local directory.*