JAM3D: tutorial

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Installation

- **step 1:**
  - Install python2 scipy stack. e.g. anaconda (python2)
  - From the commandline:

```
cd external && ./install
```

- **step 2:**
  - Enviroment variables needs to be set in your terminal session.
  - For bash they are

```
export FITPACK=path2fitpack
PYTHONPATH=$FITPACK:$PYTHONPATH
export PATH=$FITPACK/bin:$PATH
```

  - Alternatively you can source the setup files:

```
source setup.bash
```

Workflow

- **General**
  - + There are various ways in which `fitpack` can be used
  - + The enviroment variables allows you to run the code from anywhere in your system. In other words, there is no need to work within the same folder of `fitpack`
  - + As a good practice, create dedicated folders for a given analysis you want to study
- **Using the terminal**
  - + There are dedicated scripts that can be executed from commandline. They are located at `fitpack/bin/`
  - + The main script is called `jam3d`. This is useful for running the `jam3d` codes to generate TMD MC parameters via nested sampling. The code can be packaged into containers and be deployed in cluster environments.

Workflow

- **Using the Jupyer notebooks**
  - + The core libraries can also be loaded from jupyer notebooks
  - + The notebooks are more useful for visualization task such as plotting data or TMDs.
  - + This is ideal to share the software via `jupter-hub` servers.
- **Terminal or jupyter**
  - + In principle all the workflow can be set inside a jupyter notebook without ever need to run programs from the commandline.
  - + However at the beginning of any analysis where one needs to know if a particular implementation of the theory works by fitting the data, it is simpler to check from commandline if the setup works
  - + Moreover, for more complex problem where many parameters are involved in the analysis or a MC sampling is desired, is best to proceed via terminal (specially for very long runs)and use jupyter-notebooks to post-process the results

Tutorial 1: fits of unpolarized TMDs

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