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# Chapter 1

# About

Our Dropbox repository is ready for the python pedigree library (pyPedLib) project. We can all contribute now.

First create a working folder where you want to checkout your SVN repository.

```
mkdir /somewhere/on/your/computer/pyPedLib
cd /somewhere/on/your/computer/pyPedLib
svn co file://$HOME/Dropbox/our_shared_folder/pyPedLib
```
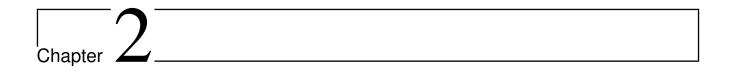
To commit changes

```
svn add xxx # google svn cheat-sheet for details
svn ci -m "message"
```

I have created several empty directories for now:

- codes: for depositing all computer scripts related to the project (please run *make* to compile)

- data: for important summary data and results.

- figures: for important result figures

- reference: for all reference papers we've been reading

- wiki: for detailed documentation of workflow, thoughts, dicussions, etc. (please run *make* to compile)

- manuscript: for drafts of manuscripts

Good luck to all of us!

# Chapter 2

# Discussion

## 2.1 `pedlib` Features

- parse *.ped file, check/correct errors in data entry, fill in missingness, and retrieve family structure related information (Biao)

- use matplotlib to plot pedigree structure with legends and marks, highlight gene flow, etc. (Hang)

- query families/individuals based on retrieved ped information (Biao?)

- calculate simple statistics, linkage/association analysis, etc. (Biao?)

- a report file based on all above can be automatically generated (?)