#activate-general-py3

activate-pheweb-py3.6

cd /imppc/labs/dnalab/share/ana\_test/pheweb\_data/pheweb-master/

cd /imppc/labs/dnalab/share/ana\_test/PheWeb/pheweb-master/

### Creating a working instance with sample data

pheweb phenolist glob --simple-phenocode 'tests/input\_files/assoc-files/\*'

pheweb phenolist unique-phenocode

pheweb phenolist read-info-from-association-files

pheweb phenolist import-phenolist -f pheno-list-categories.json tests/input\_files/categories.csv

pheweb phenolist merge-in-info pheno-list-categories.json

pheweb phenolist verify --required-columns category

# cp tests/input\_files/correlations/pheno-correlations.txt .

pheweb process

pheweb serve

#

#

#

(zcat taula\_segona.ICD272.glm.logistic.gz | head -n 1 && zcat taula\_segona.ICD272.glm.logistic.gz | tail -n 9998 | sort –k1,1V –k2,2n) | gzip -c > icd.gz

### arxius a /imppc/labs/dnalab/share/PheWeb

### markdown tret de https://github.com/statgen/pheweb/blob/master/etc/detailed-development-instructions.md

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