# Week 10 - Predictive modeling

L10-04. Predictive modeling in practice – model building

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## Software dependencies

- Code available at <a href="https://github.com/cocoanlab/interpret\_ml\_neuroimaging">https://github.com/cocoanlab/interpret\_ml\_neuroimaging</a>
- Matlab
  - Statistics and Machine Learning toolbox
  - Signal Processing toolbox
- CanlabCore Tools
   (https://github.com/canlab/CanlabCore)
- Statistical Parametric Mapping (SPM) toolbox (<a href="https://www.fil.ion.ucl.ac.uk/spm/">https://www.fil.ion.ucl.ac.uk/spm/</a>)



#### Useful functions

- CanlabCore Tools
- fmri\_data object

```
obj =
 fmri_data with properties:
         source_notes: 'Info about image source here'
                    X: []
                 mask: [1×1 fmri_mask_image]
         mask descrip: 'REMOVED: CHANGED SPACE'
   images_per_session: []
                    Y: []
              Y names: []
            Y_descrip: 'Behavioral or outcome data matrix.'
           covariates: []
      covariate names: {''}
   covariates_descrip: 'Nuisance covariates associated with data'
      history_descrip: 'Cell array of names of methods applied to this data, in order'
      additional_info: [0×0 struct]
                  dat: [352328×1 single]
          dat_descrip: []
              volInfo: [1×1 struct]
       removed_voxels: 0
       removed_images: 0
          image names: 'brainmask.nii'
             fullpath: '/Users/ladakohoutova/Desktop/CocoanLab/gitrep/CanlabCore2/CanlabCo
          files_exist: 1
              history: {1×4 cell}
```

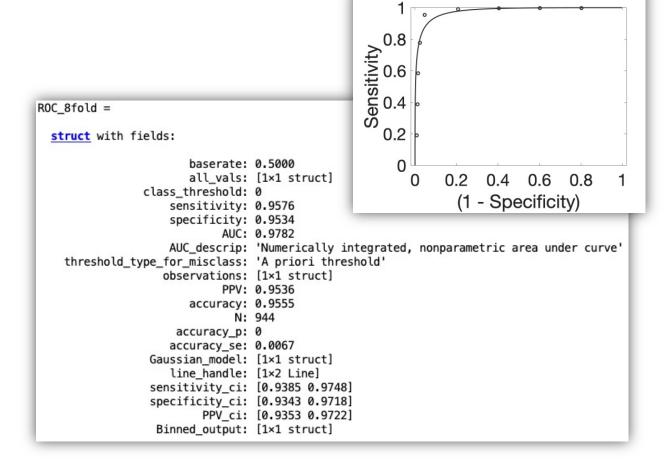
#### **Useful functions**

- CanlabCore Tools
- fmri\_data object
- predict function
  - Works on fmri\_data objects
  - Can run various algorithms (e.g,. multiple regression, SVM, SVR, PCR, etc.)
  - Cross-validation
  - Bootstrap

```
out =
 struct with fields:
                          Y: [62×1 double]
             algorithm name: 'cv svr'
              function_call: '@(xtrain, ytrain, xtest, cv_assignment) cv_svr(xtr
            function_handle: [function_handle]
                       yfit: [62×1 double]
                        err: [62×1 double]
                 error_type: 'mse'
                      cverr: 125.2375
                     nfolds: 'nfolds'
                cvpartition: [1×1 struct]
                      teIdx: {1×5 cell}
                      trIdx: {1×5 cell}
               other_output: []
      other output descrip: 'Other output from algorithm - trained on all data
            other_output_cv: []
    other_output_cv_descrip: 'Other output from algorithm - for each CV fold'
                        mse: 125.2375
                       rmse: 11.1910
                 meanabserr: 9.0577
             pred_outcome_r: 0.5219
                 weight_obj: [1x1 statistic_image]
                        WTS: []
```

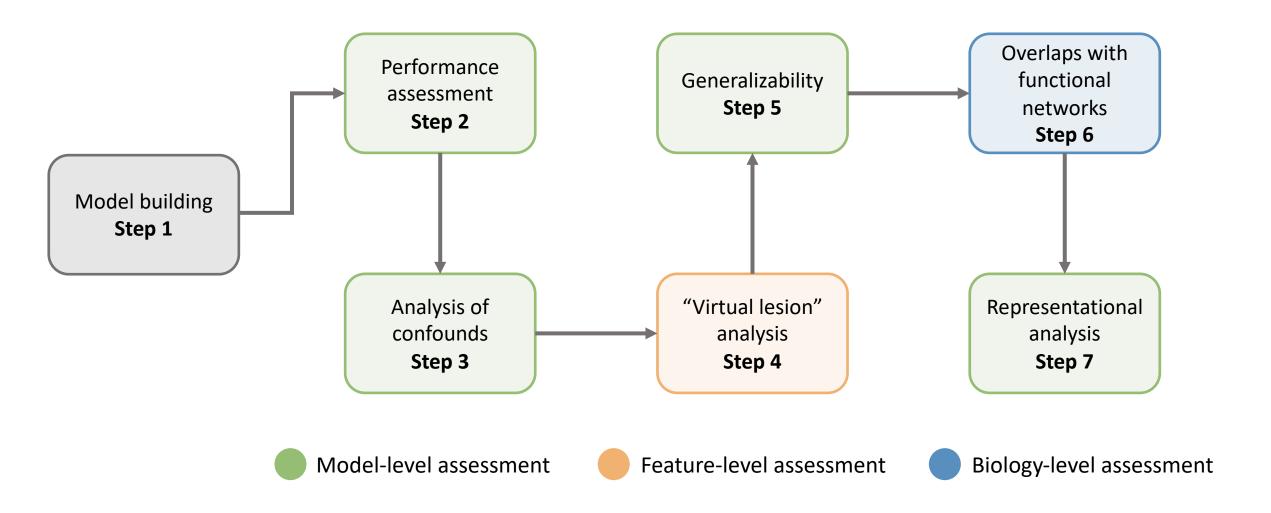
#### **Useful functions**

- CanlabCore Tools
- fmri data object
- predict function
- roc plot function
  - Calculates accuracy, sensitivity, and specificity
  - Draws ROC curve for input values and binary outcome
  - Various threshold options (e.g., 'twochoice')
- apply\_mask function
- canlab\_pattern\_similarity function





### **Tutorial workflow**





## Example data

- fMRI data from Woo et al., Nat Commun, 2014
- Binary classification heat vs. rejection
- Support Vector Machine (SVM)

