

# Pattern Recognition for Neuroimaging Toolbox: PRoNTTo

Jessica Schrouff



PRNI 2018

June 14<sup>th</sup>

NUS, Singapore



# Outline

- PRoNTTo's goals and history
- PRoNTTo for users
  - ✓ General framework
  - ✓ Modules
- PRoNTTo for developers
  - ✓ Implementation
  - ✓ Scripting examples
- PRoNTTo v3
- Hands-on session with Fabio Ferreira

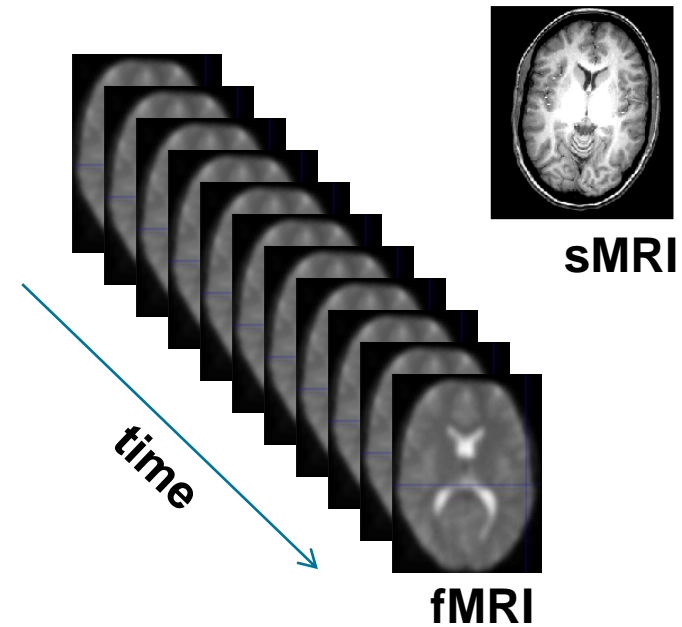
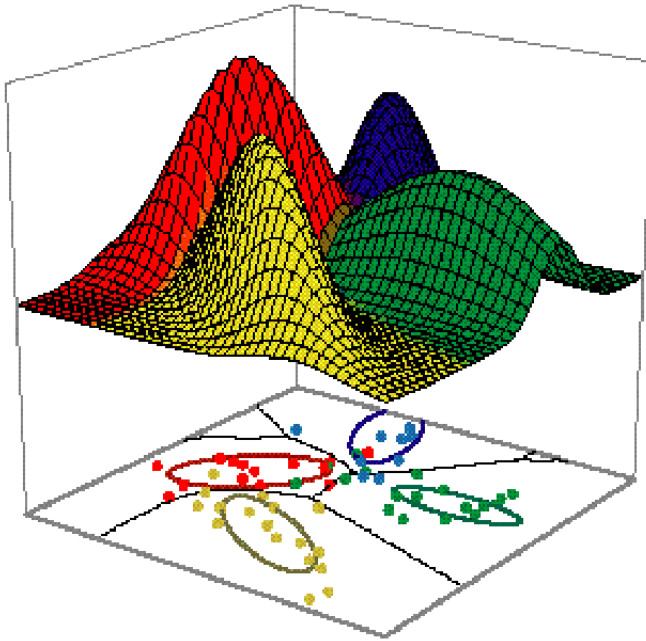


# Aims

Machine Learning  
community



Neuroscience and  
Clinical Neuroscience  
communities





# PRoNTo's history

- Pascal Harvest project: August 2011, v1.0
- Team from different backgrounds and institutions

- Releases since: v1.1, v2.0, v2.1, v3.0 to come



# PRoNTTo features

- Matlab based
- Open-source
- Interfaced: GUI and batch
- SPM compatible
- Multiple classification and regression algorithms
- Includes developments from the team member's work

Available at: <http://www.mlnl.cs.ucl.ac.uk/pronto/>



# Questions it addresses

- Classification

- Can we use brain scans to diagnose psychiatric or neurological disorders?
- Can we decode from the brain scans information about the stimuli being processed?

- Regression

- Can we predict clinical scores from brain scans?

# PRoNTTo for users

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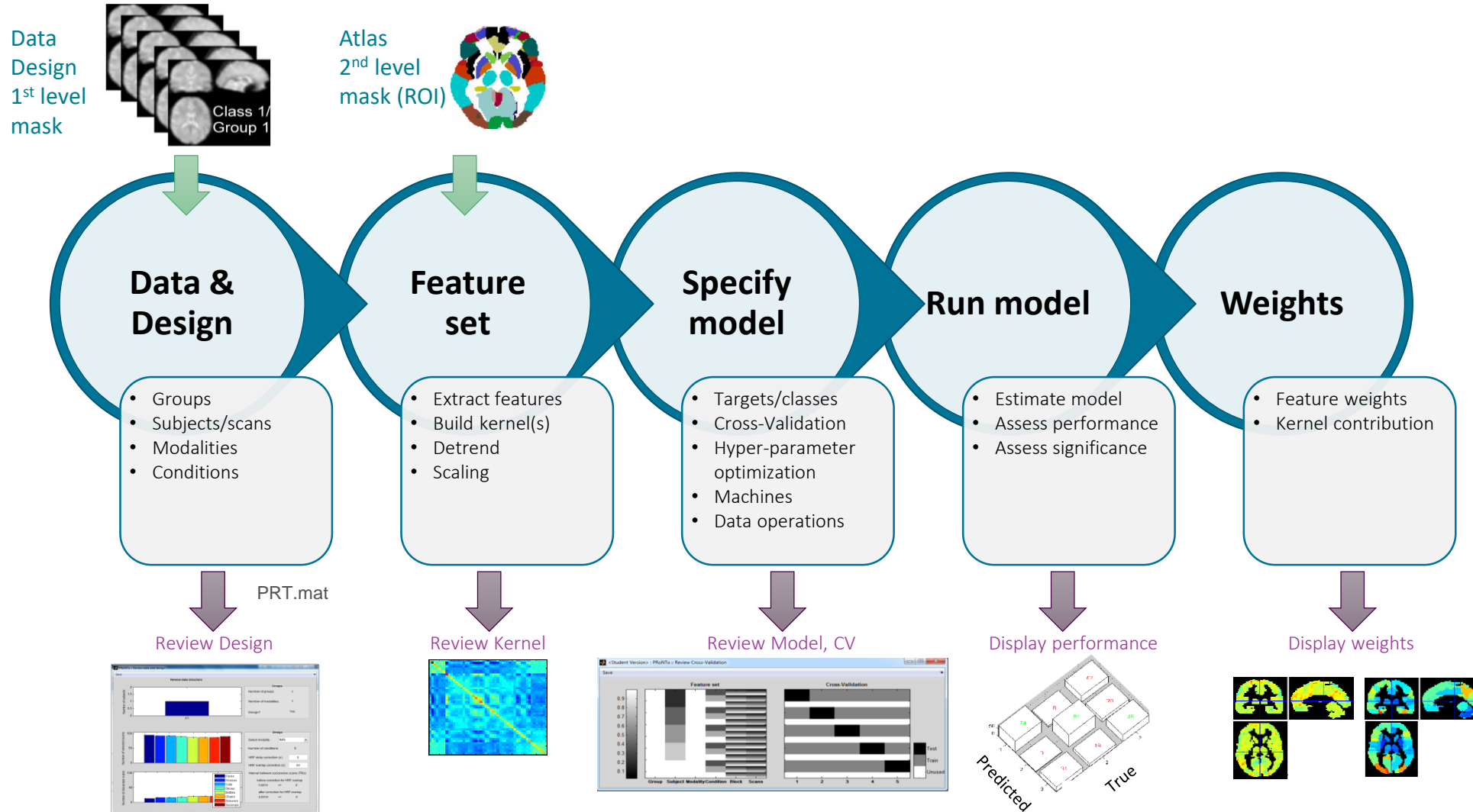
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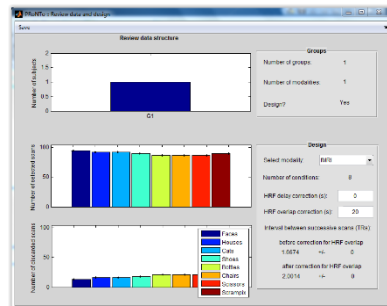

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# Framework







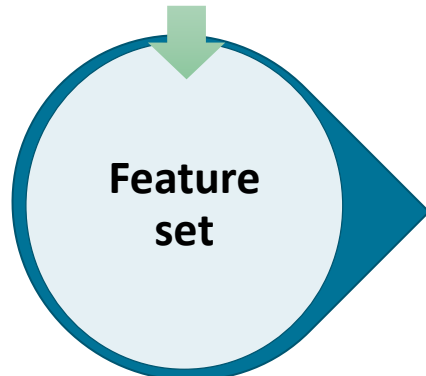
- User inputs:
  - ✓ Groups
  - ✓ Subjects
  - ✓ Modalities
  - ✓ Design
  - ✓ Covariates
  - ✓ Targets
  - ✓ Masks



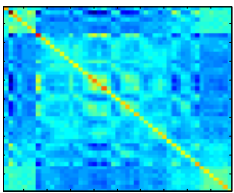


# Feature set

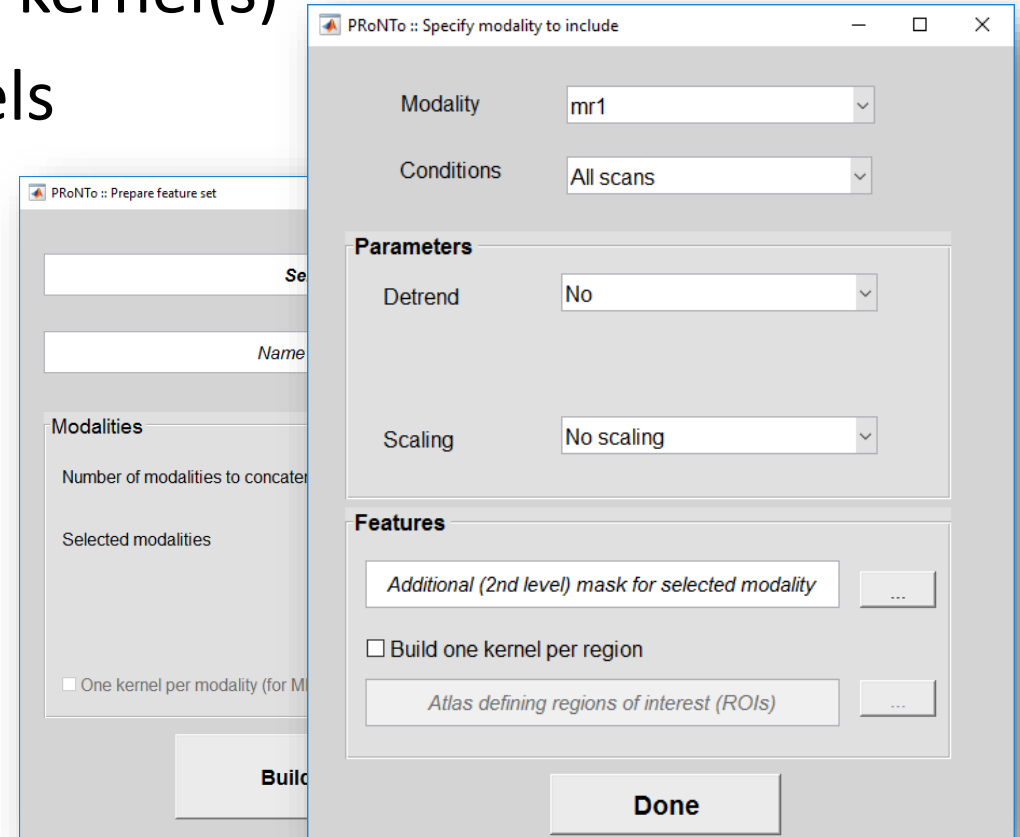
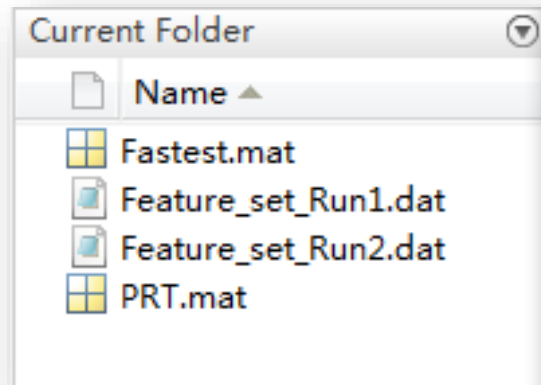
Atlas  
2<sup>nd</sup> level  
mask (ROI)



Review Kernel



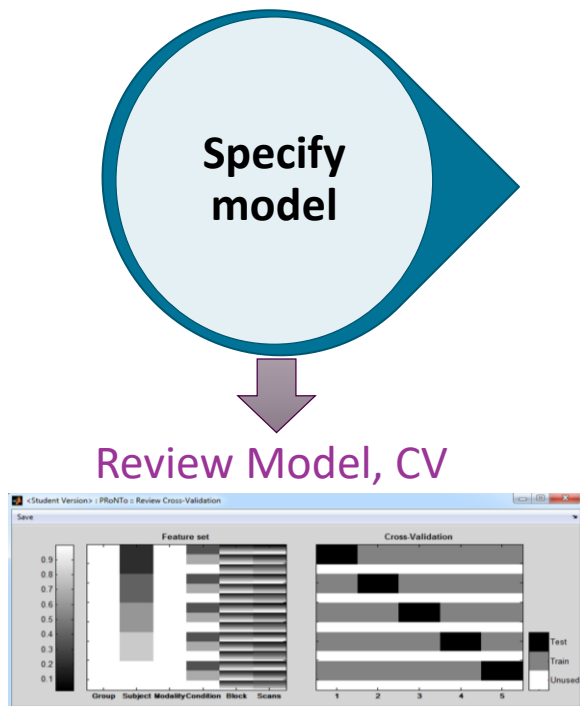
- Reads through all images in modality
- Selects features for kernel(s)
- v2: combines kernels





# Specify model

- Define the question:
  - ✓ feature set
  - ✓ classes / samples
  - ✓ machine and parameters
  - ✓ cross-validation (inner & outer)
  - ✓ data operations



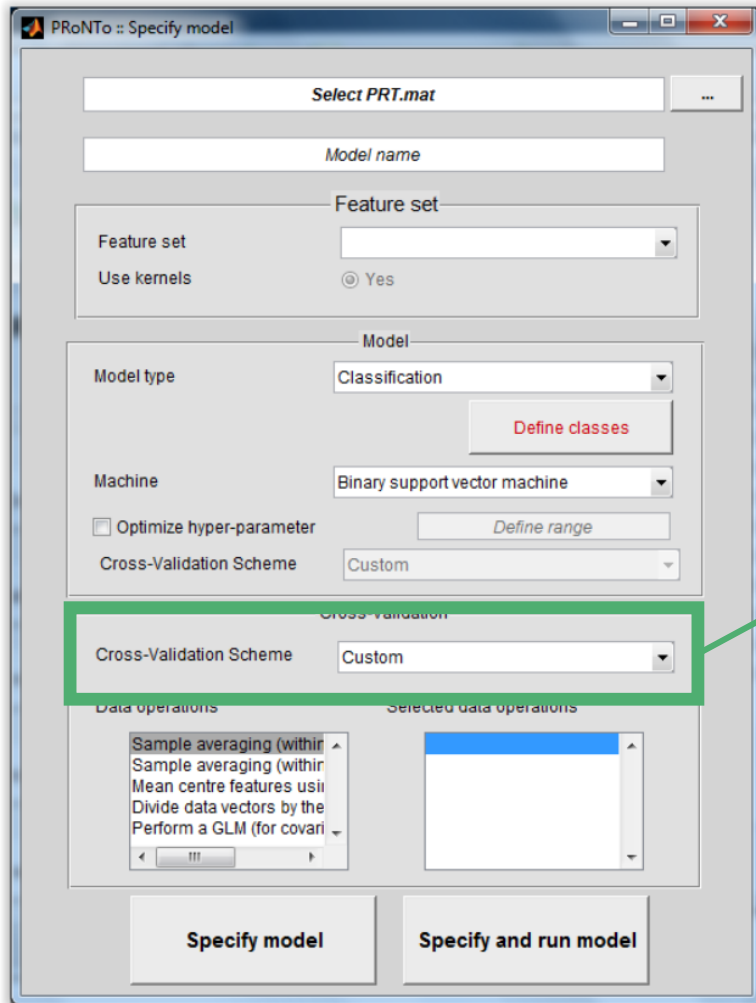


# Machines

- Classification:
  - ✓ SVM (LIBSVM)
  - ✓ Gaussian Processes (GPML)
  - ✓ L1-MKL (simpleMKL)
- Regression:
  - ✓ RVR
  - ✓ KRR
  - ✓ Gaussian Processes (GPML)
  - ✓ L1-MKL (simpleMKL)



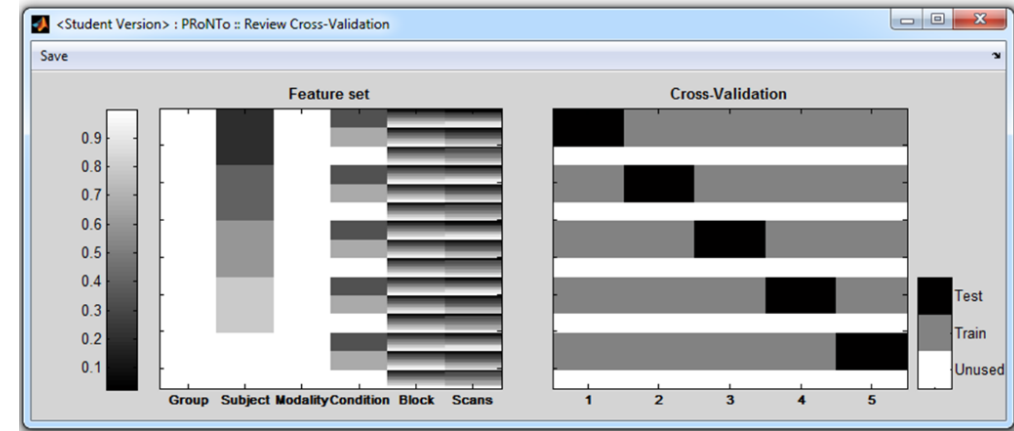
# Cross-validation



Standard approaches:

- LOSO
- LOBO
- LORO
- LOSCO
- k-fold CV

Flexible CV schemes allowed



Define CV

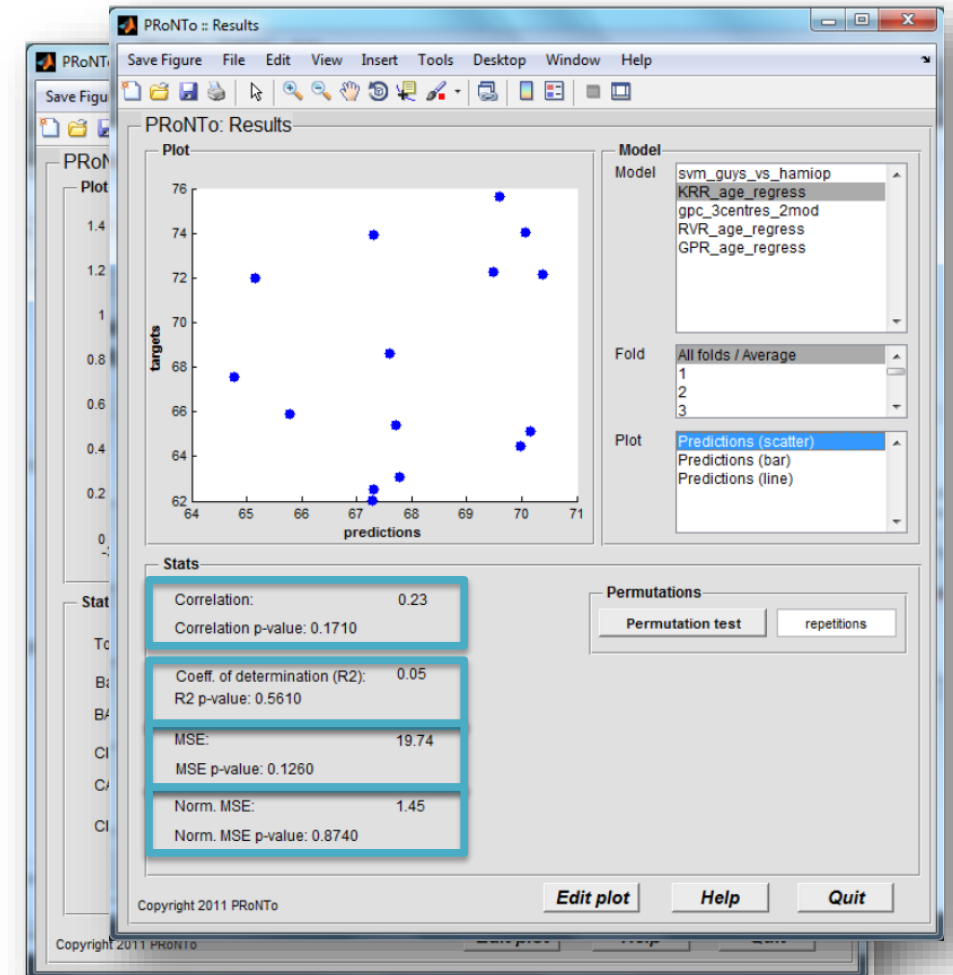
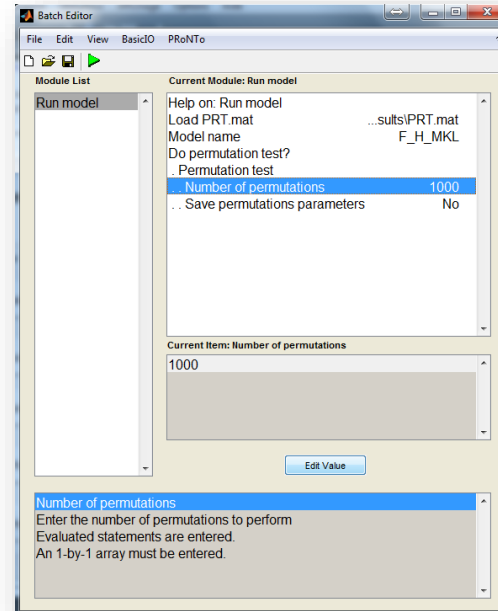
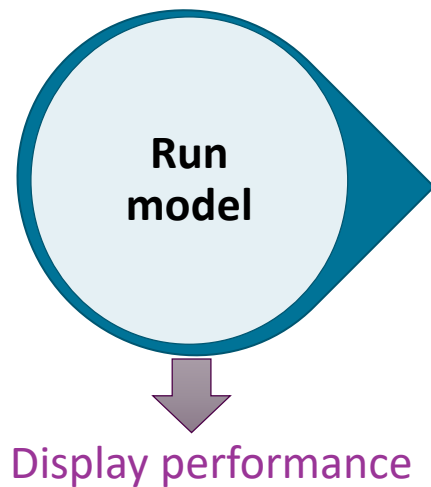
	fold 1	fold 2	fold 3	fold 4	fold 5
Faces	2	1	1	1	1
Faces	2	1	1	1	1
Faces	2	1	1	1	1
Faces	2	1	1	1	1
Faces	2	1	1	1	1
Faces	2	1	1	1	1
Faces	2	1	1	1	1
Faces	2	1	1	1	1
Faces	2	1	1	1	1
Faces	2	1	1	1	1
Faces	1	2	1	1	1
Faces	1	2	1	1	1
Faces	1	2	1	1	1
Faces	1	2	1	1	1
Faces	1	2	1	1	1
Faces	1	2	1	1	1
Faces	1	2	1	1	1

Buttons: Save, Done



# Run model

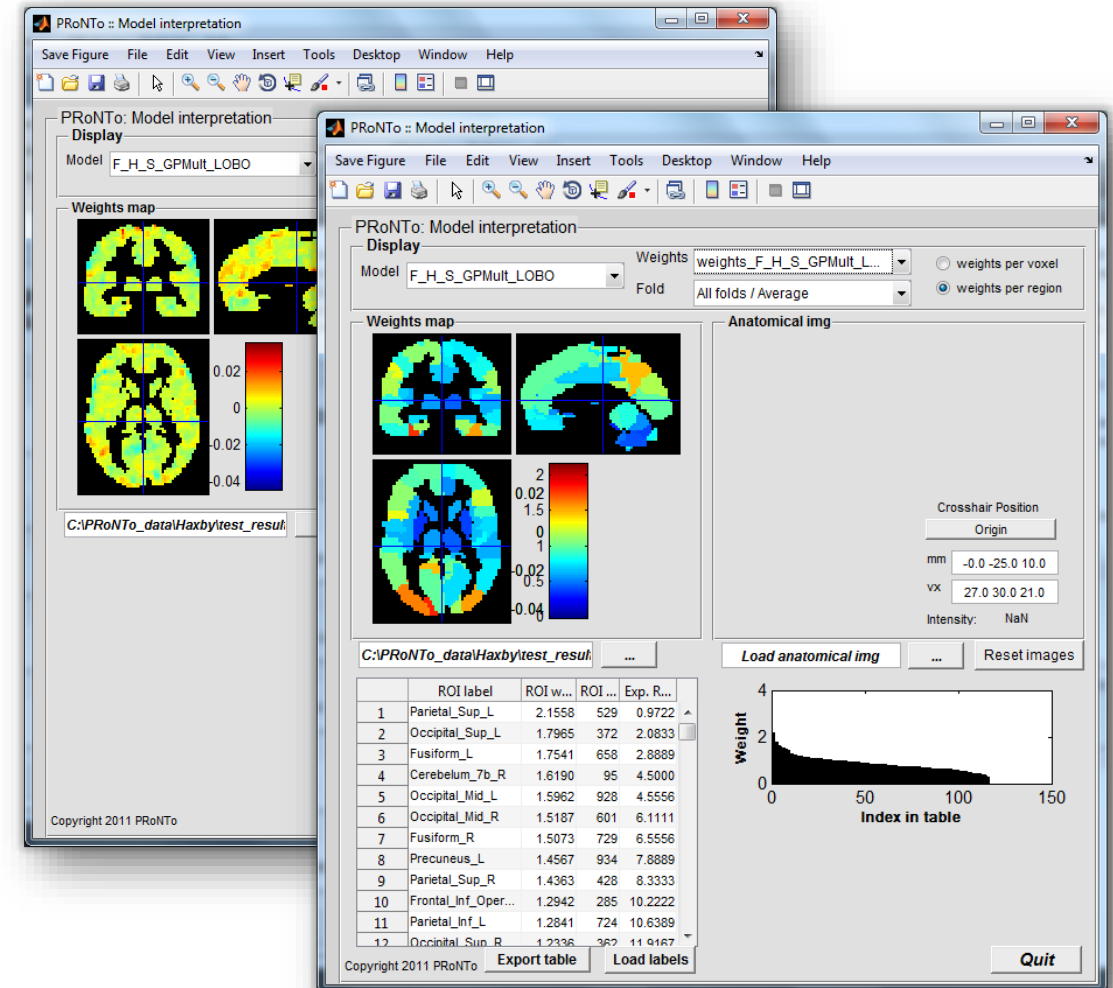
- Estimates the model
- Batch: runs permutations





# Compute weights

- Build voxel weights
- Maps back to original image
- ROI contributions:
  - ✓ average from atlas (post-hoc)
  - ✓ kernel contribution (MKL)





# Thank you!

## Questions?





# PRoNTo for developers

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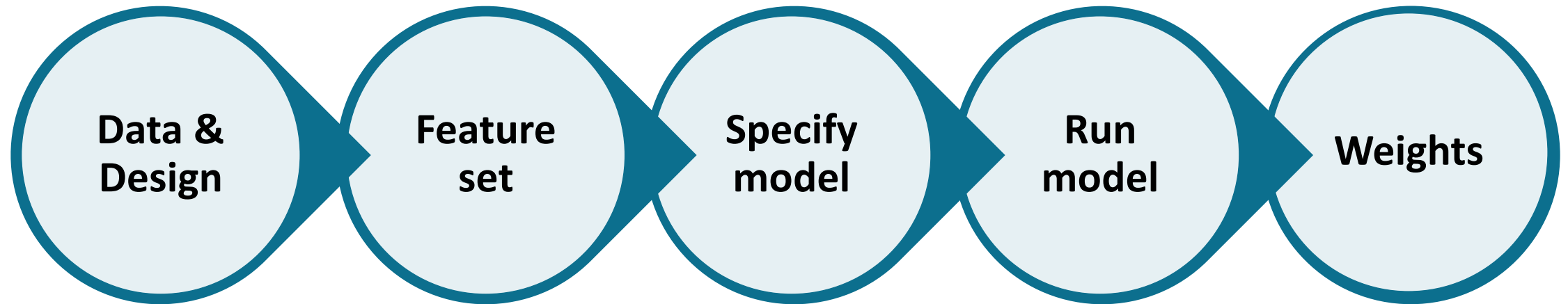
# PRoNTo for developers

- Tool box: use PRoNTo as a basis for developments
- Avoids to re-code e.g. cross-validation when new data/model
- Established framework: less prone to errors, double dipping



# PRoNTTo architecture

- Modular

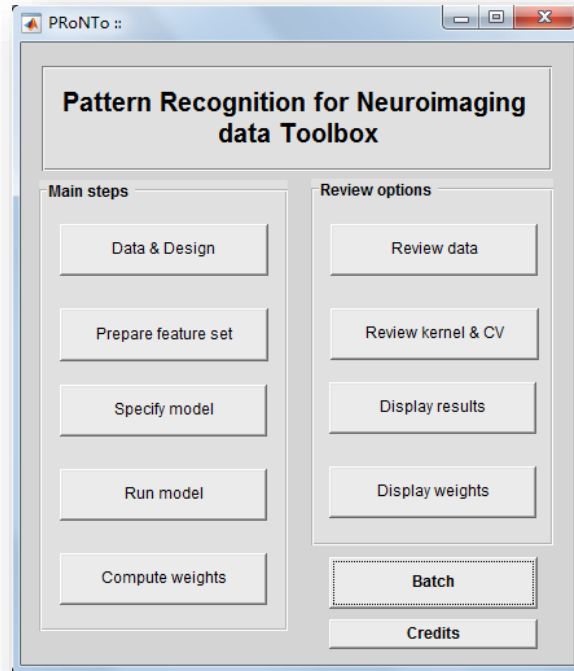


- User interfaces
- Core functions
- All written in Matlab with occasional mex interfaces

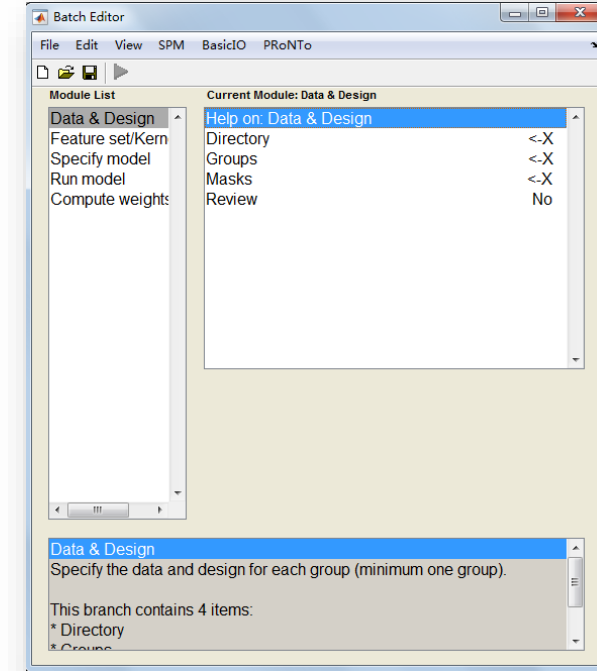


# PRoNTTo architecture

## GUI



## Batch



Core functions



# PRT structure

- Similar to SPM structure
- Saved in folder as 'PRT.mat'
- PRT has one or 2 fields per module
- Load and dig:

The screenshot shows the MATLAB environment. The 'Current Folder' pane on the left lists files including 'comb.mat', 'Feature\_set\_mr1.dat', 'Feature\_set\_mr2.dat', 'mr12.mat', 'PRT.mat', and several weight files. 'PRT.mat' is selected. The 'Command Window' on the right shows the following commands and output:

```
>> PRT  
  
PRT =  
  
struct with fields:  
  
    group: [1x1 struct]  
    masks: [1x2 struct]  
         fs: [1x1 struct]  
         fas: [1x2 struct]  
    model: [1x1 struct]  
  
>> PRT.model(1).output.stats  
  
ans =  
  
struct with fields:  
  
    con_mat: [2x2 double]  
         acc: 0.4000  
    c_acc: [2x1 double]  
    b_acc: 0.3333  
    c_pv: [2x1 double]  
    acc_lb: 0.1176  
    acc_ub: 0.7693
```

At the bottom of the Command Window, the prompt 'fx >> |' is visible.



# Core functions

- One function per module
- Ideal for scripting:
- Not for Data & Design step
- Best for running models

```
function [outfile] = prt_cv_model(PRT,in)
% Function to run a cross-validation structure on a given model
%
% Inputs:
% -----
% PRT:          data structure
% in.fname:     filename for PRT.mat (string)
% in.model_name: name for this model (string)
%
% Outputs:
% -----
% Writes the following fields in the PRT data structure:
%
% PRT.model(m).output.fold(i).targets:    targets for fold(i)
% PRT.model(m).output.fold(i).predictions: predictions for fold(i)
% PRT.model(m).output.fold(i).stats:      statistics for fold(i)
% PRT.model(m).output.fold(i).{custom}:   optional fields
%
% Notes:
% -----
% The PRT.model(m).input fields are set by prt_init_model, not by
% this function
%
% Copyright (C) 2011 Machine Learning & Neuroimaging Laboratory
```



# Scripting example - 1

- Simulated data: one feature set per SNR and sparsity
- $19 * 15 = 285$  models
- Power using PRoNTTo:
  - Home script
  - Batch to create feature set
  - Load PRT
  - Use a pre-defined model as basis
  - Replace the feature set
  - Run and extract performance

```
|function [PRT] = pronto_analysis(fname,prtname,channel_file)

load(prtname)
path = spm_fileparts(prtname);
% Replace file name by new file name
PRT.group.subject.modality.scans = fname;
PRT = rmfield(PRT,{'fs','fas','model'});
save(fullfile(path,'PRT.mat'),'PRT')

% Build feature set
batch_create_feature_set(prtname,channel_file)
load(prtname)

% Specify models
batch_specify_models_pronto(prtname)
load(prtname)

% Run models
in.fname = prtname;
in.model_name = 'SVM';
prtname = prt_cv_model(PRT,in);
```



# Scripting example - 2

- Permutations can be lengthy
- Can run code on cluster
- Different strategies:
  - one job per xx permutations
  - using parfor
  - spmd
  - Batch or prt\_permutations
  - Careful with graphical/workspace output

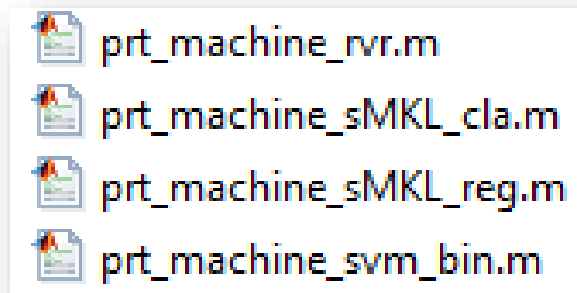
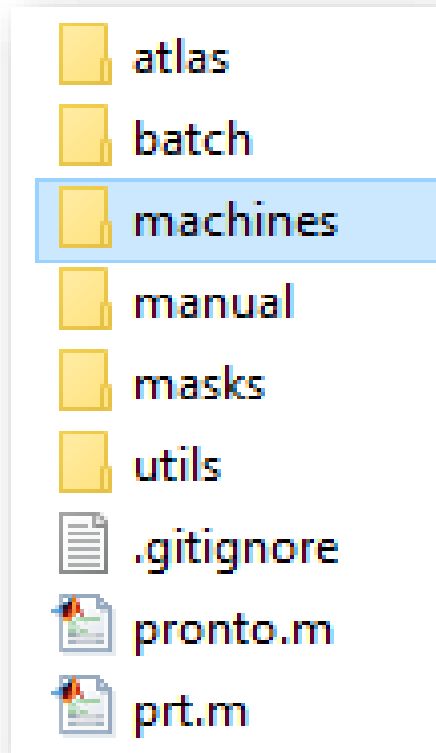
```
function [] = prt_permutation(PRT, n_perm, modelid, path, flag)
% Function to compute permutation test
%
% Inputs:
% -----
% PRT:      PRT structure including model
% n_perm:   number of permutations
% modelid:  model ID for model to test and model to copy permutations from
%           (optional). Can hence be of size 1x1 or 1x2.
% path:     path
% flag:     boolean variable. set to 1 to save the outputs for each
%           permutation. default: 0
%
```



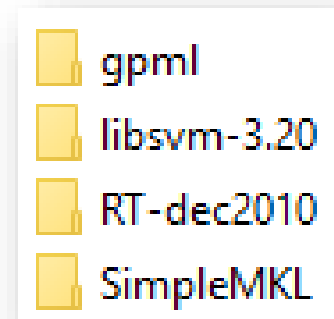


# PRoNTTo machines

- PRoNTTo interfaces libraries



Wrapper functions



Third-party libraries



# New machine

- Can interface your classification/regression algorithm



prr\_machine\_esvr.m

```
function output = prr_machine_esvr(d,args)
% Run Epsilon-SVR - wrapper for libSVM
% FORMAT output = prr_machine_esvr(d,args)
% Inputs:
%   d - structure with data information
%       .train - training data (cell array of [Ntr x D]). Each m
%               of the data. This is used for multiple kernel learning
%       .test  - testing data (cell array of [Nte x D])
%       .tr_targets - training labels (for classification or regression) (column vector)
%       .use_kernel - flag, is data in form of features (false)
%       args - libSVM arguments
% Output:
%   output - output of machine (struct).
% * Mandatory fields:
%   .predictions - predictions of classification or regression
% * Optional fields:
%   .func_val - value of the decision function
%   .type - which type of machine the
```

Re-arrange  
inputs/outputs  
and arguments







esvr\_train.m  
esvr\_predict.m

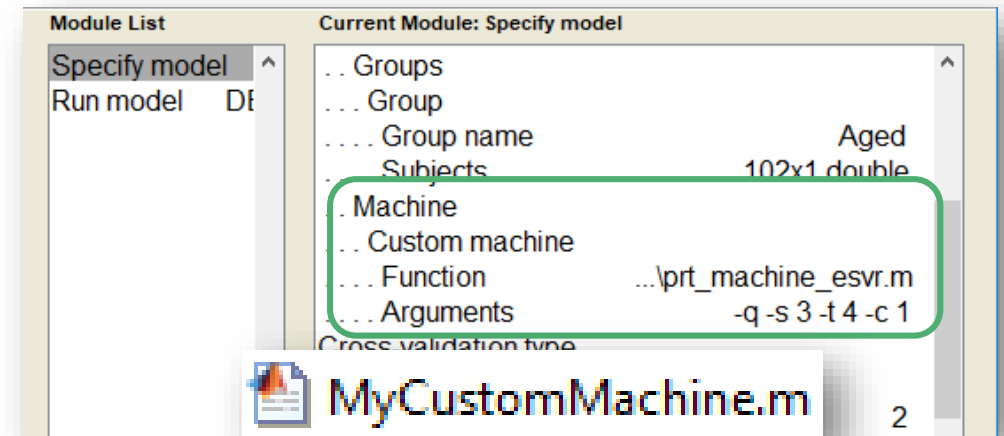


# New machine: further considerations

- labels: 1 for class 1, 2 for class 2, ...
- Hyper-parameter optimization: careful with string arguments
- Use 'custom machine'
- Compiled machine?
- Weight computation:
  - Default: linear kernel
  - If not: need to specify weight function

 prt\_weights\_bin\_linkernel.m  
 prt\_weights\_gpclap.m  
 prt\_weights\_sMKL\_cla.m  
 prt\_weights\_sMKL\_reg.m

$$\rightarrow w = \sum \alpha x_i$$



$$w \neq \sum \alpha x_i$$



# Contributing

- Yes!
- Next releases in Github
- Need to interface: GUI and batch
- Backwards compatibility
- Matlab backwards compatibility and toolbox codes
- Coming soon: developer's manual



# Thank you!

## Questions?



# PRoNTo v3.0

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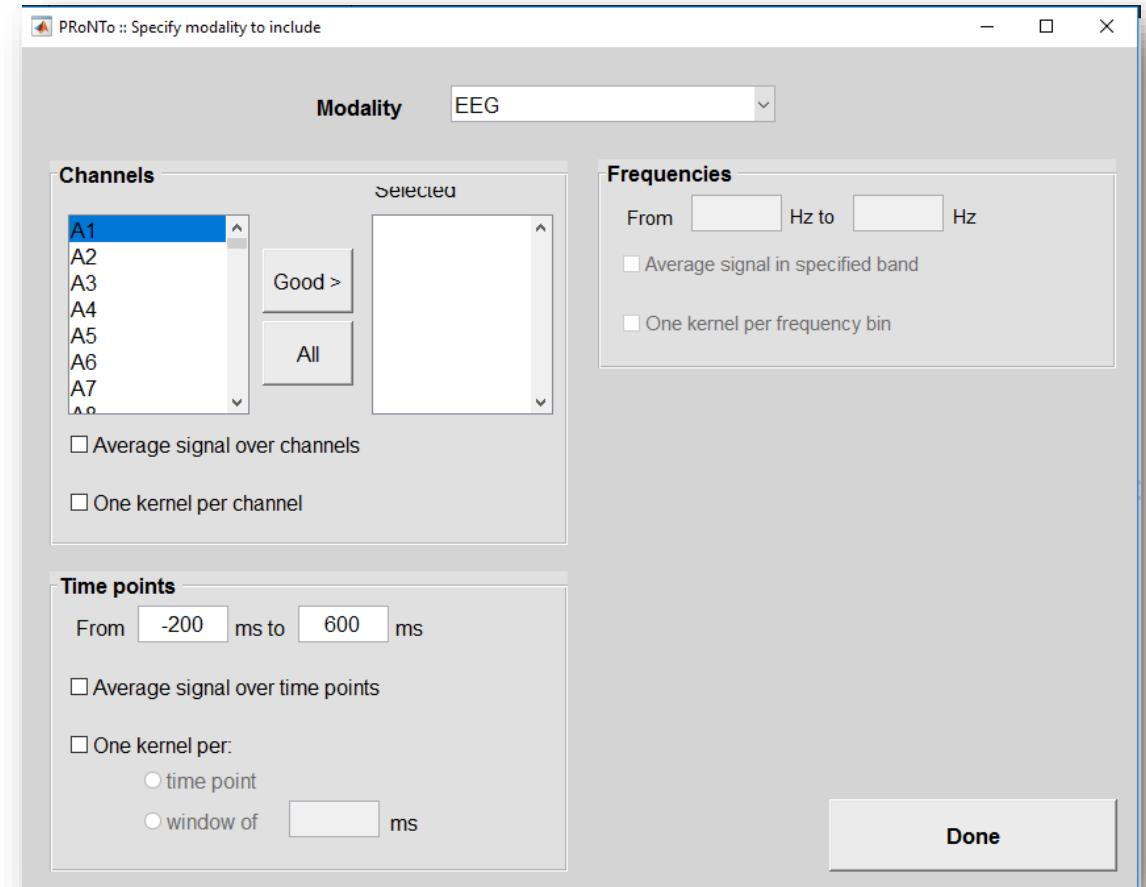
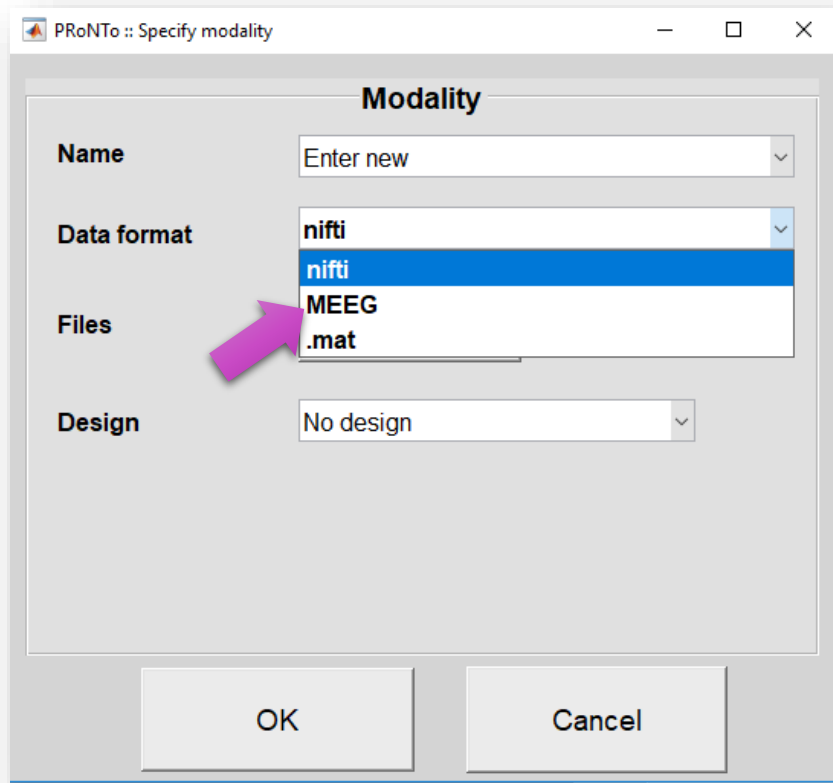
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# New input formats

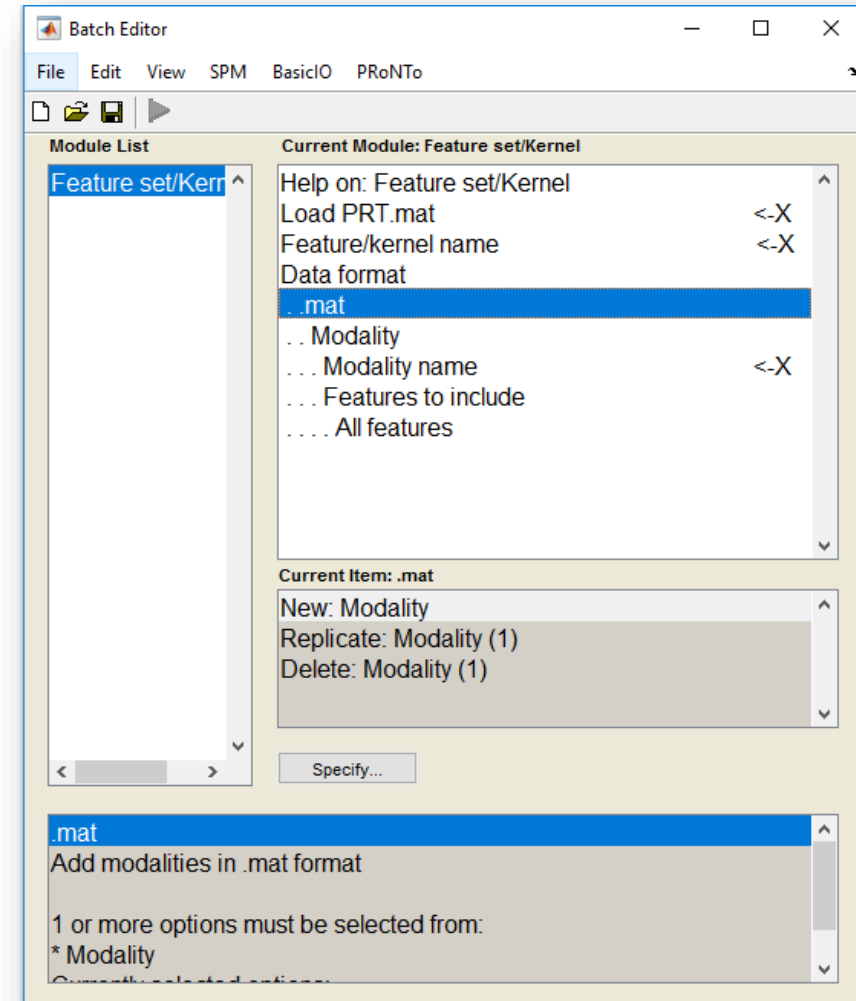
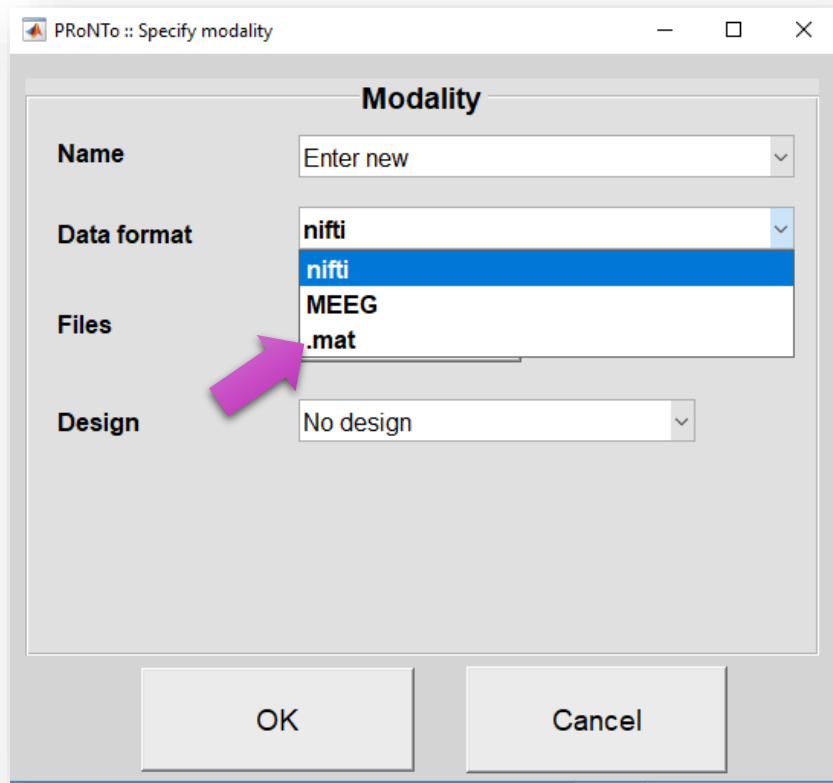
- SPM MEEG





# New input formats

- .mat







# New functionalities

- Non-kernel methods
- Combining different data formats (e.g. EEG and fMRI)
- Multi-Task Learning
- Test model module: share PRT and weight maps
- and much more ...



# Thank you!

## Suggestions?



# Hands-on session

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# Demo

- OASIS data set
- 50 demented – 50 non-demented
- Confounds: age and gender (boolean)
- Two features extracted: grey and white matter
- **Goal:** classify demented from non-demented