PRoNTo: Pattern Recognition for Neuroimaging Toolbox

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Introduction

Mass univariate analyses have recently been complemented by the use of *multivariate pattern analyses*, in particular using machine learning based predictive models [1]. These analyses focus on predicting a variable of interest (e.g. mental state 1 vs. mental state 2, or patients vs. controls) from the pattern of brain activation/anatomy over a set of voxels. Due to their multivariate properties, these methods can achieve relatively greater sensitivity and are therefore able to detect subtle, spatially distributed activations and patterns of brain anatomy.

While these tools can help investigating brain function or the evolution of a disease, their use often requires (high-level) programming skills. For instance, one sophisticated software package currently available (PyMVPA, [2]) allows advanced machine learning modeling of neuroimaging data but it does not provide graphical interfaces nor comprehensive displays of results.

Therefore, the goal of this project was to develop a user-friendly and open-source toolbox that could make machine learning modeling available to every neuroscientist.

Methods

PRoNTo [3] is a Matlab-based, SPM compatible toolbox, which can be used in three ways: graphical user-interface, Matlab batch system (developed at [4]) or scripting function calls. The toolbox is organized in modules (Fig. 1), allowing for flexible Multi-Variate Pattern Analyses (MVPA) based on machine learning models.

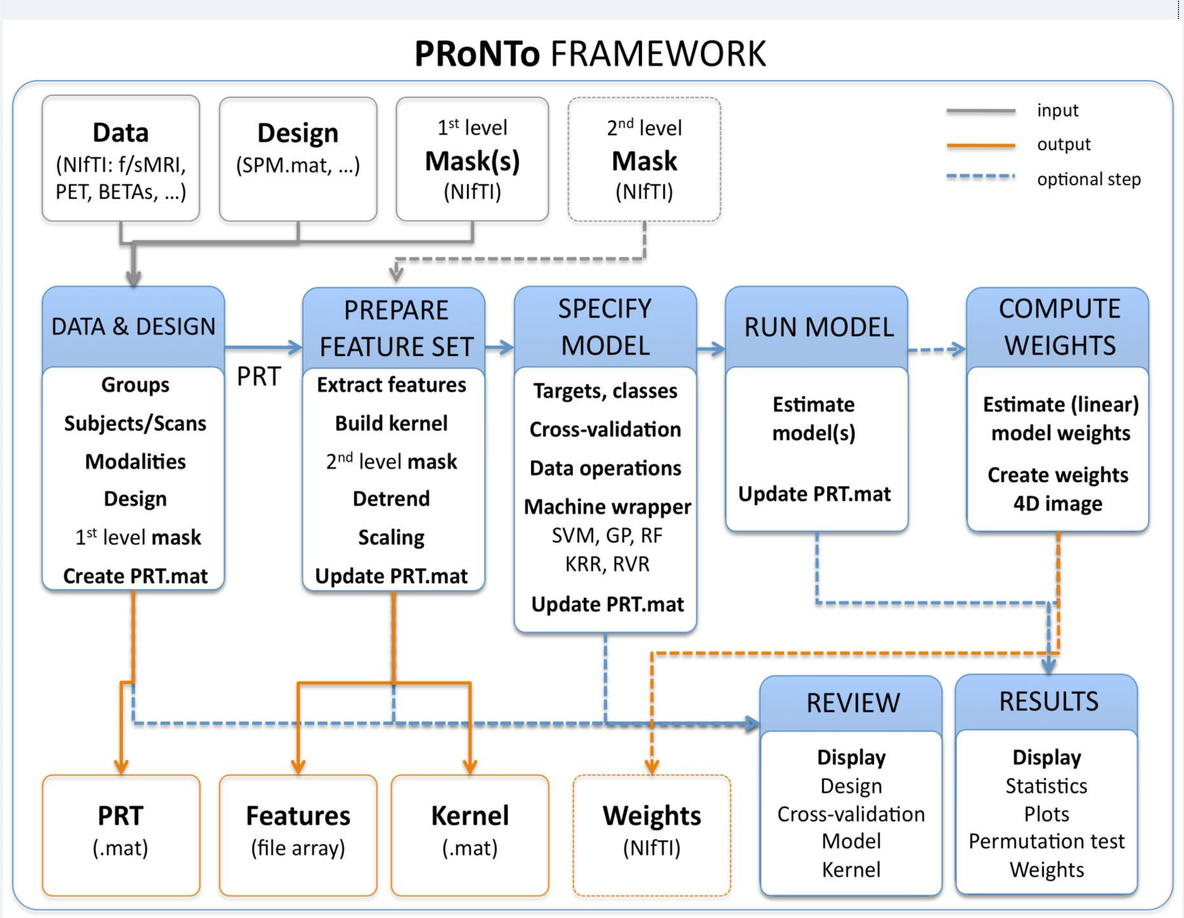

Fig. 1: PRoNTo framework. The main modules are represented in blue, with their respective inputs (in grey) and outputs (in orange). They form the main analysis pipeline. Optional steps are represented by dashed arrows. Finally, the 'Review' and 'Results' modules contain the different displays available for reviewing data, design, model, cross-validation or results.

Results

PRoNTo provides a user-friendly and flexible environment to address different research questions, such as:

1. Does the pattern of activation in brain regions A, B and C encode information about a variable of interest? (Fig. 2)
2. How do we account for the hemodynamic response function (HRF) in pattern recognition analyses and how much does correcting for the HRF affect classification results?
3. Which type of features discriminates best between groups (e.g. patients vs. controls or young vs. old subjects)?
4. Can we predict continuous measures from brain scans, and how do we deal with continuous clinical values? (Fig. 3A).
5. Can we predict the scanners on which different brain scans were acquired? (Fig. 3B)

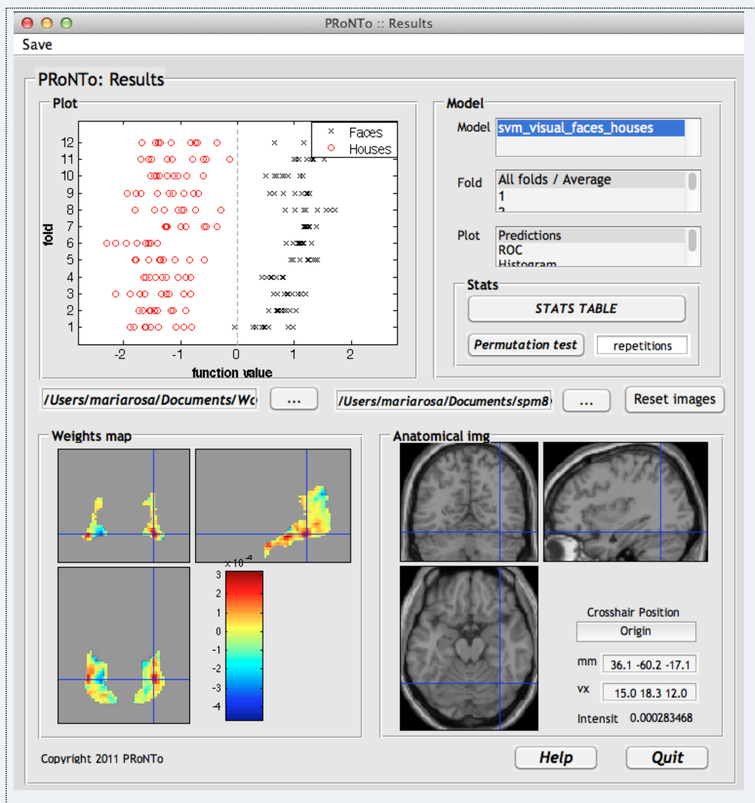

Fig. 2: PRoNTo main (right) and results (left) interfaces. PRoNTo outputs include: predicted values (per fold), histograms of function values for each class, ROC curves, 3D confusion matrices, model stats, permutation test results and weights visualisation. Plots from Fig.2 are for SVM [5] classification of houses vs. faces (Haxby dataset [6]) using a visual cortex mask.

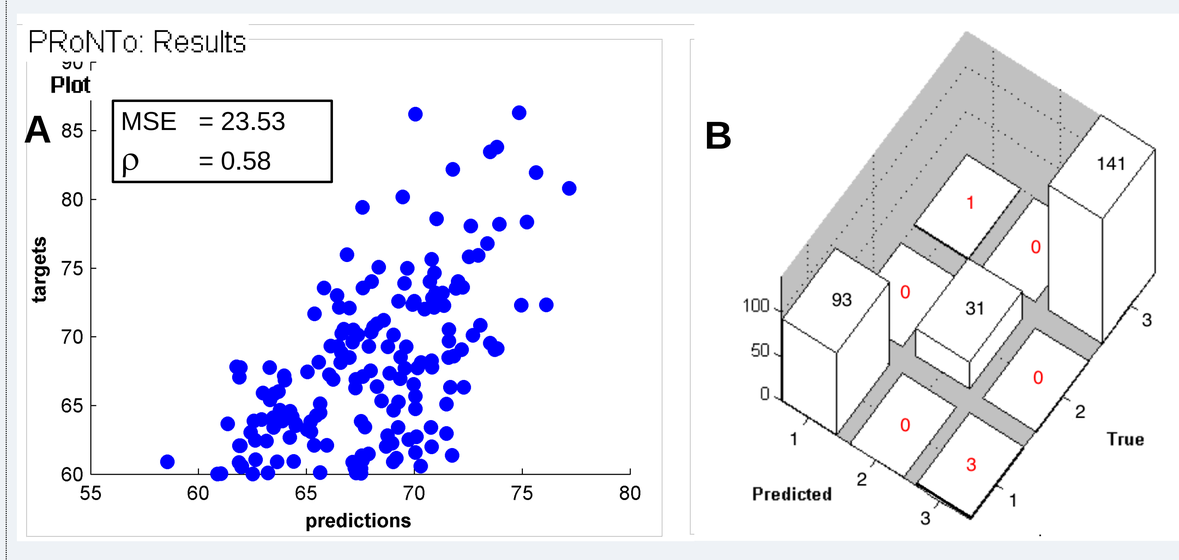

Fig. 3: IXI dataset [7]. A Scatter plot of the predictions from the regression performed on subjects aged 60 to 90 according to their respective targets (age), with the Mean Squared Error (MSE) and correlation between predictions and targets (ρ). **B** Confusion matrix from the classification between centers from subjects aged 20-30 and 60-90.

Conclusions

PRoNTo = Pattern Recognition for Neuroimaging Toolbox

- ***Free Matlab-based software for pattern recognition***
- ***Available at: http://www.mlnl.cs.ucl.ac.uk/pronto/ with manual and tutorials***
- ***Comprehensive, user-friendly software framework***
- ***Compatible with SPM, but also with graphical interfaces, batching and scripting***
- ***Flexible and accommodating multiple modalities (e.g. sMRI, fMRI, PET, …)***
- ***Modular design to be easily extended: feature selection and extraction, validation procedures or classification/ regression models.***

References

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