

Pitfalls: Accuracies

Underestimating information Classification accuracies reflect the result of a complex sampling of single cell populations. Because a voxel might sample more than a million neurons the information might be underestimated at the level of voxels.

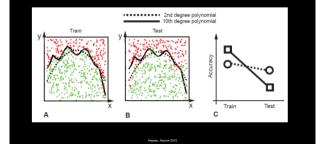
Overestimating information The hemodynamic delay might integrate information across longer timescales than neuronal integration time windows. Thus, the single-cell population information might be overestimated.

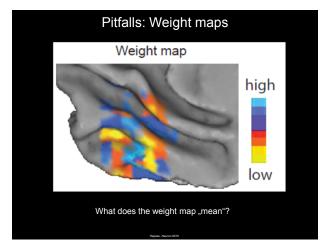
Comparison across areas Different regions might have different sampling patterns, different numbers of neurons and voxels, different SNRs, different hemodynamic response efficiencies, etc. Thus, a direct comparison of information across regions is not possible.

Processing options Levels of accuracy depend on partitioning of data into training and test

Pitfalls: Circularity and overfitting

Proper cross-validation If different classifiers and parameters are used (linear, nonlinear, parametric, nonparametric, etc.) this needs to be done in a nested cross-validation, otherwise accuracies can be biased.

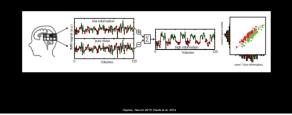


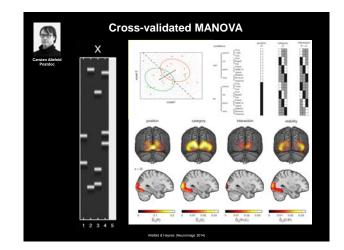


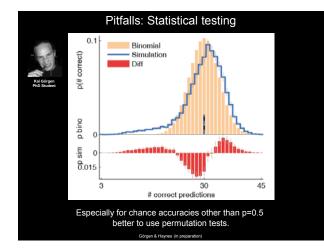
Pitfalls

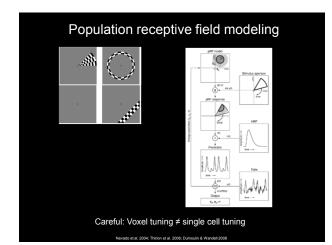
A weight map pertains to a classifier as a whole and does not (directly) allow to interpret the involvement of individual voxels → presurgical mapping

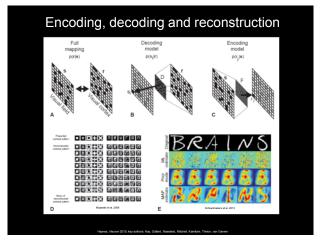
If a voxel has a positive weight this does not imply that this voxel has "information" about the labels.

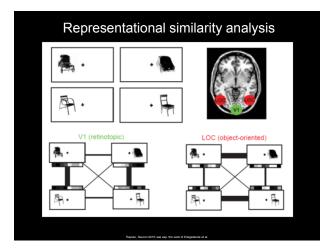


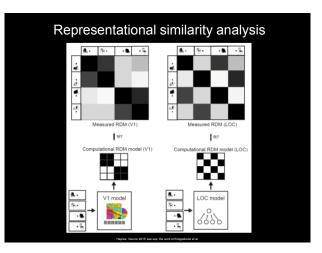














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