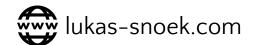






Multivariate pattern analysis

Spinoza fMRI Course





About me

- PhD-student at the University of Amsterdam, lab of Steven Scholte
- Interested in emotion (perception), face perception, and (fMRI) methodology/ computational modelling
- Teaching two courses on fMRI analysis

- Teach you the basics of "multivariate pattern analysis", MVPA (the how, what, and why)
 - Enough to get you started
- Mostly about "decoding" (machine learning)
- For beginners!

- Meant to be interactive ask questions!
- Conceptual, rather than mathematical
- Focuses on <u>f</u>MRI (but applicable to EEG/MEG, structural MRI, etc.)
- Not hands-on
 - But I'll be here tomorrow to help with analyses!

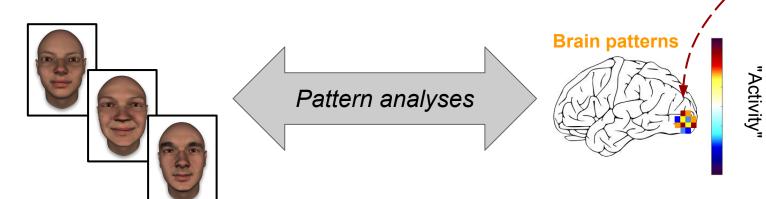
- Introduction
- Why?
 - Why look at patterns instead of single voxels?
- What?
 - Decoding and related concepts
- How?
 - How to set up a complete decoding pipeline

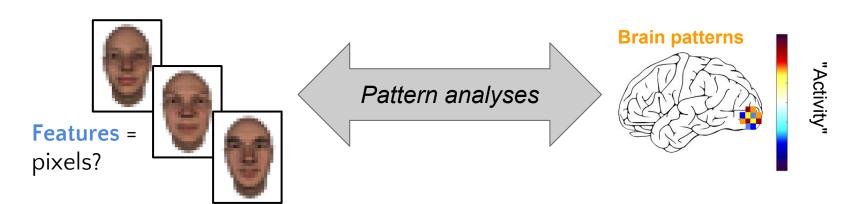
- Introduction
- Why?
- What?
- How?

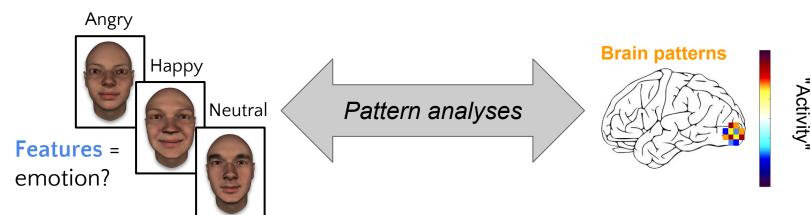
- Introduction
- Why?
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- How?

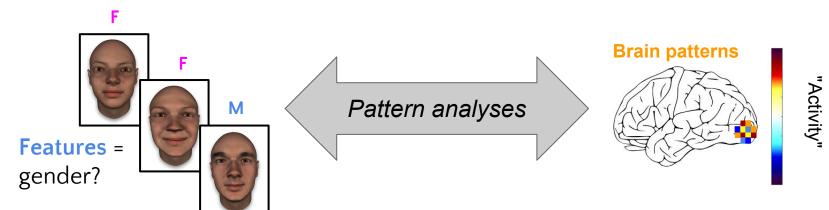
"Multivariate" (sometimes "multivoxel") refers to the brain patterns (>1 voxel)

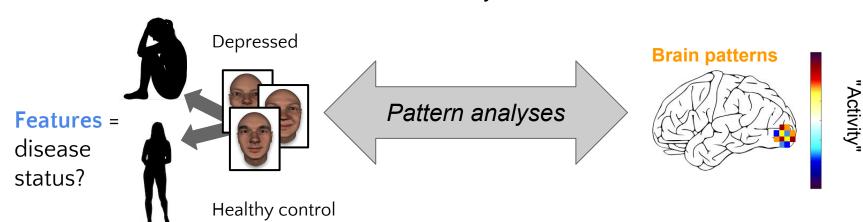
What is MVPA?







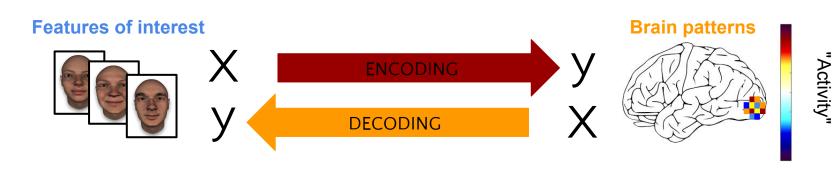




- There are many different types of MVPA!
 - "Decoding" (machine-learning)
 - Representational similarity analysis (RSA)
 - Pattern component modeling
 - Cross-validated MANOVA
- Common ground: they operate on patterns of voxels

MVPA vs. univariate analysis

- "Decoding" models (topic of today) are a specific type of MVPA
- Relative to "encoding" models, decoding models differ in the "direction of analysis"





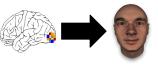
Analysis landscape

Encoding: [5]





Decoding:



Univariate:

Statistical Parametric Mapping (mass-univariate)

pRF models

777

MANOVA

Multivariate:

Pattern component modelling

Machine learning ("decoding")

Inverted encoding models

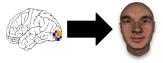


Analysis landscape

Encoding:



Decoding:



Univariate:

Statistical Parametric
Mapping (mass-univariate)

pRF models

???

MANOVA

Multivariate:

Pattern component modelling

Machine learning ("decoding")

Inverted encoding models

Test your understanding!

Tomas measures the gray-matter density of a 100 subjects.

He then wants to investigate whether the gray-matter density in the hypothalamus is predictive of whether someone is male or female.

Encoding?



Decoding?

Test your understanding!

Steven shows TV-commercials which are either boring, funny, or neutral.

He then wants to investigate which brain regions respond more to funny than to boring commercials.

Encoding?

?

Decoding?

Test your understanding!

Noor show subjects images of different complexity ('visual clutter').

She then wants to analyze whether these complexity parameters can explain the voxel patterns in early visual cortex.

Encoding?

?

Decoding?

Contents

- Introduction
- Why?
- What?
- How?

Why <u>pattern</u> analyses?

- Why look at patterns instead of single voxels?
- Three reasons:
 - One practical
 - One theoretical
 - One instrumental

Practical reason

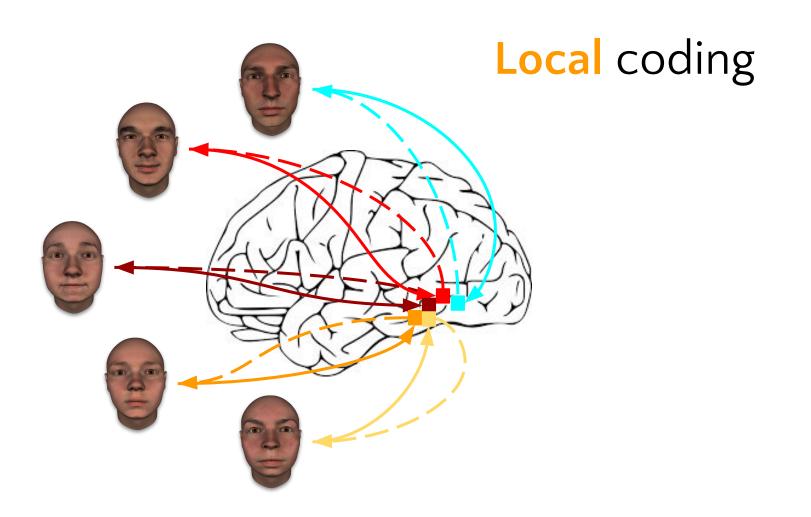
- "It's more sensitive" than univariate analyses
- Effect sizes are often larger in MVPA
- (If you ask me: that's comparing apples and oranges)
- But there are also theoretical reasons for analyzing patterns

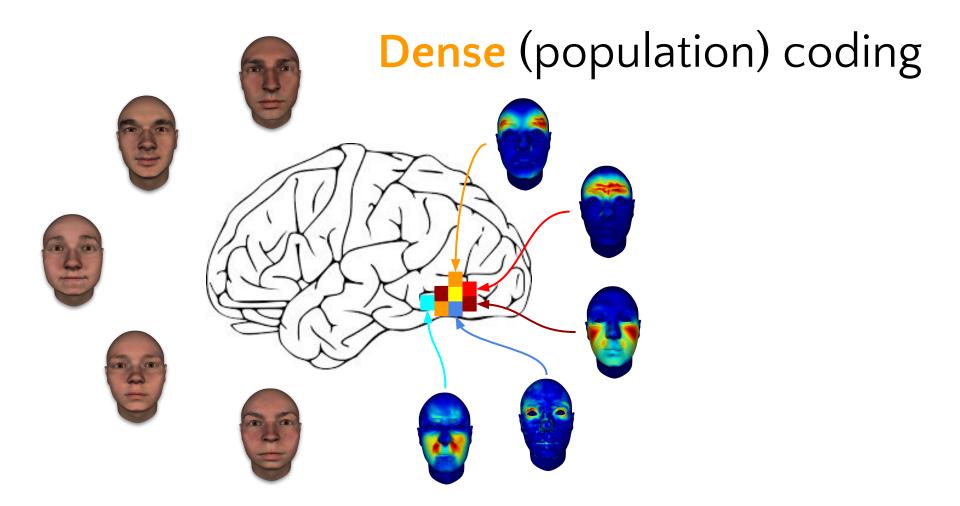
Neural correlations, population coding and computation

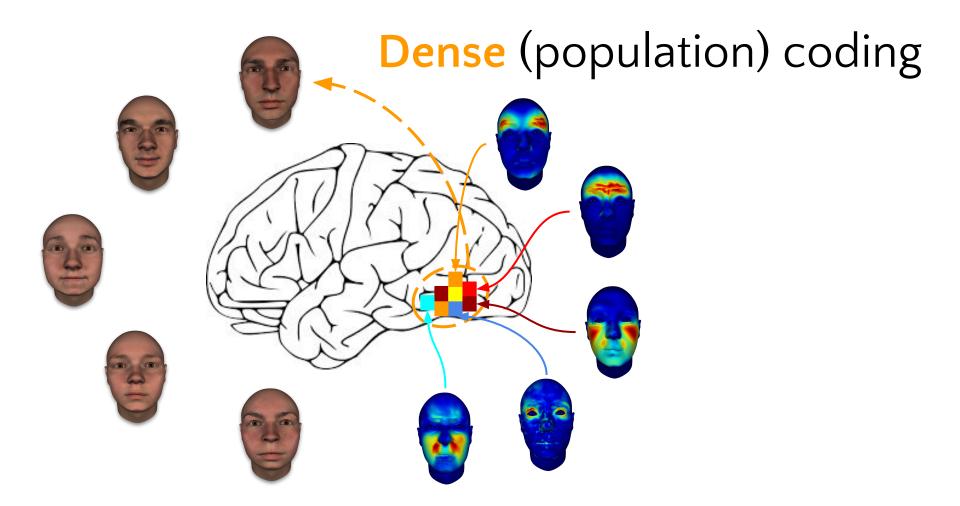
Bruno B. Averbeck*, Peter E. Latham¹ and Alexandre Pouget*

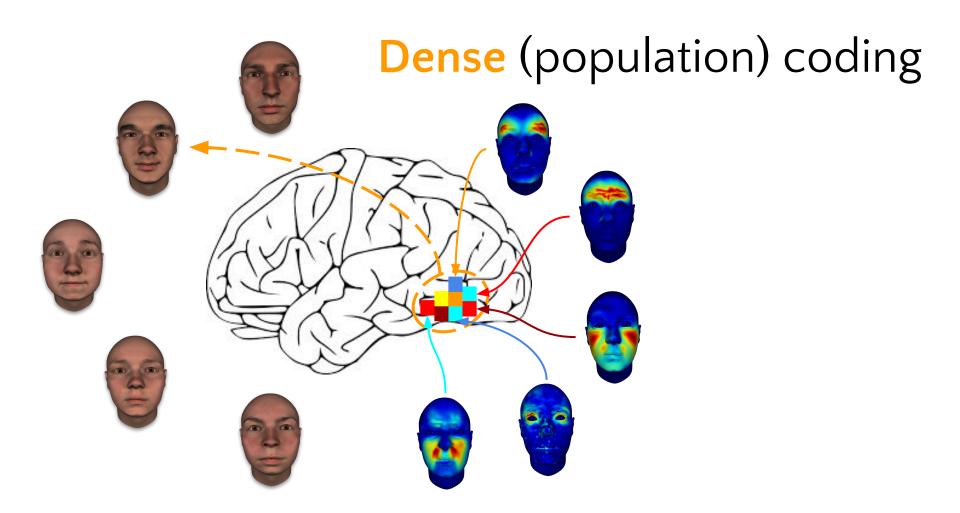


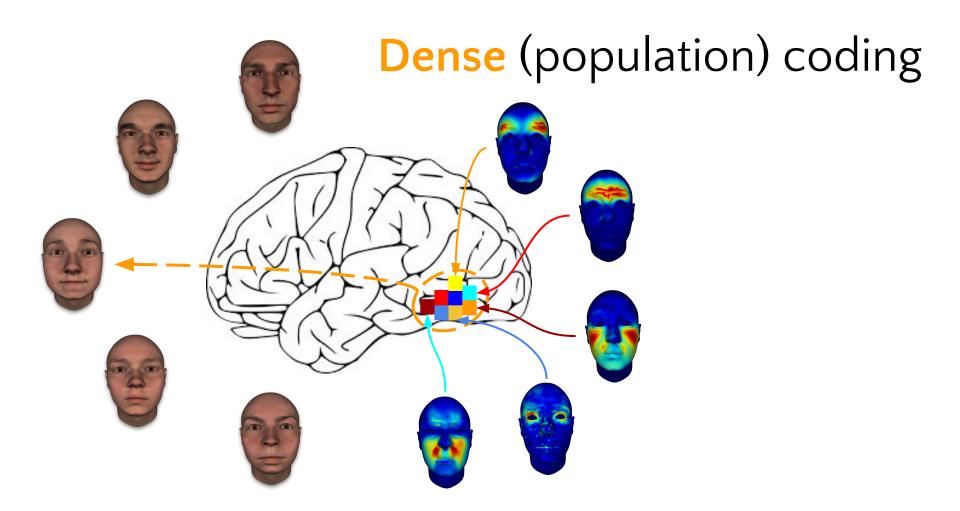
- MVPA fits well with the notion of distributed/dense (population) coding
- Information is not encoded in single or few neurons (or even voxels), but in distributed populations of neurons (voxels)











Instrumental reasons

- As opposed to many other methods, decoding models are predictive
- They can predict new ("out of sample") ...
 - Stimuli (brain reading / reconstruction)

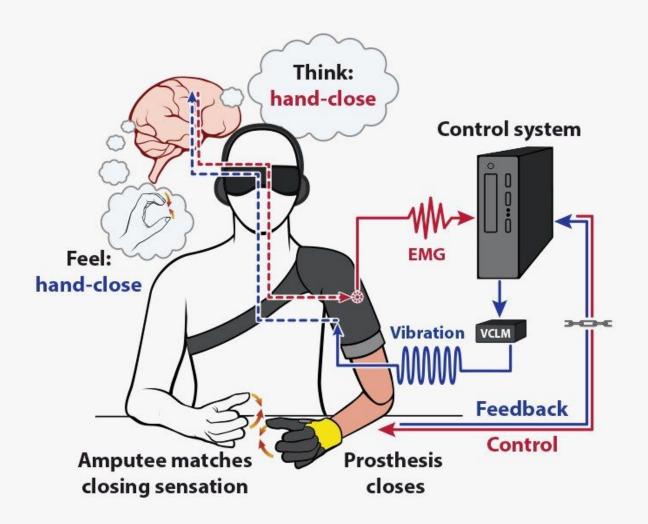
Presented clip



Clip reconstructed from brain activity

Instrumental reasons

- As opposed to many other methods, decoding models are predictive
- They can predict new ("out of sample") ...
 - Stimuli (brain reading / reconstruction)
 - Motor actions



Instrumental reasons

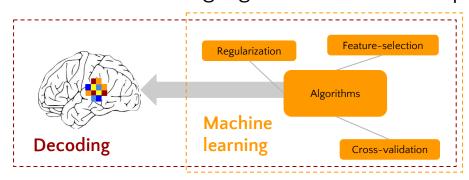
- As opposed to many other methods, decoding models are predictive
- They can predict new ("out of sample") ...
 - Stimuli (brain reading / reconstruction)
 - Motor actions (brain-machine interfaces)
 - Disease development (biomarkers; next talk!)

Contents

- Introduction
- Why?
- What?
- How?

Terminology

- Decoding ≈ machine learning
 - Generic name for brain → stimulus/task analyses;
 - Also: neuroimaging-specific name for application of machine learning algorithms and techniques

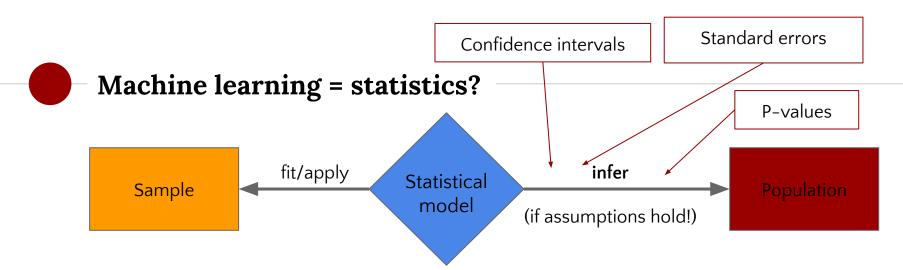


Machine learning = statistics?

- Defining machine learning is (in a way) trivial:
 - "Algorithms that learn how to model the data without an explicit instruction how to do so"
- But how it that different from traditional statistics?
 - Like the familiar GLM (linear regression, t-tests)?
 - Similar, but different ...

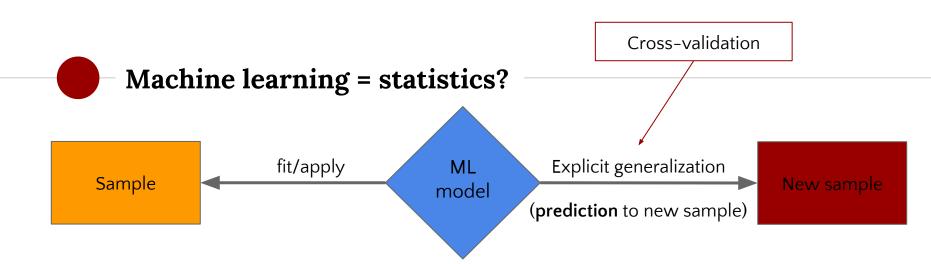
- They have different origins:
 - Statistics is a subfield from mathematics
 - Machine learning is a subfield from computer science
 - "Science vs. engineering"
- They have a different goal:
 - Statistical models aim for inference about the population based on a limited sample
 - Machine learning models aim for accurate prediction of new samples

- Psychologists (you included) are taught traditional statistics: how to make inferences about general psychological "laws" based on a limited sample:
 - "I've tested the reaction time of 40 people (sample) before and after drinking coffee ...
 - ... and based on the significant results of a paired sample t-test,
 t(39), p < 0.05 (statistical test) ...
 - ... I conclude that caffeine improves reaction times (statement about population)

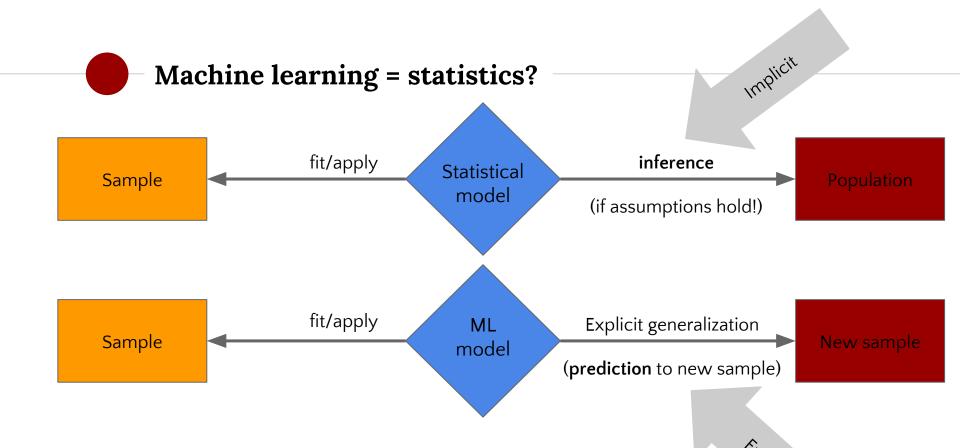


- Crucially: we are quite certain that our findings in the sample will generalize to the population, if and only if assumptions of the model hold (and sample = truly random)
- Uses concepts like standard errors, confidence intervals, and p-values to generalize the model to the population

- ML models do not aim for inference, but aim for prediction
 - Instead of assuming findings will generalize to the population, ML analyses in fact *literally check* whether it generalizes;
 - It's like they're saying: "I don't give a shit about assumptions - if it works, it works."



- Instead of assuming that the findings from the model will generalize beyond the sample, ML tests this explicitly by applying this to ("predicting") a new sample
- New sample is concretely part of your dataset! (not like "the population")



- While having a different goal, in the end both types of models simply try to explain the data;
- Take for example linear regression:
 - It has a statistics 'version' (as defined in the GLM) ...
 - ... and an ML 'version' (using a mathematical technique called gradient descent to find the optimal βs)

So ...?

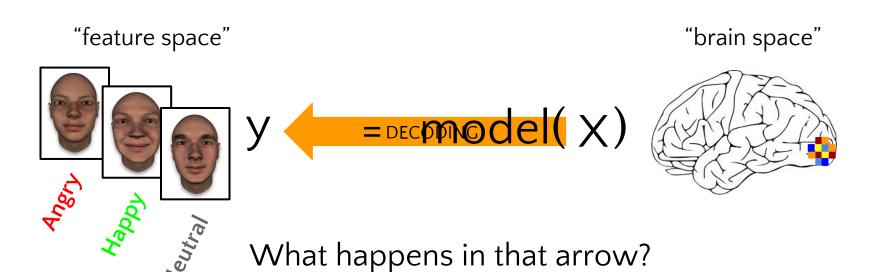
- As said, statistics and ML are the same, yet different;
 - o Both aim to model the data (with different techniques) ...
 - ... but have a different way to generalize findings
- "But why do we have to learn a whole new paradigm (ML), then?", you might ask ...

Good question!

- Traditional statistical models do not fare well with high-dimensional problems
 - In decoding: dimensionality = amount of voxels
- Neuroimaging data likely violates many assumptions of traditional statistical models ...
- Sometimes, decoding analyses actually need prediction specifically: e.g., predict clinical treatment outcome

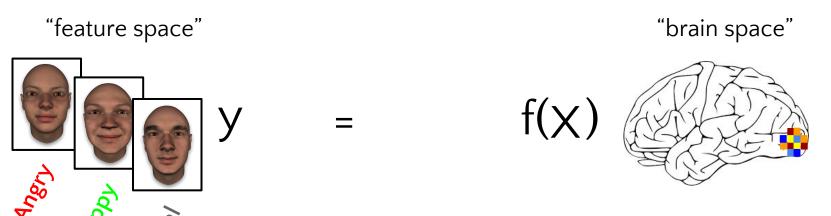


What is decoding?





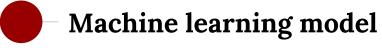
Back to the brain

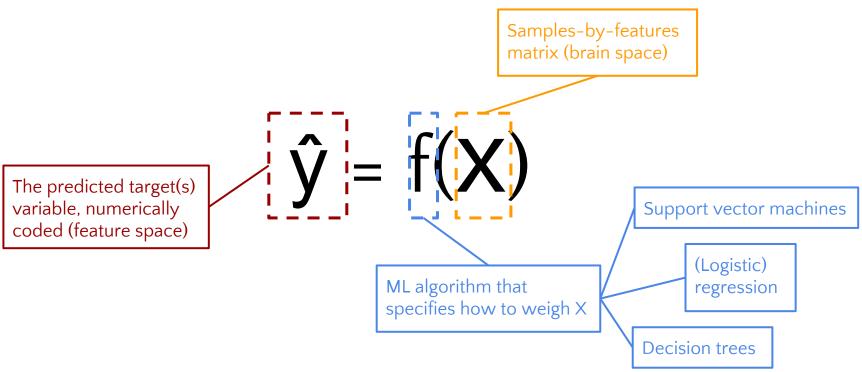


What happens in that arrow?

Machine learning model

- Machine learning algorithms try to model the features (X) such that they approximate the target (y)
- In fMRI (decoding): can the voxel activities (X) be linearly combined ("weighted") such that they approximate the feature-of-interest (y)?





β denotes the weighting parameters (or just "parameters" or "coefficients") for our features (in X)

$$\hat{y} = f(X) = X\beta$$

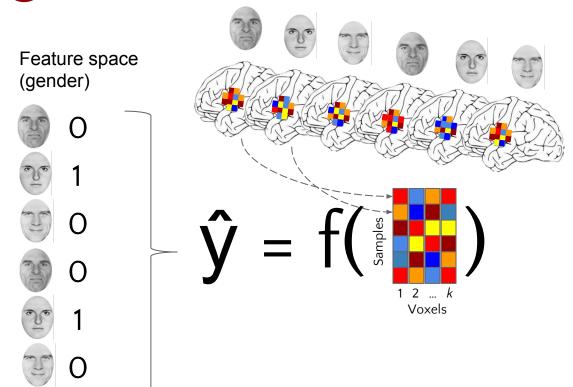
Xβ denotes the (matrix) product of the weighting parameters and X - which means that y is approximated as a weighted linear combination of features

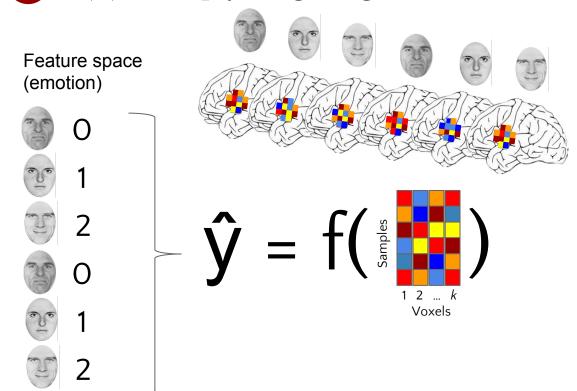
Linear vs. non-linear

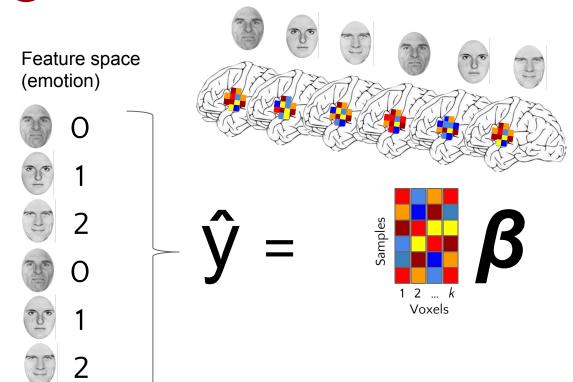
- Disclaimer: the "Xβ" term implies that it is a linear model (i.e. a linear weighting of features)
- Decoding analyses almost always use linear models, because most world ↔ brain relations are probably linear (cf. Naselaris et al., 2011)
- Non-linear models exist, but are rarely used
 - Also because they often perform worse than linear models

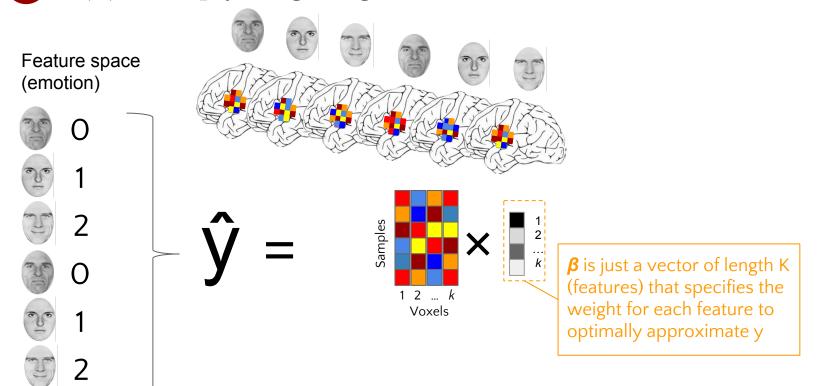
$$\hat{y} = f(X)$$





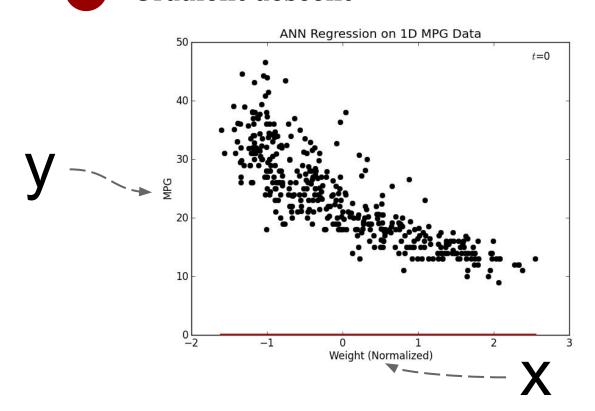






- But **how** does f(X) find the "optimal" weights β ?
- Depends on the specific (linear) ML algorithm!
 - Usually by (intelligently) trying out different values for β until it doesn't improve anymore ("gradient descent")
- Not part of this lecture!

Gradient descent



Model: $y = \beta_0 + X\beta_1$

- Start with $\beta_0 = 0$ and $\beta_1 = 0$
- Update **β** in 'the right direction'
- Repeat until fit doesn't get (much) better ("convergence")

Summary

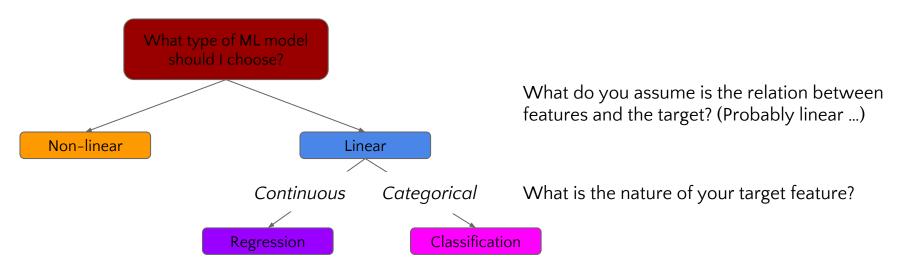
- ML models (f) find parameters (β) that weigh features (X) such that they optimally approximate the target (y)
- Applied to fMRI: we make a model from the brain (X) to the world (y) by optimally weighing voxels!



Questions so far?

Flavors of ML algorithms

• ML algorithms – f() – exist in different 'flavors'





Regression vs. classification

Regression

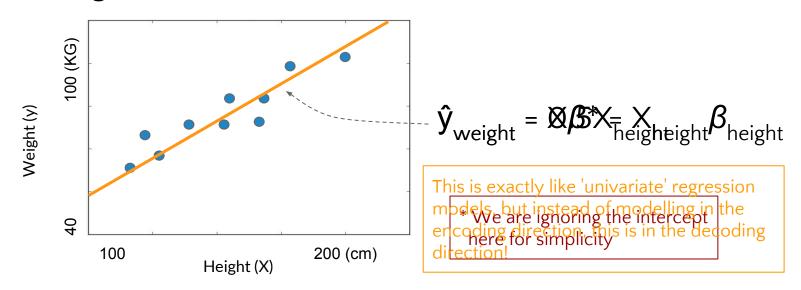
- Target (y) is continuous
- "Predict someone's weight based on someone's height"
- Example models: linear regression, ridge regression, LASSO

Classification

- Target (y) is categorical
- "Predict someone's gender based on someone's height"
- Example models: support vector machine (SVM), logistic regression, decision trees,

Regression

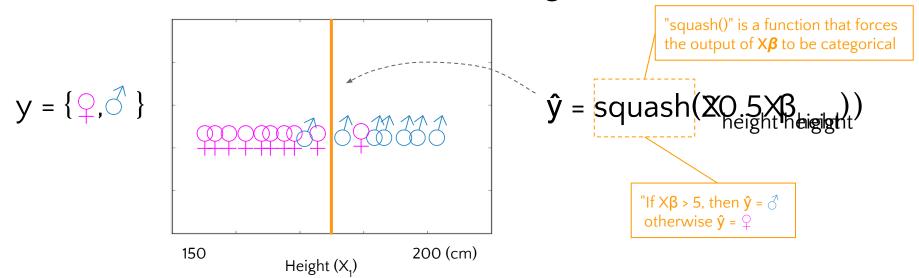
Regression models a continuous variable





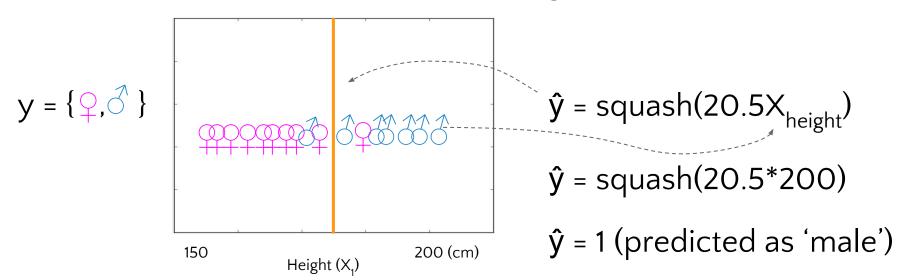
Regression vs. classification

Classification models a categorical variable



Regression vs. classification

Classification models a categorical variable



Test your knowledge!

Subjects perform a memory task in which they have to give responses. Their responses can be either correct or incorrect.

I want to analyze whether the patterns in parietal cortex are predictive of whether someone is going to respond (in)correctly.

Classification



Regression

Test your knowledge!

During fMRI acquisition, subjects see a set of images of varying emotional valence (from 0, very negative, to 100, very positive).

I want to decode stimulus valence from the bilateral insula.

Classification



Regression

Test your knowledge!

Subjects perform an attentional blink task in the scanner (during which we measure fMRI).

I want to predict whether someone has a relatively high IQ (>100) or low IQ (<100) based upon the patterns in dorsolateral PFC during the attentional blink task.

Classification

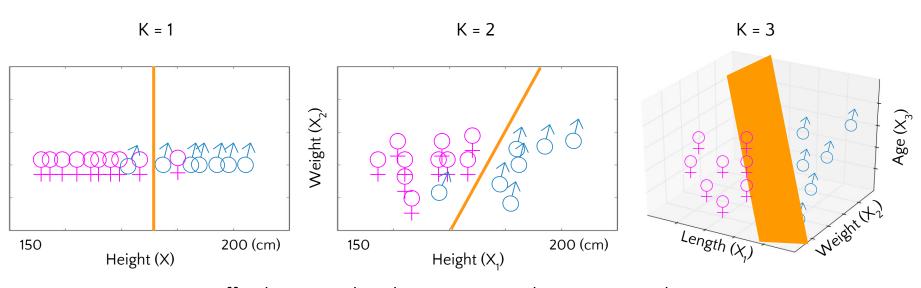


Regression

Regression & classification

- Both types of model try to approximate the target by 'weighting' the features (X)
 - Additionally, classification algorithms need a "squash" function to convert the outputs of Xβ to a categorical value
- The examples were simplistic (K = 1); usually, ML models operate on high-dimensional data (K > 200,000)!

Dimensionality



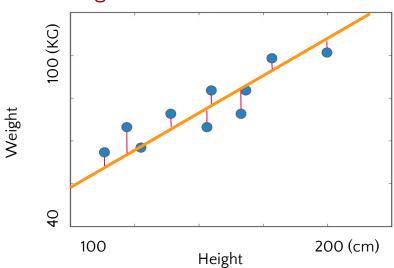
K = >3? Difficult to visualize, but process is the same: weighting features such that a multidimensional plane is able to separate classes as well as possible in K-dimensional space

Model performance

- We know what ML models do (find weighting parameters β to approximate y), but how do we evaluate the model?
- In other words, what is the model performance ("fit")?

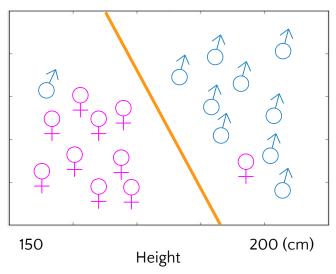
Model performance





 R^2 = 0.92 [explained variance] MSE = 8.2 [mean deviation² from prediction]

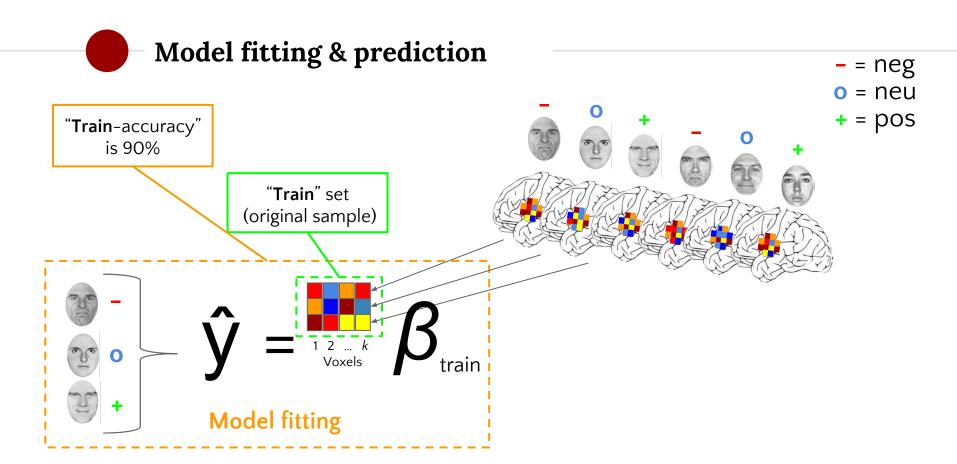
Classification

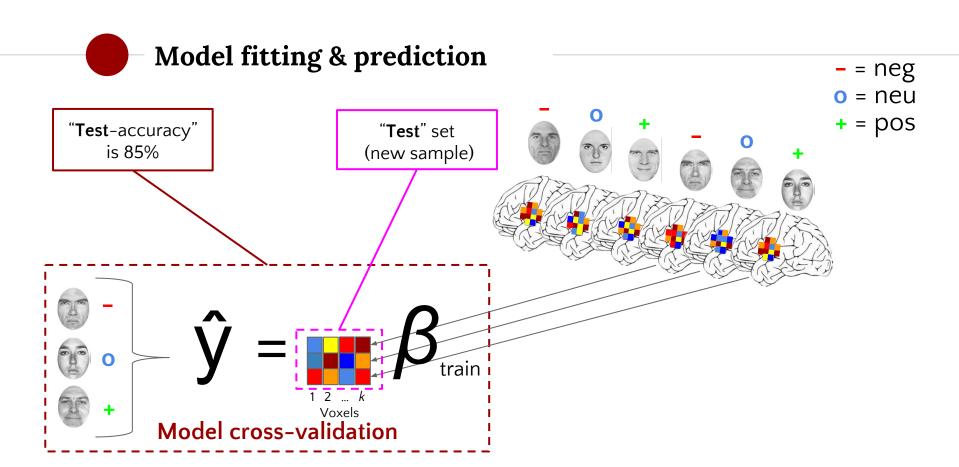


Accuracy = 18 / 20 = 90% [percent correct]

Model performance

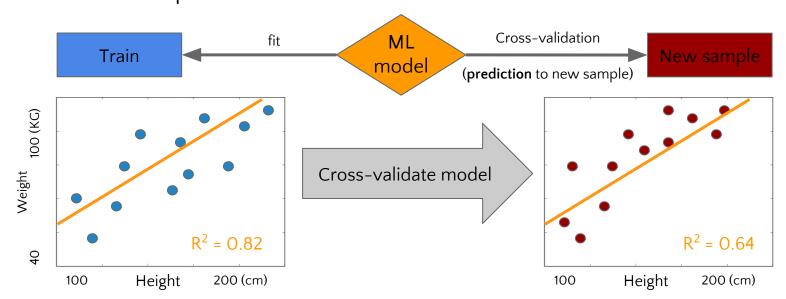
- Performance is often evaluated not only on the original sample, but also on a "new sample"
- This process is called "cross-validation"





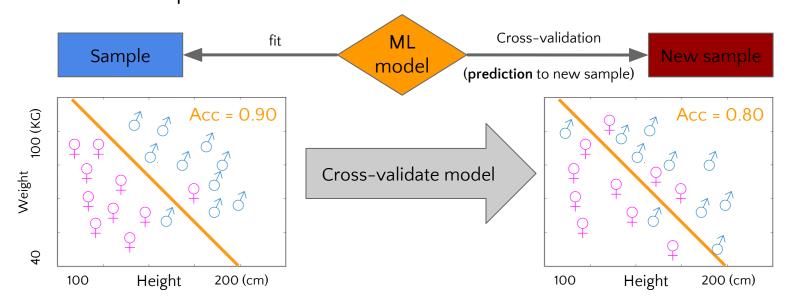
Model performance

 Model performance is often evaluated on a new ("unseen") sample: cross-validation



Model performance

 Model performance is often evaluated on a new ("unseen") sample: cross-validation



Why do we want (need) to do cross-validation?

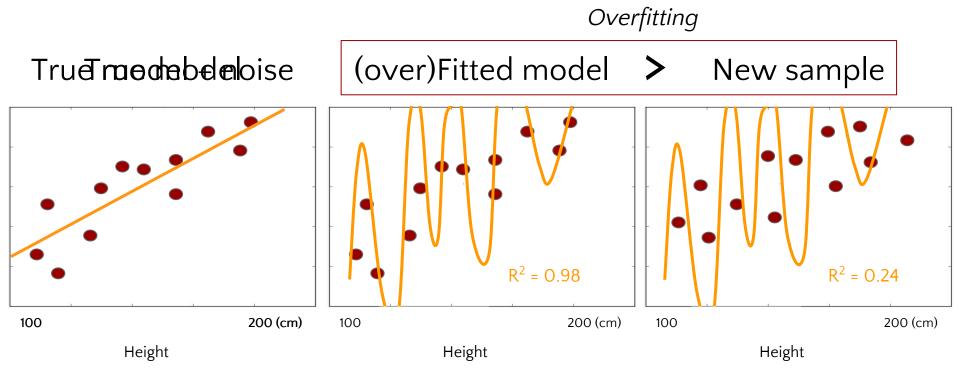
Model fit ≠ good prediction



Overfitting

- When your fit on your train-set is better than on your test-set, you're overfitting
- Overfitting means you're modelling noise instead of signal





Overfitting

- Overfitting = modeling noise
- Noise = random (uncorrelated from sample to sample)
- Therefore, a model based on noise will not generalize

- A small sample/feature-ratio often causes overfitting
- When there are few samples or many features, models may fit on random/accidental relationships



 When there are few samples, models may fit on random/accidental relationships



















When there are few samples, models may fit on random/accidental relationships

















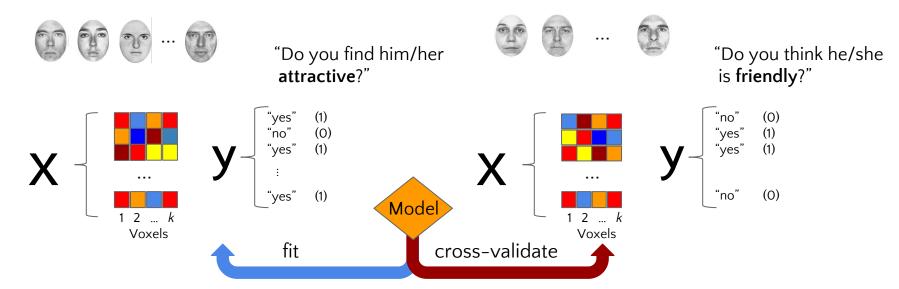
- Two options:
 - Gather more data (not always feasible)
 - Reduce the amount of features (more about this later)
 - [Regularization beyond the scope of this course!]
- Feature selection/extraction is an often-used technique in decoding analyses
 - Discussed later ("How?")

Cross-decoding!

- Sometimes, decoding analyses use a specific form of cross-validation to perform cross-decoding
- In cross-decoding, you aim to show "informational overlap" between two types of representations

Cross-decoding!

 For example: suppose you have the hypothesis that attractiveness drives the perception of friendliness



Summary

- ML models find weights to approximate a continuous (regression) or categorical (classification) dependent variable (y)
- Good fit ≠ good generalization ...
- ... therefore, cross-validate the model!
- Optimize the sample/feature ratio to reduce overfitting (spurious feature-DV correlations)
- Cross-decoding uses cross-validation to uncover shared representations ('informational overlap')

Contents

- Introduction
- Why?What?
- How?

Slides online

• If we're out of time (very likely), you can check the rest of the slides online:

https://tinyurl.com/MVPA-SPINOZA

I'll be here tomorrow to help with (multivariate) analyses!

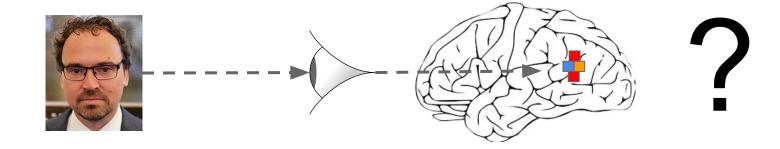
A typical decoding pipeline

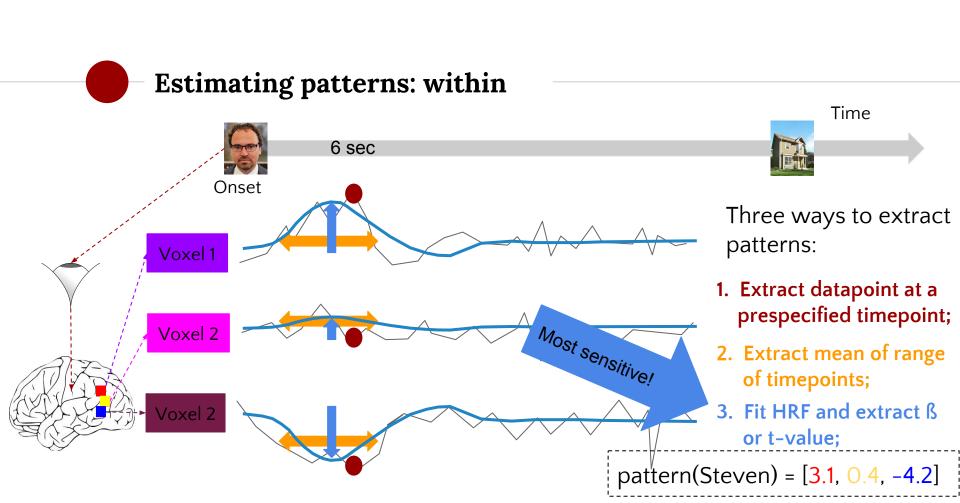
- O. Pattern extraction & preparation
 - 1. Partitioning train/test
- 2. Feature selection/extraction
- 3. Model fitting (TRAIN)
- 4. Model generalization (TEST)
- 5. Statistical test of performance
- 6. Optional: plot weights

A typical decoding pipeline

- O. Pattern extraction & preparation
 - Partitioning train/test
- 2. Feature selection/extraction
- 3. Model fitting (TRAIN)
- 4. Model generalization (TEST)
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- 6. Optional: plot weights

How do we get here?





Estimating patterns: within

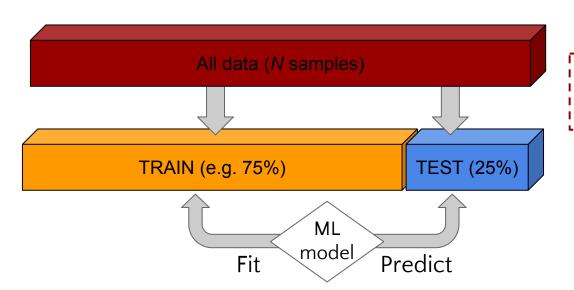
- The design(-matrix) used in within-subject pattern analyses is often called a single-trial design
- Thus, you estimate a pattern for each instance of your feature-of-interest ("trial")

Estimating patterns: within Time

A typical decoding pipeline

- O. Pattern extraction & preparation
- 1. Partitioning train/test
- 2. Feature selection/extraction
- 3. Model fitting (TRAIN)
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- 5. Statistical test of performance
- 6. Optional: plot weights

• Hold-out CV



Only cross-validate once!

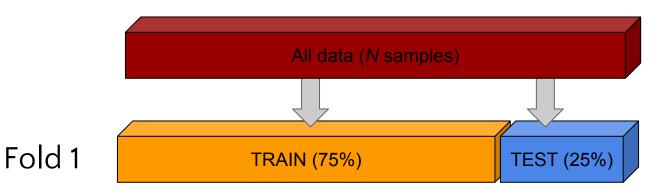
Kind of a "waste" of data ... Reuse data?

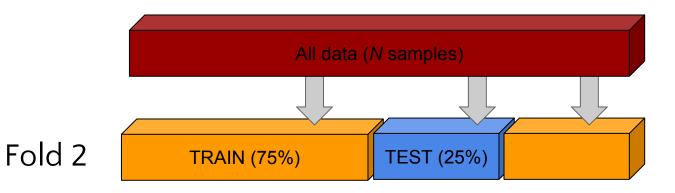
Leads to high "variance" of the model (little confidence) ...

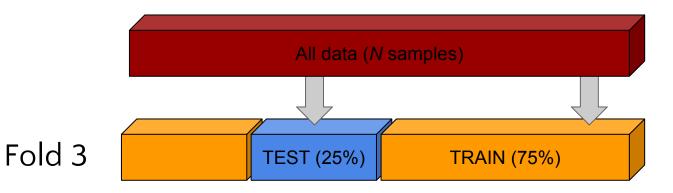
Step 1: Partitioning

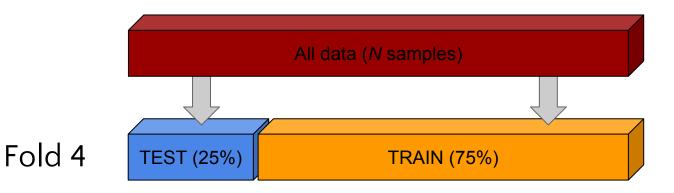
- Hold-out CV
- Advantage: computationally efficient (only fit model once!)
 - Recommended for very large datasets (N > 1000)
- Disadvantage: not very "robust" (especially for small datasets
 - If your test-set has only 10 samples, your estimated cross-validated accuracy may be spurious!

- How to reduce variance? (increase robustness)
- Iteratively create partitions!
 - Into different folds: K-fold cross-validation



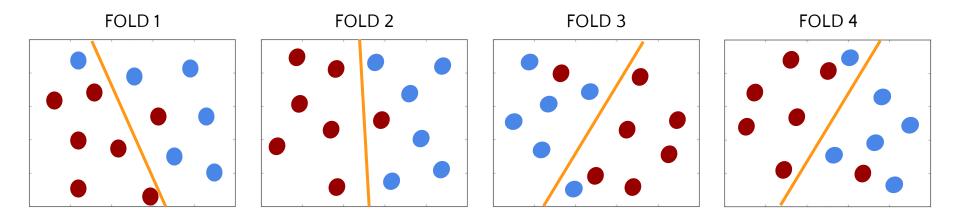








 Often-heard question: "but now we fit 4 potential completely different models!"



- Often-heard question: "but now we fit 4 potential completely different models!"
- True! Conclusion should be: "a model with these features (X) is able to predict with x% accuracy"
- Not: "this *specific* model ($X\beta$) is able to predict with x% accuracy"

- How to reduce variance? (increase robustness)
- Iteratively create partitions!
 - Into different folds: K-fold cross-validation
- Average of fold-wise performance is more robust than just a single performance estimate (i.e., more robust)!

A typical decoding pipeline

- O. Pattern extraction & preparation
 - Partitioning train/test
- 2. Feature selection/extraction
- 3. Model fitting (TRAIN)
- 4. Model generalization (TEST)
- 5. Statistical test of performance
- 6. Optional: plot weights

Feature selection

- Goal: high sample/feature ratio!
- MRI: often many features (voxels), few samples (trials/instances/subjects)
- What to do???



- Reducing the dimensionality of patterns:
 - Select a subset of features (feature selection)
 - Transform features in lower-dimensional components (feature extraction)

Feature selection vs. extraction

- Ideas for feature selection?
 - ROI-based (e.g. only hippocampus);
 - (Independent!) functional mapper;
 - Data-driven selection: univariate feature selection

Feature selection vs. extraction

- Ideas for feature selection?
 - ROI-based (e.g. only hippocampus);
 - (Independent!) functional mapper;
 - Data-driven selection: univariate feature selection

Univariate feature selection

- Use univariate difference scores (e.g. t-value/F-value) to select features
- Only select a subset of the voxels with the highest scores

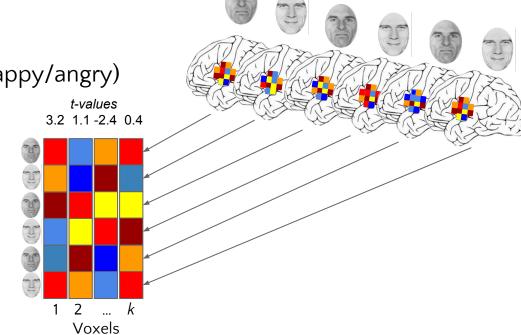


Univariate feature selection

Steps:

Calculate test-statistic
 (t-test for difference happy/angry)

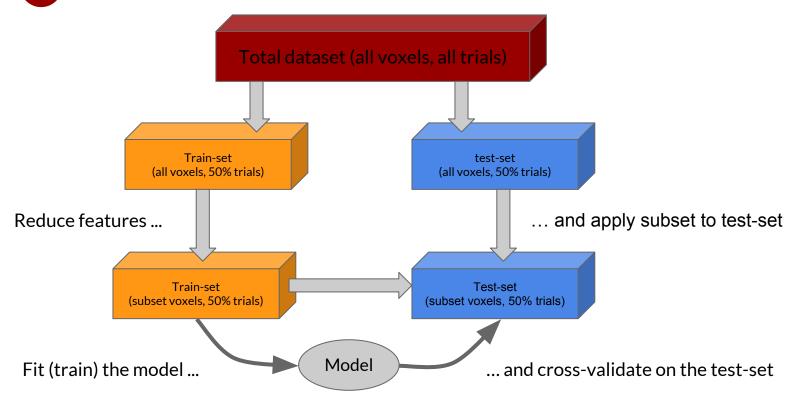
2. Select only the "best"
100 voxels (or a percentage)



Cross-validation in FS

- Importantly, data-driven feature selection needs to be cross-validated!
 - Performed on train-set only!





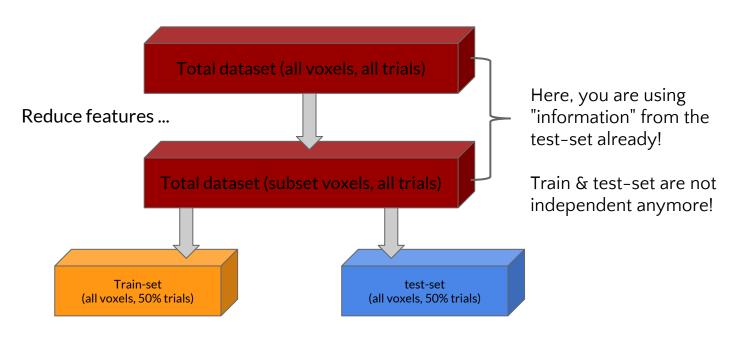
ToThink:

Why do you need to cross-validate your feature selection?

Isn't cross-validating the model-fit enough?

ToThink:

Why do you need to cross-validate your feature selection?



Feature selection vs. extraction

- Ideas for feature extraction?
 - PCA
 - Averaging within regions ("downsampling")



-60,000 features (voxels)

-110 features (brain regions)

A typical decoding pipeline

- O. Pattern extraction & preparation
 - Partitioning train/test
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- When is a particular model performance "good enough"?
- Decoding analyses use significance tests to infer whether decoding performance (R² or % accuracy) would generalize to the population

- Remember, if you want to statistically test something, you need to have a null- and alternative hypothesis:
 - H₀: performance = chance level
 - H_a: performance > chance level

- What is chance level?
- \bullet R^2 ?
 - Cross-validated R² null: 0
- Accuracy?
 - 1 / number of classes
 - Decode negative/positive/neutral? Chance = 33%

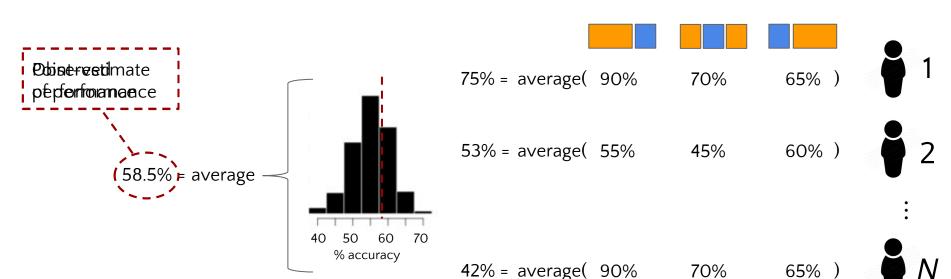




- Observed performance is measured as the average cross-validated performance $(R^2 / \% \text{ accuracy})$
- Slightly different for within/between subject analyses:
 - Within: average performance across subjects
 - Between: average performance across folds

Statistics: within-subject

Take e.g. a 3-fold cross-validation setup



Statistics: within-subject

- H_a: 58.5 > 50
- Subject-wise average performance estimates represent the data points
- Assuming independence between subjects, we can use simple parametric statistics*
 - t-test(N 1) of observed performance (i.e. 58.5%)
 against the null performance (i.e. 50%)

Prevalence inference

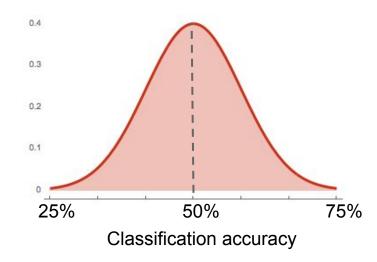
- Assuming independence between subjects, we can use simple parametric statistics*
- *Actually: not really ...

Valid population inference for information-based imaging: From the second-level *t*-test to prevalence inference

Carsten Allefelda.*., Kai Görgena.1, John-Dylan Haynesa,b,1

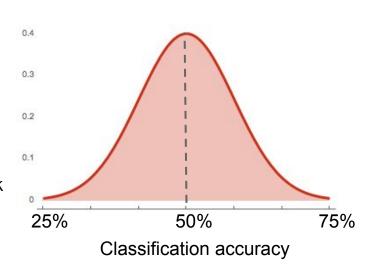
Prevalence inference

 Parametric statistics (in decoding) assume that you're testing against a symmetric null distribution



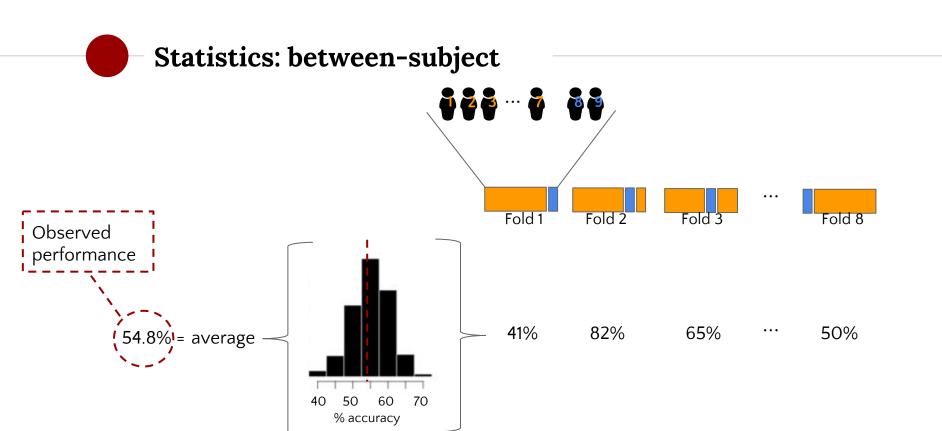
Prevalence inference

- Parametric statistics (in decoding) assume that you're testing against a symmetric null distribution
 - Assumes below-chance accuracy is possible
 - But this is not possible on a population level!
 - It's like testing the average travel time from house → work against H₀ = 0
 - Negative time???



Prevence inference

- Solution: test the prevalence of an effect (≈ how many subjects show an above-chance performance)
- Beyond the scope of this course ...
 - But a possible topic for your final project!

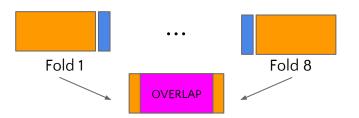


Statistics: between-subject

- H_a: 54.8 > 50
- Fold-wise performance estimates represent data points
- Problem: different folds contain the same subjects







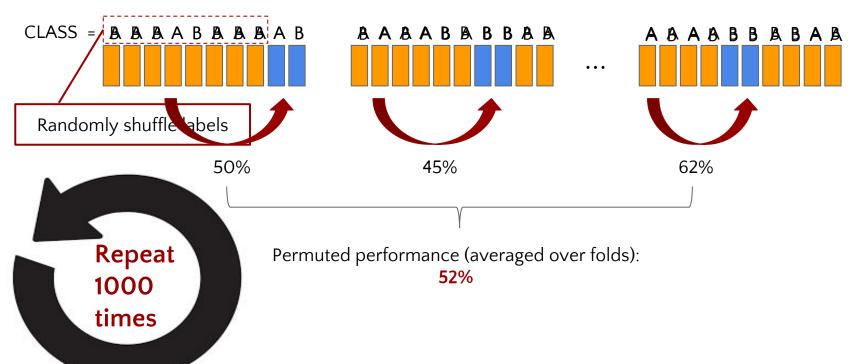
- Problem: different folds contain the same subjects
- Consequence: dependence between data points
 - Violates assumptions of many parametric statistical tests
- Solution: non-parametric (permutation) test

Statistics: between-subject

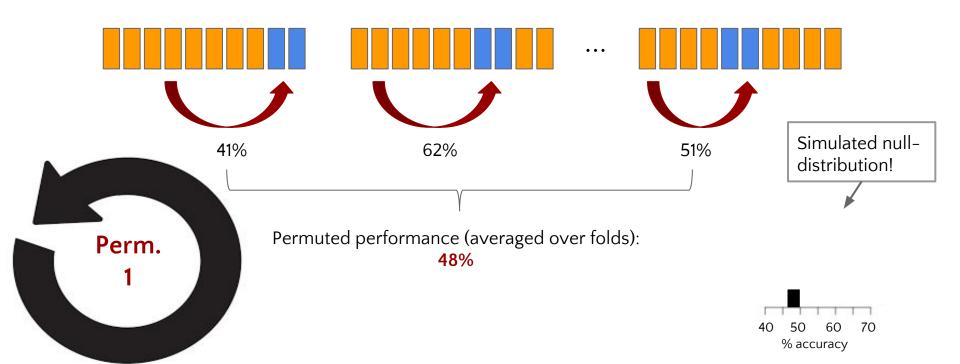
- Permutation tests do not assume (the shape of) a null-distribution, but "simulate" them
- To simulate the null-distribution (results expected when H₀ is true), permutation tests literally simulate "performance at chance"

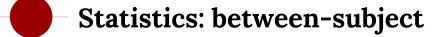


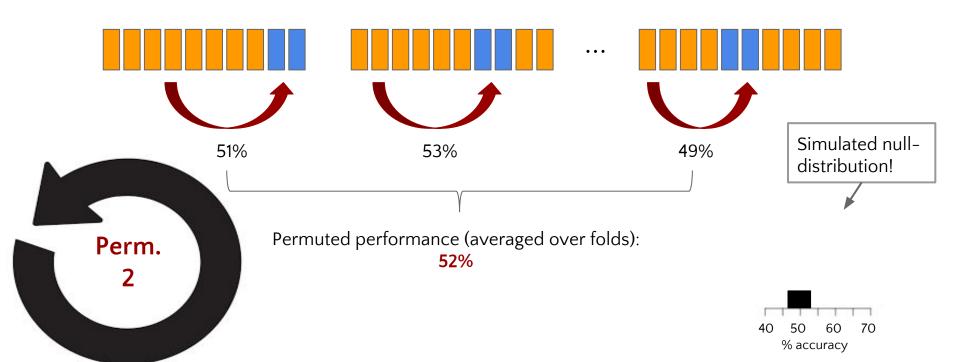
Statistics: between-subject

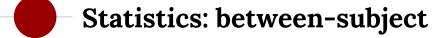


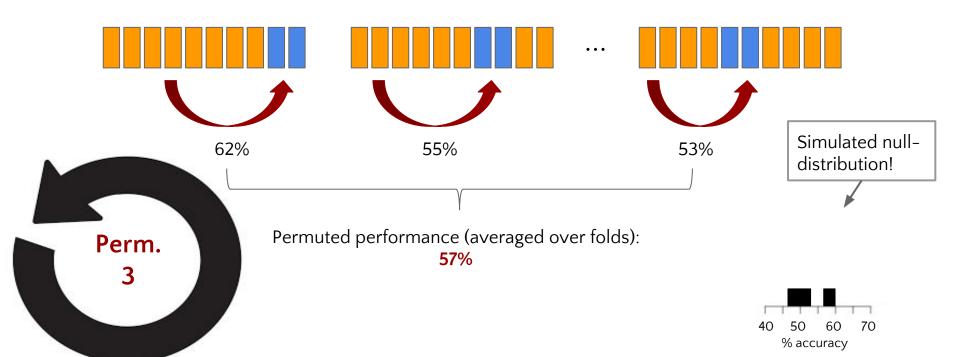


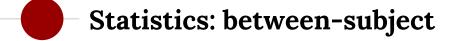


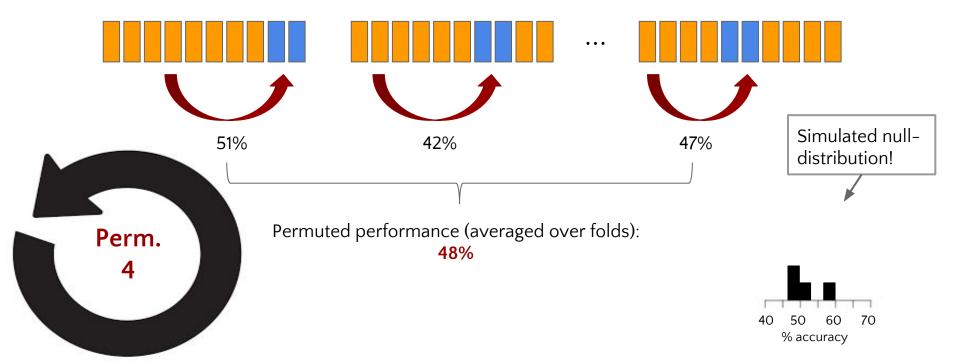


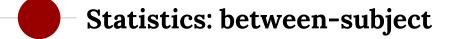


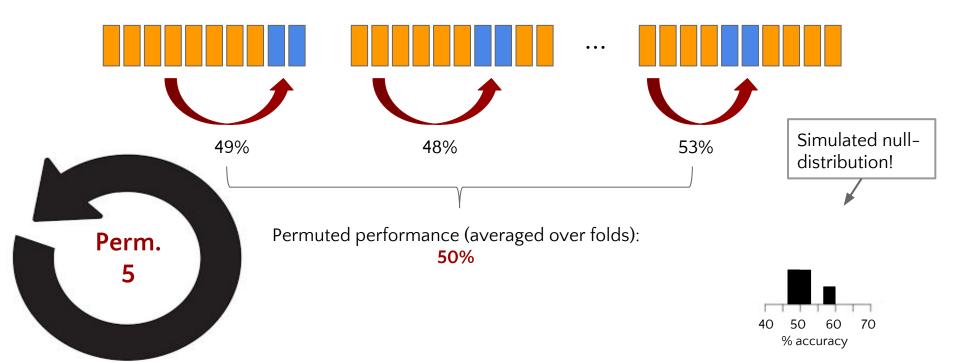


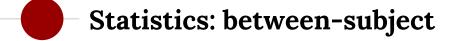


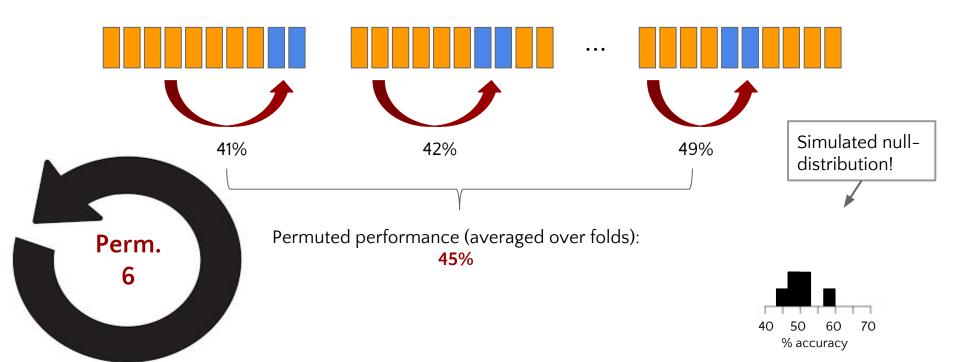


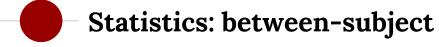


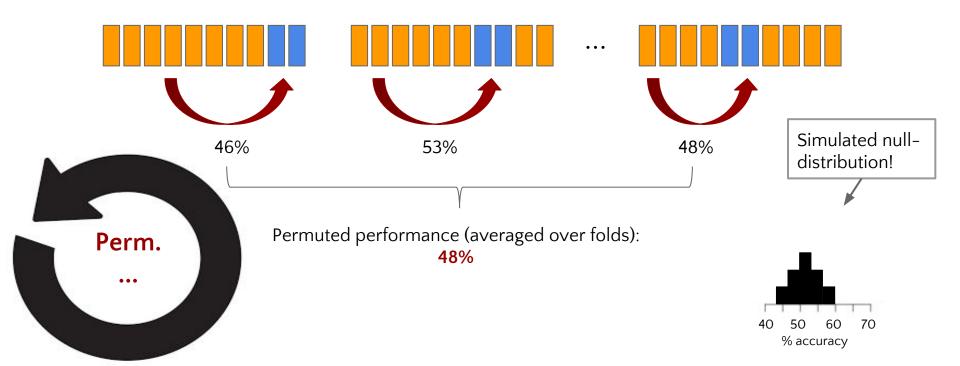




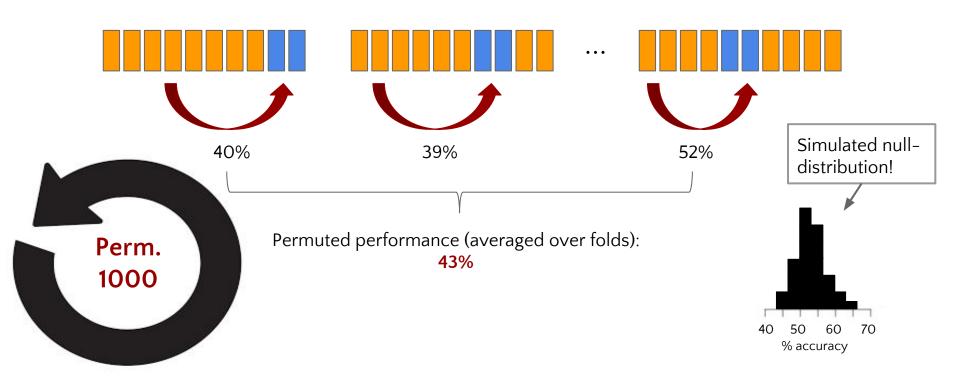












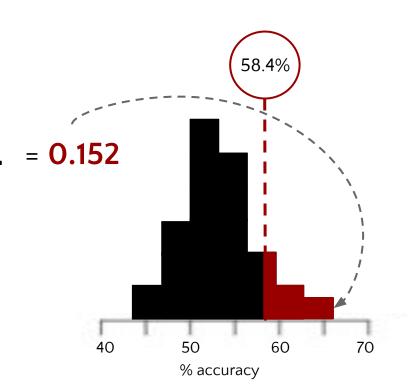


Statistics: between-subject

"Non-parametric" **p-value** =

∑(null-scores ≯52bserved-score)

Number of Commutations



A typical decoding pipeline

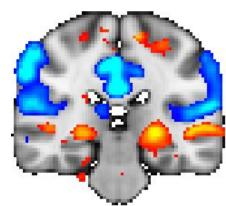
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If there is time left!

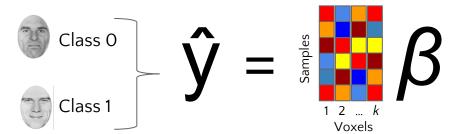
Often, researchers (read: reviewers) ask:

"Which features are important for which class?"

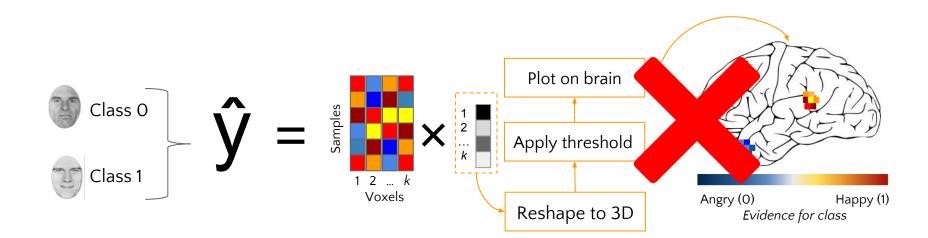
- What they want:
- Intrinsic need for blobs?



- Technically, weights (β) in *linear* models are interpretable: higher = more important
 - Also, the following is assumed (but wrong):
 - Negative weights: evidence for class 0
 - Positive weights: evidence for class 1



• Technically, weights (β) in *linear* models are interpretable: higher = more important

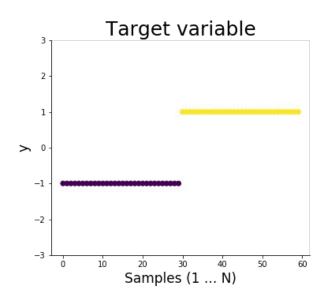


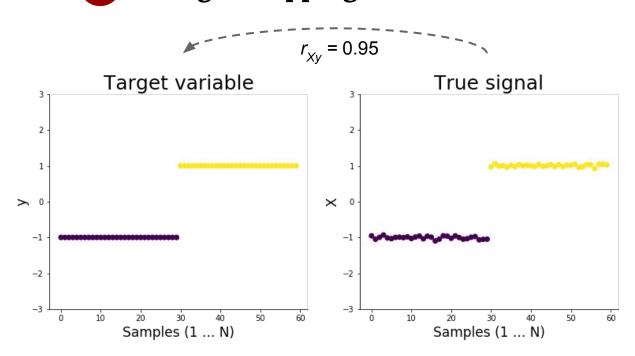
 Haufe et al. (2014, NeuroImage) showed that high weights ≠ class importance

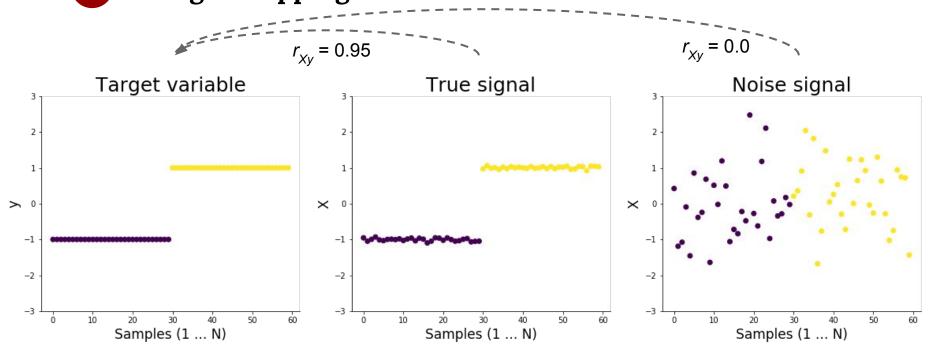
... A widespread miscon-

ception about multivariate classifier weight vectors is that (the brain regions corresponding to) measurement channels with large weights are strongly related to the experimental condition. In fact, such conclusions can be unjustified.

*voxels







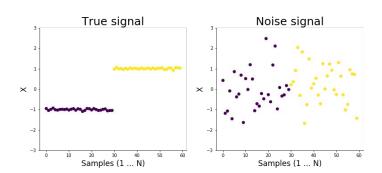
What could you do instead if somebody asks

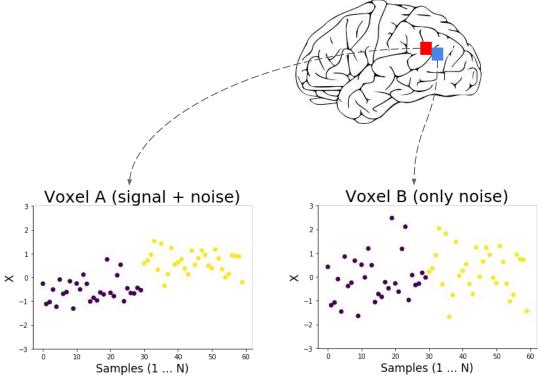
for pretty brain pictures related to your

decoding analysis?

$\hat{y} = X_A \beta_A + X_B \beta_B$

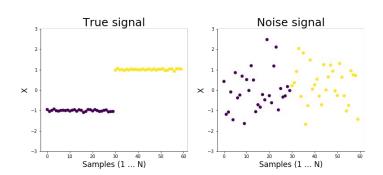


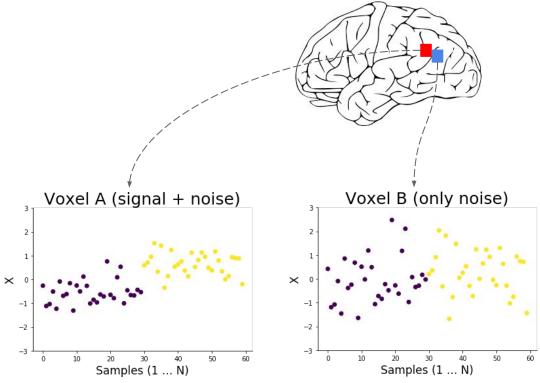




$\hat{y} = X_A \cdot 1 + X_B \cdot -1$







- Haufe et al. (2014, NeuroImage) showed that high weights ≠ class importance
- Features (voxels) may function like (class-independent) "filters"
 - E.g. reflect physiological noise
- Features with high weights may be completely unrelated to the target (y)!

- Just do a mass-univariate analysis!
 - MVPA has a different goal
- Conclusion: (like always) choose the analysis best suited for your question!

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Estimate and extract patterns such that X = N-samples by N-features (voxels)

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Use hold-out or K-fold partitioning

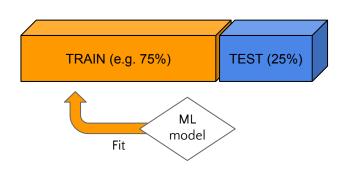
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Feature selection (voxel subset)

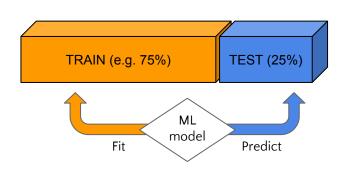
Reduce the amount of features

Feature extraction (voxels → components)

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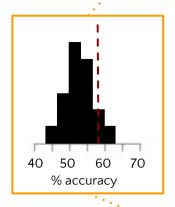


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Parametric test against chance (within-subject)



Permutation test against simulated null (between- subject)

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Do not plot weights! A (complementary) univariate analysis would suffice

Recommended literature

- Abraham et al. (2014): about the scikit-learn package for decoding analyses
- Pereira et al. (2009): tutorial-style paper about decoding analyses
- Ritchie et al. (2017): what are you actually measuring with decoding?
 - Highly recommended!

Thanks!