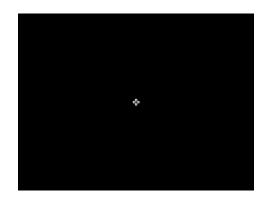
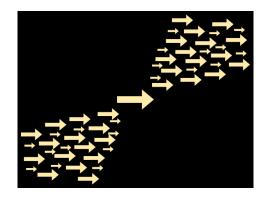
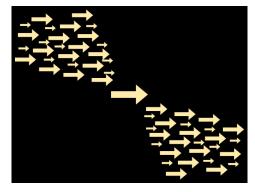
Tutorial – Analysing your own data

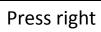
Task

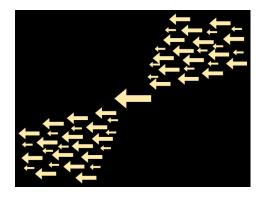


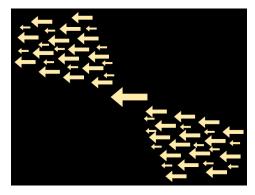
Fixation











Press left

Design

- First run: Block design same direction of arrow shown in blocks of 15 seconds with null blocks included.
- Second run: Event related design direction of arrow changed every 3 seconds with null trials included.

Today's tutorial

• First hour: Create your own preprocessing (and glm) pipeline for one subject.

• Break: Distribution of topics for final presentation MED-Students.

Second hour: Use a batch and script to process the data.

Organize data

- behav Behavioral data
- 👢 functional Functional MRI data for analysis
- Image of the property of th
- physlog Physiological measurements (not available)
- \mathbb{L} scandata Original raw data \rightarrow Never touch this during analysis
- structural Anatomical/Structural MRI scans for analyis

Behavioral data

- BehaviorSummary01.mat
- BehaviorSummary02.mat
- BehavRun01.mat
- BehavRun02.mat
- tRArrowRegs01.mat
- 1 LRArrowRegs02.mat
- 1 LRPressRegs01.mat
- 1 LRPressRegs02.mat
- MedgeRegs01.mat
- MedgeRegs02.mat

- Behavior analysis (Errors etc.)
- All behavioral data
- Regressors (left arrow vs. right arrow)
- Regressors (left press vs. right press)
- Regressors (7-13 wedge vs. 5-11 wedge)

Prepare mri data

- b0map_01_ec1_typ0.nii
- b0map_01_ec1_typ3.nii
- b0map_01_ec2_typ0.nii
- b0map_01_ec2_typ3.nii
- b0map_02_ec1_typ0.nii
- b0map_02_ec1_typ3.nii
- b0map_02_ec2_typ0.nii
- b0map_02_ec2_typ3.nii
- fmri01.nii
- fmri02.nii
- skstruct.nii

−B0 field maps

- -fMRI data (T2*) → Copy to folder functional
- -Structural data (T1) → Copy to folder structural

Try to setup a preprocessing pipeline

• Hint: Try to put a pipeline together that you think is reasonable, it does not have to be exactly the one we used last week.

Try to setup a glm

- Use one of the regressor types LRArrowRegsXX, LRPressRegsXX, WedgeRegsXX for the two runs.
- Hint: You can use the batch of last week as a starting point.

MED students presentations

- Form 4-5 groups of 2-3 people each.
- Each group will give one presentation about their analysis.
- Within your analysis you should present a specific question (you can come up with your question):
 - E.g. how do results differ between regressors (e.g. LRArrow vs. LRPress)
 - How do results differ across participants?
 - Compare different pipelines, e.g. for preprocessing (with and without slice time correction, ...)
 - How do the results change, when motion regressors are included or not, or with and without derivatives of the HRF.

MED students presentations

- On Nov. 6 you will present these analysis. Every person needs to present a short part of the presentation (1-2 slides per person).
- We will then discuss your results together.

Break

Analysis scripts

• Use the two analysis scripts (download ZIP from homepage):

- teach_prepro_subject.m
- teach_glm_subject.m