

# MRI pilot

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## Abstract

### Run an MRI pilot at Spinoza REC.

#### **This protocol will help you running your pilot.**

Make sure to read this protocol before coming to the pilot so you know what is expected of you and which choices you will be going to make.

During the pilot the researcher runs the task for the first time. Spinoza personnel will help you set up the sequences and assist you with the stimulus set up. Also we will try to help you with getting a good workflow for your scan time.

There are a couple of things that are generally done during a pilot:

- The researcher checks if the tasks are running properly and as expected;
- The researcher makes an estimation of the amount of time necessary to run one participant to eventually be able to make a feasible planning of the project;
- The MR-operator (from Spinoza REC) sets up a protocol on the scan computer;
- If desired, the person that is present from the Spinoza REC may advise you in aspects of the stimulus equipment, scan workflow and planning of the project

In our experience, it's best to have an experienced participant during the pilot.

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## Protocol

### Workflow for pilot

#### **Step 1.**

#### **This protocol will help you running your pilot.**

*Note: you will be assisted by Spinoza staff. They will help you setting up the sequences (scan protocol).*

Make sure to read this protocol before coming to the pilot in order to know what is expected of you and which choices you will be going to make. Use this protocol as a checklist during the pilot.

## Step 2.

### What will be done during the pilot?

During the pilot the researcher runs the experiment (including scanning) for the first time. Spinoza staff will help you set up the sequences and assist you with the stimulus set up. Also we will try to help you with getting a good workflow for your scan time.

There are a couple of things that are generally done during a pilot:

- The researcher checks if the experimental tasks are running properly and as expected;
- The researcher estimates the amount of time necessary to run one participant to eventually be able in order to make a feasible planning of the project;
- The MR-operator (from the Spinoza Centre) creates a protocol on the scan computer;
- If desired, the person that is present from the Spinoza Centre may advise you in aspects of the stimulus equipment, scan workflow, and planning of the project

### Participant for the pilot

## Step 3.

### We advice you to use an experienced participant for your pilot.

Preferably, this person is *not* a colleague or friend (in case of an incidental finding).

Even if the participant is experienced, he or she should go through the normal routine for participating in MRI research. As such, he or she should ...:

- have the opportunity to read the **information folder** about MRI research at our centre;
- fill in and sign an **MRI screening form**;
- fill in and sign a **General Practitioner Informed Consent**;
- fill in and sign a **study-specific Informed Consent**;

Additionally, make sure that the pilot participant knows that the current session is a pilot run. This way the participant understands that some things may a bit longer (due to unforeseen issues during the pilot) and, moreover, this allows the participant to give valuable feedback on the

experiment/protocol.

Create scan protocol ('exam card')

#### Step 4.

##### Create your scan protocol.

During the pilot, you will (together with the MR-operator) create a selection of scans ('exam card') to run during your experiment, which most likely includes:

- a 'SmartBrain' (survey scan)
- a high-resolution T1-weighted anatomical scan
- one or more functional (BOLD-fMRI) scans (we offer the option of [multiband](#) scans)
- B0-scan or 'top-up' scans (from which you can create a 'fieldmap', reflecting the magnetic field's inhomogeneity).

Depending on your experiment/analysis, your selection may also include a high-resolution T2-weighted anatomical scan and/or scans for diffusion weighted imaging. Ideally, you have already discussed your desired scans during the introduction meeting.

#### Step 5.

##### Name your scans appropriately.

If you're using the centre's QC/preprocessing service, it is very important to name your scans (and thus the resulting MRI files) according to the BIDS-format.

*If you're not using the centre's QC/preprocessing service, you may give whatever name to your scans/files and skip the rest of the instructions listed in this step.*

We have already named the templates of our standard scans such that they only require minimal editing to make them BIDS-compatible. BIDS uses key-value pairs in filenames to denote parameters/information about the file itself. The structure is as follows:

- `key1-value1_key2-value2_[optionalKey-optionalValue]`

We have pre-formatted our standard exam cards such that they already contain the appropriate keys. We've included placeholders, formatted as *(this\_is\_a\_placeholder)*, for values which you should replace with the appropriate information. For example, our standard (non-multiband) functional EPI

(3mm, TR=2000ms) is named:

- *task-(taskname)\_acq-SeqSense2Mm3[\_run-(nr)]\_bold*

(Note: the *acq* - 'acquisition' - value specifies the specific type of scans, which here refers to a Sequential scan with *Sense* factor 2, and a 3 millimeter isotropic spatial resolution.)

It is then up to the researcher to replace the *(taskname)* with the appropriate value (e.g., *workingmemory* or *Nback* - completely up to the researcher, but only use alphanumeric symbols). The parts between square brackets, *[...]*, are optional. If you, for example, have two runs of an *Nback* task, you should name them:

- *task-Nback\_acq-SeqSense2Mm3\_run-1\_bold*
- *task-Nback\_acq-SeqSense2Mm3\_run-2\_bold*

If you don't have different runs, you may leave out the *run* key-value pair (e.g., *task-Nback\_acq-SeqSense2Mm3\_bold* is just fine).

In fact, you likely only have to format the names of the functional (EPI) scans (and the corresponding topup-scans, if included). Most other types of scans (e.g., B0, DWI, and T1-weighted/T2-weighted scans) are already completely pre-formatted and do not need editing (but exceptions arise when, for example, you want to run two T1-weighted scans; in that case, you need to add a *run-(nr)* key-value pair yourself). The MR-operator will assist you in this process.

Check your experiment/paradigm

## Step 6.

**Check whether your experimental paradigm/task runs as expected.**

Check the following things regarding your experimental paradigm/task during the pilot:

- Does the paradigm start at the first scanner pulse? (The *Before data acquisition* explains how to

sync your task with your experiment)

- When using response buttons, check whether these are working and logged as expected;
- Visually inspect the experimental paradigm/task during the scan;
- Are the log files stored on the D-drive, data not on the D drive will be deleted without any notice;
- Ask the participant whether the task was clearly explained and if he/she could read (hear and see) everything properly;

## Check pilot data

### Step 7.

#### Check your data after the pilot.

We advise you to check your pilot data for artifacts or other issues after the pilot.

- Check whether you received the (MRI) data files as expected (proper file format, right file size, etc.)
- Check whether the logfiles of the paradigm include all the expected information (esp. stimulus/response onsets and the onset of the first scanner pulse);
- Convert your scans from PAR/REC (or DICOM) format to nifti (using, e.g., [dcm2nii](#)) and inspect your anatomical and functional scans visually (using e.g. FSLView)

In case of unexpected artifacts, let Lukas (L.Snoek@uva.nl) or Tinka (t.beemsterboer@uva.nl) know.

## Start your project!

### Step 8.

#### You're ready to start your project!

Now, you are ready to start your project by making bookings in Calpendo ([spinozarec.calpendo.com](https://spinozarec.calpendo.com))!

*Good luck!*