

Standard Operating Procedures of the HCPh project

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The Human Connectome PHantom (HCPH) study: Standard Operating Procedures

These SOPs correspond to a pre-registered report

These documents correspond to a pre-registration¹ (<https://doi.org/10.17605/OSF.IO/VAMQ6>). Please check the corresponding registered report (<https://osf.io/fh8mc>) (direct download) to get a better understanding of what these SOPs implement.

The experiments and hypotheses were pre-registered to further guarantee research rigor and seek early scrutiny and feedback from experts in the field, thereby generating consensus on data collection and analysis. Researchers increasingly perceive pre-registration as a tool to maximize research transparency, improve study planning, and eliminate incentives conducive to dubious practices in the search for positive outcomes. By pre-registering the study, we will maximize the impact and usefulness of this work.

Future reports and public communications of results of this project will be pre-registered whenever that is possible.

Thanks to César Caballero-Gaudés and Stefano Moia

We highly appreciate the decisive help we have received from César and Stefano to bring together the physiology component of this project.

César provided very valuable feedback at the earliest stages of the design of the project and has also facilitated it with key feedback (including a visit to show their settings at BCBL).

Stefano helped edit our registered report, and traveled to Lausanne twice to help us on the spot with the BIOPAC and calibration.

Thanks to Garikoitz Lerma-Usabiaga

Gari filmed several versions of the *Mundaka clip*, that allowed us to edit the final clip that is presented during the resting state fMRI.

Thanks to Inès de Riedmatten and Arthur Spencer

Inès has contributed with excellent materials to the initial versions of these SOPs, and re-enabled the trigger issuing by our dMRI sequence (which had disappeared after a scanner's software upgrade...) Arthur helped us with more recent aspects regarding the gas analyzer calibration and has supported us in other meaningful ways.

Summary

Unveiling how the brain's structure defines its distributed function and modulates the dynamics of processing holds the promise of triggering a revolution in neuroscience and applications to mental health and neurodegenerative diseases. Magnetic resonance imaging ([MRI](#)) has proven a valuable, non-invasive way of probing both the architecture and activity of the brain *in-vivo*, with sufficient spatial and temporal resolution to understand many aspects of its function. Although a large body of literature has shown strong correlations between structural and functional networks at the larger scales² (<https://doi.org/10.1016/j.jneumeth.2010.01.014>),³ (<https://doi.org/10.1073/pnas.0811168106>),⁴ (<https://doi.org/10.1073/pnas.1219562110>),⁵ (<https://doi.org/10.1038/s41467-018-04614-w>), the accumulated unreliability of [MRI](#) measurements from the scanner and through further steps of the research workflow impedes the link between structure, function, and dynamics at clinically relevant spatial and temporal scales. In particular, the measurements obtained with [MRI](#) are highly indirect, spatiotemporally uncertain, and confounded by other sources of [MR](#) signal. This complexity provides an immense informatics challenge that crosses multiple imaging modalities, including structural, functional, and dynamic connectivity approaches to understanding the human brain. Nonetheless, functional and structural networks extracted from [MRI](#) have proven sufficient levels of reliability to discriminate between individuals⁵ (<https://doi.org/10.1038/s41467-018-04614-w>),⁶ (<https://doi.org/10.1371/journal.pbio.0060159>),⁷ (<https://doi.org/10.1038/nn.4135>),⁸ (<https://doi.org/10.1038/s41598-018-25089-1>), and such reliability has proven stable from months to years⁹ (<https://doi.org/10.1016/j.neuroimage.2019.02.002>). Therefore, it is critical to characterize the reliability of this network's phenotyping before these analytical approaches may be applied clinically¹⁰ (<https://doi.org/10.1038/s41562-019-0655-x>),¹¹ (<https://doi.org/10.1001/jamapsychiatry.2020.4272>). In this project, we will first optimize the research workflow of [MR](#) network analyses to maximize the reliability of functional and structural connectivity matrices (so-called connectomes). Indeed, these matrices have been shown to contain large ratios of false positives and false negatives in both the functional¹² (<https://doi.org/10.1016/j.neuroimage.2011.10.018>) and the structural¹³ (<https://doi.org/10.1016/j.neuroimage.2016.06.035>),¹⁴ (<https://doi.org/10.1038/s41467-017-01285-x>) cases. We hypothesize that such improvements in sensitivity and specificity of functional and structural networks generalize across scanners and subjects, allowing the univocal identification of individuals from their brain's networks ("fingerprinting"). In order to be able to statistically separate and characterize the sources of signal variation, the project involves acquiring large amounts of repeated data on a small number of individuals. This approach has recently been dubbed "precision [MRI](#)"¹⁵ (<https://doi.org/10.1016/j.neuron.2017.07.011>) and focuses on individual differences rather than group differences. The data acquisition approach is structured in three efforts with varying numbers of subjects, repetitions, and scanning devices. The first two, called "Cohort I" and "Cohort II" are sequential in time, and collected on three different devices. Cohort I involves a single individual who will undergo

a total of 60 scanning sessions. Subsequently, Cohort II involves six (6) individuals and a total of twelve (12) sessions each. Finally, "Cohort III" is a quality control set involving 18 individuals and a total of two sessions each in a single scanner. In total, the project plans for repeated MRI acquisition on 25 healthy, adult human subjects, across three different 3.0 Tesla (T) MRI scanners available at CHUV. In addition to the new data, the project will reuse existing, open-access data to pilot various aspects of the MRI processing and analysis workflow to further support the overall reliability of the findings.

Impact

Overall, this project will equip researchers with a framework for the extraction of reliable and precise structural, functional and dynamic networks that permit their joint modeling and analysis with interpretable and reproducible methods. The project will publicly release two highly valuable datasets necessary for the improvement of the workflow for structural and functional network extraction under open access and reuse terms. Upon conclusion, this study will mark a turning point for MRI research as a fundamental resource for academic training and a necessary assessment to unlock clinical applications in the long-term with the improvement of the reliability of MRI-network analyses. At a local scale, the project will substantially contribute to ensuring the reliability of the MRI clinical workflow that routinely aids medical decisions at CHUV.

Change History

All notable changes to these SOPs are documented below, starting with the most recent version of the document.

You found an error

If you want to check the list of open issues, please proceed to our [issue tracker](https://github.com/TheAxonLab/hcph-protocol/issues) (<https://github.com/TheAxonLab/hcph-protocol/issues>).

If you have identified a problem, a typo, or something missing, and you know it is not in our tracker, please report it by [creating a new issue](https://github.com/TheAxonLab/hcph-protocol/issues/new) (<https://github.com/TheAxonLab/hcph-protocol/issues/new>).

0.4.0 (<https://github.com/TheAxonLab/hcph-protocol/releases/tag/0.4.0>) (September 27, 2023)

[Compare with 0.3.0](https://github.com/TheAxonLab/hcph-protocol/compare/0.3.0...0.4.0) (<https://github.com/TheAxonLab/hcph-protocol/compare/0.3.0...0.4.0>)

Enhancements, new features, and additions

- Add report pre-registered on OSF and fix references ([f9a8360](https://github.com/TheAxonLab/hcph-protocol/commit/f9a8360efd56e8ab33876b68f0c51012c47f6cb1) (<https://github.com/TheAxonLab/hcph-protocol/commit/f9a8360efd56e8ab33876b68f0c51012c47f6cb1>) by Oscar Esteban (<https://github.com/oesteban>)).
- Replace --merge true with --how merge in datalad updates ([d297d45](https://github.com/TheAxonLab/hcph-protocol/commit/d297d45c9f4ab837702b748bb961277fecdf07ac) (<https://github.com/TheAxonLab/hcph-protocol/commit/d297d45c9f4ab837702b748bb961277fecdf07ac>) by Oscar Esteban (<https://github.com/oesteban>)).
- Add DataLad documentation for synchronizing and adding new data ([5d57e74](https://github.com/TheAxonLab/hcph-protocol/commit/5d57e74) (<https://github.com/TheAxonLab/hcph-protocol/commit/5d57e74>) by Oscar Esteban (<https://github.com/oesteban>)).
- Add a .zenodo.json with the intent of connecting Zenodo ([ee429ea](https://github.com/TheAxonLab/hcph-protocol/commit/ee429ea4ef72479fd6b0e8baf5a650f3f20e9a81) (<https://github.com/TheAxonLab/hcph-protocol/commit/ee429ea4ef72479fd6b0e8baf5a650f3f20e9a81>) by Oscar Esteban (<https://github.com/oesteban>)).
- Play nice with Apache license in heuristic, better documentation ([2dffffc](https://github.com/TheAxonLab/hcph-protocol/commit/2dffffcc8fae8fb4abd4f3c7ed275a9960c41178) (<https://github.com/TheAxonLab/hcph-protocol/commit/2dffffcc8fae8fb4abd4f3c7ed275a9960c41178>) by Oscar Esteban (<https://github.com/oesteban>)).

Bug Fixes

- Datalad DOI and link ([fc6311836865c3b564610601e19d5f917f5602ef](https://github.com/TheAxonLab/hcph-protocol/commit/fc6311836865c3b564610601e19d5f917f5602ef)) by Oscar Esteban (<https://github.com/oesteban>)).
- Escape HTML special characters ([e54c468b08520de764ba3cf6c8650f3f50bbc204](https://github.com/TheAxonLab/hcph-protocol/commit/e54c468b08520de764ba3cf6c8650f3f50bbc204)) by Oscar Esteban (<https://github.com/oesteban>)).
- Escaping characters ([737edce814c7ca1b4dda1ffee850cce08cdf73fa](https://github.com/TheAxonLab/hcph-protocol/commit/737edce814c7ca1b4dda1ffee850cce08cdf73fa)) by Oscar Esteban (<https://github.com/oesteban>)).
- Remaining bugs in heuristic file ([443493c6f91fe59ee9656362253d2d0388456043](https://github.com/TheAxonLab/hcph-protocol/commit/443493c6f91fe59ee9656362253d2d0388456043)) by Oscar Esteban (<https://github.com/oesteban>)). Related issues/PRs: #179 (<https://github.com/TheAxonLab/hcph-protocol/issues/179>)
- Revise heuristic after testing it ([ca49867f1712e61cefb0327d91f05e9a966d6013](https://github.com/TheAxonLab/hcph-protocol/commit/ca49867f1712e61cefb0327d91f05e9a966d6013)) by Oscar Esteban (<https://github.com/oesteban>)).
- Overhaul of the data-management section with DataLad ([5afcd97004f96d8314e5eaf034d152d8cf2d1b8d](https://github.com/TheAxonLab/hcph-protocol/commit/5afcd97004f96d8314e5eaf034d152d8cf2d1b8d)) by Oscar Esteban (<https://github.com/oesteban>)). Related issues/PRs: #100 (<https://github.com/TheAxonLab/hcph-protocol/issues/100>), #163 (<https://github.com/TheAxonLab/hcph-protocol/issues/163>), #160 (<https://github.com/TheAxonLab/hcph-protocol/issues/160>)

0.3.0 (<https://github.com/TheAxonLab/hcph-protocol/releases/tag/0.3.0>) (September 06, 2023)

Compare with 0.2.0 (<https://github.com/TheAxonLab/hcph-protocol/compare/0.2.0...0.3.0>)

Enhancements, new features, and additions

- Replace unicode symbols with octicons/fontawesome icons ([675e1ff](https://github.com/TheAxonLab/hcph-protocol/commit/675e1ff) (<https://github.com/TheAxonLab/hcph-protocol/commit/675e1ff>)) by Oscar Esteban (<https://github.com/oesteban>)).
- Add ET description to intro ([8bf5278d47150d6c4df454c7d8906aec279952b4](https://github.com/TheAxonLab/hcph-protocol/commit/8bf5278d47150d6c4df454c7d8906aec279952b4)) by Oscar Esteban (<https://github.com/oesteban>)). Related issues/PRs: #146 (<https://github.com/TheAxonLab/hcph-protocol/issues/146>), #153 (<https://github.com/TheAxonLab/hcph-protocol/issues/153>)
- Deep revision of the PR ([1fefef2d98b4b10bb255aa908a544e68bb14fa467](https://github.com/TheAxonLab/hcph-protocol/commit/1fefef2d98b4b10bb255aa908a544e68bb14fa467)) by Oscar Esteban (<https://github.com/oesteban>)).

- Added a safety check for the desiccant chamber color ([7c13efc \(https://github.com/TheAxonLab/hcph-protocol/commit/7c13efc30625935bd8c0369174de7a2ea6f53f5f\)](https://github.com/TheAxonLab/hcph-protocol/commit/7c13efc30625935bd8c0369174de7a2ea6f53f5f) by Alexandre Cionca (<https://github.com/acionca>)).

Bug Fixes

- Scanner name leak ([71a5e81d1e8c3dc4c8bbf8f01d88163870551ae7](https://github.com/TheAxonLab/hcph-protocol/commit/71a5e81d1e8c3dc4c8bbf8f01d88163870551ae7)) by Alexandre Cionca (<https://github.com/acionca>)).
- Indentation for rendering / show admonition folded ([0747ffe \(https://github.com/TheAxonLab/hcph-protocol/commit/0747ffe8ebb272e3558f090709faae5d3a89d35b\)](https://github.com/TheAxonLab/hcph-protocol/commit/0747ffe8ebb272e3558f090709faae5d3a89d35b) by Oscar Esteban (<https://github.com/oesteban>)).
- Typos ([ae572d919dbd33e3b21b2efbc47a97c250982c79](https://github.com/TheAxonLab/hcph-protocol/commit/ae572d919dbd33e3b21b2efbc47a97c250982c79)) by Céline Provins (<https://github.com/celprov>)).
- Add missing picture in emergency procedures section ([e977607 \(https://github.com/TheAxonLab/hcph-protocol/commit/e977607933c444a306639f61431ef99874b8f431\)](https://github.com/TheAxonLab/hcph-protocol/commit/e977607933c444a306639f61431ef99874b8f431) by Oscar Esteban (<https://github.com/oesteban>)). Related issues/PRs: #89 (<https://github.com/TheAxonLab/hcph-protocol/issues/89>)

0.2.0 (<https://github.com/TheAxonLab/hcph-protocol/releases/tag/0.2.0>) (August 29, 2023)

Compare with 0.1.0 (<https://github.com/TheAxonLab/hcph-protocol/compare/0.1.0...0.2.0>)

Enhancements, new features, and additions

- Change icon of quote admonitions ([fbadaed \(https://github.com/TheAxonLab/hcph-protocol/commit/fbadaedc37d61e2b2f137cede897fd608433142e\)](https://github.com/TheAxonLab/hcph-protocol/commit/fbadaedc37d61e2b2f137cede897fd608433142e) by Oscar Esteban (<https://github.com/oesteban>)).
- Large overhaul, including initial flowchart of the experiment ([0e0d390 \(https://github.com/TheAxonLab/hcph-protocol/commit/0e0d390931ba13b96374a14cf8ea495f782eda85\)](https://github.com/TheAxonLab/hcph-protocol/commit/0e0d390931ba13b96374a14cf8ea495f782eda85) by Oscar Esteban (<https://github.com/oesteban>)).
- Add explanation in SOPs and code to run defacing ([2d8982c \(https://github.com/TheAxonLab/hcph-protocol/commit/2d8982c11368678b7141c31cc575d62eada474e7\)](https://github.com/TheAxonLab/hcph-protocol/commit/2d8982c11368678b7141c31cc575d62eada474e7) by Céline Provins (<https://github.com/celprov>)).
- Add codespell ([61717daacaddc4d2a5cbb60893e1ea3504aa184e](https://github.com/TheAxonLab/hcph-protocol/commit/61717daacaddc4d2a5cbb60893e1ea3504aa184e)) by Oscar Esteban (<https://github.com/oesteban>)).
- Add folder structure of the BIDS dataset ([c3d0a2a \(https://github.com/TheAxonLab/hcph-protocol/commit/c3d0a2a01a7bbe2fc953c28c709ceeba2ede6479\)](https://github.com/TheAxonLab/hcph-protocol/commit/c3d0a2a01a7bbe2fc953c28c709ceeba2ede6479) by Oscar Esteban (<https://github.com/oesteban>)). Related issues/PRs: #94 (<https://github.com/TheAxonLab/hcph-protocol/issues/94>)

- Add tape for head motion ([2dbae4d7c359ef48fc058861708ce6750bfc8ce4](https://github.com/TheAxonLab/hcph-protocol/commit/2dbae4d7c359ef48fc058861708ce6750bfc8ce4)) by Oscar Esteban (<https://github.com/oesteban>). Related issues/PRs: #87 (<https://github.com/TheAxonLab/hcph-protocol/issues/87>)
- Add STP100D and MMBT-S manuals ([9feb3366ad617219f3cbcb8a6fdbbe77bbaea382e](https://github.com/TheAxonLab/hcph-protocol/commit/9feb3366ad617219f3cbcb8a6fdbbe77bbaea382e)) by Oscar Esteban (<https://github.com/oesteban>).
- Improve some admonitions ([de3f034568d4c08684b72bd3f9457c246cb69849](https://github.com/TheAxonLab/hcph-protocol/commit/de3f034568d4c08684b72bd3f9457c246cb69849)) by Oscar Esteban (<https://github.com/oesteban>).

Bug Fixes

- Stop leaking host name ([5a42d8574b6a4b9157f2bbe3bb2445eaef9e6be5](https://github.com/TheAxonLab/hcph-protocol/commit/5a42d8574b6a4b9157f2bbe3bb2445eaef9e6be5)) by Oscar Esteban (<https://github.com/oesteban>). Related issues/PRs: #122 (<https://github.com/TheAxonLab/hcph-protocol/issues/122>)
- Refactor of the preliminary section, separating an intro from it ([19b4571589a49cabd22fa2b092bd7a9ada006c40](https://github.com/TheAxonLab/hcph-protocol/commit/19b4571589a49cabd22fa2b092bd7a9ada006c40)) by Oscar Esteban (<https://github.com/oesteban>).
- Trim trailing spaces, change admonition type ([6e16e80baa13299b57785d46a15599dd8569c044](https://github.com/TheAxonLab/hcph-protocol/commit/6e16e80baa13299b57785d46a15599dd8569c044)) by Oscar Esteban (<https://github.com/oesteban>).
- Revert removal of indentation in script file ([9be8d05](https://github.com/TheAxonLab/hcph-protocol/commit/9be8d05)) ([9be8d055b8e21fc3ae56cf6d41d23ad46fd02b3d](https://github.com/TheAxonLab/hcph-protocol/commit/9be8d055b8e21fc3ae56cf6d41d23ad46fd02b3d)) by Oscar Esteban (<https://github.com/oesteban>)).
- Reorder some incongruent steps, move sound, light and ventilation ([e1f4b4b35d1bf9db422a10469b26fc8be16c7e](https://github.com/TheAxonLab/hcph-protocol/commit/e1f4b4b35d1bf9db422a10469b26fc8be16c7e)) by Oscar Esteban (<https://github.com/oesteban>)).
- Use octicons and fontawesome ([09927cc63e16b9cdd5a82d6c566b124e9d78d255](https://github.com/TheAxonLab/hcph-protocol/commit/09927cc63e16b9cdd5a82d6c566b124e9d78d255)) by Oscar Esteban (<https://github.com/oesteban>)).
- Inconsistencies in the ET's eye-coverage setting and calibration ([15cebe21044daa79d2ce8e04332a9af420b36cf3](https://github.com/TheAxonLab/hcph-protocol/commit/15cebe21044daa79d2ce8e04332a9af420b36cf3)) by Oscar Esteban (<https://github.com/oesteban>)).
- Misplaced ET description and minor revisions ([60475e7ad21cd4f595beb381dc9a69fc897fdb25](https://github.com/TheAxonLab/hcph-protocol/commit/60475e7ad21cd4f595beb381dc9a69fc897fdb25)) by Oscar Esteban (<https://github.com/oesteban>)). Related issues/PRs: #99 (<https://github.com/TheAxonLab/hcph-protocol/issues/99>)
- Spell check and indentation with spaces ([2c2cdeb979ffecb485def7bc48d70f677f37659](https://github.com/TheAxonLab/hcph-protocol/commit/2c2cdeb979ffecb485def7bc48d70f677f37659)) by Oscar Esteban (<https://github.com/oesteban>)).

- Add a note regarding disruption on BIDS names after session 14 ([1da4810516dc6a08e6362bef464bb1d0bd150080](https://github.com/TheAxonLab/hcph-protocol/commit/1da4810516dc6a08e6362bef464bb1d0bd150080)) by Oscar Esteban (<https://github.com/oesteban>)).
- Wrong number of sessions at index page ([1adb77de68e241c395f4ccb6dd425b8d655fd96e](https://github.com/TheAxonLab/hcph-protocol/commit/1adb77de68e241c395f4ccb6dd425b8d655fd96e)) by Oscar Esteban (<https://github.com/oesteban>)).
- Typo ([abe827c22b9c5f57fa949a02d7c3eeb42b346f41](https://github.com/TheAxonLab/hcph-protocol/commit/abe827c22b9c5f57fa949a02d7c3eeb42b346f41)) by Oscar Esteban (<https://github.com/oesteban>)).
- Improve the key listening ([ead2438129b1898bc2696590ff6d21e446fa3a46](https://github.com/TheAxonLab/hcph-protocol/commit/ead2438129b1898bc2696590ff6d21e446fa3a46)) by Oscar Esteban (<https://github.com/oesteban>)).

Maintenance and Continuous Integration

- Update git-changelog config ([29d79f07de8ad9ddca3fdbef3f73f96e05633509](https://github.com/TheAxonLab/hcph-protocol/commit/29d79f07de8ad9ddca3fdbef3f73f96e05633509)) by Oscar Esteban (<https://github.com/oesteban>)).
- Fix file path and run black for style ([164d8f1d7e09528118efa5547dc1c11b0c79ef8a](https://github.com/TheAxonLab/hcph-protocol/commit/164d8f1d7e09528118efa5547dc1c11b0c79ef8a)) by Oscar Esteban (<https://github.com/oesteban>)).

0.1.0 (<https://github.com/TheAxonLab/hcph-protocol/releases/tag/0.1.0>) (June 29, 2023)

The first release of these SOPs. Currently, the document is still a work in progress, with the Data management, Preprocessing, and Release of data yet to be written.

Compare with first commit (<https://github.com/TheAxonLab/hcph-protocol/compare/51fb53f255aa8ee25b1ecb38b3429c400fabea3...0.1.0>)

Enhancements, new features, and additions

- Rename study-settings file ([f53526ecec5cbe26679f8bbcfea134306571cde7](https://github.com/TheAxonLab/hcph-protocol/commit/f53526ecec5cbe26679f8bbcfea134306571cde7)) by Oscar Esteban (<https://github.com/oesteban>)).
- Add task timings and references ([b21c7171139a4a19060fc648e41cf1dc019a05e7](https://github.com/TheAxonLab/hcph-protocol/commit/b21c7171139a4a19060fc648e41cf1dc019a05e7)) by Oscar Esteban (<https://github.com/oesteban>)). Related issues/PRs: #73 (<https://github.com/TheAxonLab/hcph-protocol/issues/73>) Co-authored-by: Elodie Savary (<https://github.com/esavary>)

- Add *phys2bids* commandline ([0d22fd7 \(https://github.com/TheAxonLab/hcp-h-protocol/commit/0d22fd71d28f59c405b5f01fab18127780be6ea2\)](https://github.com/TheAxonLab/hcp-h-protocol/commit/0d22fd71d28f59c405b5f01fab18127780be6ea2) by Oscar Esteban (<https://github.com/oesteban>)).
- Change theme, add chuv logo, update data-storage ([a00e833 \(https://github.com/TheAxonLab/hcp-h-protocol/commit/a00e83325f02110c0c1a7a3389def10339475115\)](https://github.com/TheAxonLab/hcp-h-protocol/commit/a00e83325f02110c0c1a7a3389def10339475115) by Oscar Esteban (<https://github.com/oesteban>)).
- Refining the participant preparation ([f450fd2 \(https://github.com/TheAxonLab/hcp-h-protocol/commit/f450fd208ceb83fa0c800be6e71e6231c2a0a25a\)](https://github.com/TheAxonLab/hcp-h-protocol/commit/f450fd208ceb83fa0c800be6e71e6231c2a0a25a) by Oscar Esteban (<https://github.com/oesteban>)).
- Sectioning the participant preparation ([84a4ee1 \(https://github.com/TheAxonLab/hcp-h-protocol/commit/84a4ee1b6a306fafda8e7c7332db423003986d0b\)](https://github.com/TheAxonLab/hcp-h-protocol/commit/84a4ee1b6a306fafda8e7c7332db423003986d0b) by Oscar Esteban (<https://github.com/oesteban>)).
- Revise *@celprov* (<https://github.com/celprov>)'s code ([a011894 \(https://github.com/TheAxonLab/hcp-h-protocol/commit/a0118947eb563bfd6e329d73a82abe7702c76c2\)](https://github.com/TheAxonLab/hcp-h-protocol/commit/a0118947eb563bfd6e329d73a82abe7702c76c2) by Oscar Esteban (<https://github.com/oesteban>)).
- Minimal, stylistic changes ([030a9ca \(https://github.com/TheAxonLab/hcp-h-protocol/commit/030a9ca\)](https://github.com/TheAxonLab/hcp-h-protocol/commit/030a9ca) by Oscar Esteban (<https://github.com/oesteban>)).
- Remove comment about starting recordings as it is now covered by #71 (<https://github.com/TheAxonLab/hcp-h-protocol/issues/71>) ([e4fa2cf \(https://github.com/TheAxonLab/hcp-h-protocol/commit/e4fa2cf\)](https://github.com/TheAxonLab/hcp-h-protocol/commit/e4fa2cf) by Oscar Esteban (<https://github.com/oesteban>)).
- Overhaul of the scanning section of the SOPs ([732c963 \(https://github.com/TheAxonLab/hcp-h-protocol/commit/732c9632d91a6f537af026227e178d10c48030c7\)](https://github.com/TheAxonLab/hcp-h-protocol/commit/732c9632d91a6f537af026227e178d10c48030c7) by Oscar Esteban (<https://github.com/oesteban>)).
- Add emergency procedures ([fc52766 \(https://github.com/TheAxonLab/hcp-h-protocol/commit/fc52766e9793ad516155df01d54b57f27f1e94c1\)](https://github.com/TheAxonLab/hcp-h-protocol/commit/fc52766e9793ad516155df01d54b57f27f1e94c1) by Céline Provins (<https://github.com/celprov>)).
- Miscellaneous improvements and picture addition ([b9b74c0 \(https://github.com/TheAxonLab/hcp-h-protocol/commit/b9b74c0\)](https://github.com/TheAxonLab/hcp-h-protocol/commit/b9b74c0) by Céline Provins (<https://github.com/celprov>)).
- Add info on how to configure the Acknowledge software and record physiocal signals ([f32187555b9a399b5cafab56530318bd29a38d84](https://github.com/TheAxonLab/hcp-h-protocol/commit/f32187555b9a399b5cafab56530318bd29a38d84)) by Céline Provins (<https://github.com/celprov>)).
- Add information about the outputs of the different sequences to better explain the procedure ([c7db90a \(https://github.com/TheAxonLab/hcp-h-protocol/commit/c7db90a\)](https://github.com/TheAxonLab/hcp-h-protocol/commit/c7db90a) by Hélène Lajous (<https://github.com/helenelajous>)).
- Add info about cleaning procedure ([f15155a \(https://github.com/TheAxonLab/hcp-h-protocol/commit/f15155a5103b53c6f6526d6a9e07aca03f3b0388\)](https://github.com/TheAxonLab/hcp-h-protocol/commit/f15155a5103b53c6f6526d6a9e07aca03f3b0388) by Hélène Lajous (<https://github.com/helenelajous>)).
- Correct typos and add info in case you know which exam will be run next ([3d82aee \(https://github.com/TheAxonLab/hcp-h-protocol/commit/3d82aee\)](https://github.com/TheAxonLab/hcp-h-protocol/commit/3d82aee)

[3d82aee5b703eb812e6c23ecd4bca84b05eb173f](#) by Hélène Lajous (<https://github.com/helenelajous>).

- Add details about how to switch to advanced user mode to save a protocol ([8e5c46a](#) (<https://github.com/TheAxonLab/hcph-protocol/commit/8e5c46a02ea0f725b3e2404329b3428ce31df3a7>) by Hélène Lajous (<https://github.com/helenelajous>)).
- Add details and correct a few typos ([fdd742d](#) (<https://github.com/TheAxonLab/hcph-protocol/commit/fdd742de2266e0ab2e7aa76252619c52c207c200>) by Hélène Lajous (<https://github.com/helenelajous>)).
- Review comments ([1745329](#) (<https://github.com/TheAxonLab/hcph-protocol/commit/1745329924878c5dc81b6b7d1697b93029a1f61b>) by Oscar Esteban (<https://github.com/oesteban>)).
- Add picture of the ET attached ([eaa3a8a](#) (<https://github.com/TheAxonLab/hcph-protocol/commit/eaa3a8a3b7b8a9f6e18ef1b5b469ab04de516fee>) by Oscar Esteban (<https://github.com/oesteban>)).
- Setup *mkpdfs* plugin ([2d6f9fd](#) (<https://github.com/TheAxonLab/hcph-protocol/commit/2d6f9fd1d7819943adb0312bf397945a0be5ac19>) by Oscar Esteban (<https://github.com/oesteban>)).
- Make it louder ([6d6cce4](#) (<https://github.com/TheAxonLab/hcph-protocol/commit/6d6cce44cfcd39b00af88617c45a9beb48050d3>) by Oscar Esteban (<https://github.com/oesteban>)).
- Add info box about moving the mirror slightly to the right ([589fd63](#) (<https://github.com/TheAxonLab/hcph-protocol/commit/589fd6387dc4c6a35b1a0ec94cbd57c8d3400297>) by Oscar Esteban (<https://github.com/oesteban>)).
- Add warning about attachment of infrared mirror ([00c214d](#) (<https://github.com/TheAxonLab/hcph-protocol/commit/00c214d26232700293199788b40615422ddab683>) by Oscar Esteban (<https://github.com/oesteban>)).
- Miscellaneous improvements and image additions ([a74aa6d](#) (<https://github.com/TheAxonLab/hcph-protocol/commit/a74aa6d4989b3bcf600086140fa79788ca53b6cb>) by Céline Provins (<https://github.com/celprov>)).
- Give instructions on how to switch on the scanner ([c83ad23](#) (<https://github.com/TheAxonLab/hcph-protocol/commit/c83ad232a763e7aaf7ce427f1ceb98d6d4a3b29e>) by Hélène Lajous (<https://github.com/helenelajous>)).
- Improve how the scanner is switched off ([f95d559](#) (<https://github.com/TheAxonLab/hcph-protocol/commit/f95d55990c4106d8e6b19b2bf0693ab7536830b7>) by Hélène Lajous (<https://github.com/helenelajous>)).
- Say you want to turn the key ([85180b4](#) (<https://github.com/TheAxonLab/hcph-protocol/commit/85180b44d3b0d825e245cb3baac8e3da1d9703de>) by Hélène Lajous (<https://github.com/helenelajous>)).
- [heudiconv heuristic] Do not deduplicate if run is found ([5f15cca](#) (<https://github.com/TheAxonLab/hcph-protocol/commit/5f15ccaf59aa974b56a98de2b94be571e4562e15>) by Oscar Esteban (<https://github.com/oesteban>)).

- Add phone call script ([8b10d1c96cb8fd1e0bb3a3233e53e329f2443584](https://github.com/TheAxonLab/hcph-protocol/commit/8b10d1c96cb8fd1e0bb3a3233e53e329f2443584)) by Céline Provins (<https://github.com/celprov>).
- Add what to do if the alarm rings ([f89e39977e01aa39866742c66b3ff473182dd586](https://github.com/TheAxonLab/hcph-protocol/commit/f89e39977e01aa39866742c66b3ff473182dd586)) by Céline Provins (<https://github.com/celprov>).
- Replace BIOPAC setup photo with Ines' annotated one ([8e97af771d0bf7758cf86468d551248e5f8e0d14](https://github.com/TheAxonLab/hcph-protocol/commit/8e97af771d0bf7758cf86468d551248e5f8e0d14)) by Céline Provins (<https://github.com/celprov>).
- Add missing bibliography ([a667955e1f7a604ffda222c73bd4062d04be9d2](https://github.com/TheAxonLab/hcph-protocol/commit/a667955e1f7a604ffda222c73bd4062d04be9d2)) by Céline Provins (<https://github.com/celprov>).
- Addition of miscalleneous information and of many missing pictures ([20ad2bd88603b6e84ca82e045fb9227d12fda17c](https://github.com/TheAxonLab/hcph-protocol/commit/20ad2bd88603b6e84ca82e045fb9227d12fda17c)) by Céline Provins (<https://github.com/celprov>).
- Add link to reproin ([dd4978f5bcc6aa323cbe1e97f5a2986c6760e042](https://github.com/TheAxonLab/hcph-protocol/commit/dd4978f5bcc6aa323cbe1e97f5a2986c6760e042)) by Oscar Esteban (<https://github.com/oesteban>).
- Add a filter to show missing secrets as REDACTED or replace values ([61451c847c3553d85c9c406f3df317400314ea69](https://github.com/TheAxonLab/hcph-protocol/commit/61451c847c3553d85c9c406f3df317400314ea69)) by Oscar Esteban (<https://github.com/oesteban>).
- Improvements to the data management section ([2a176c15d3bba5fc06f177b4b42af7f011de8c2f](https://github.com/TheAxonLab/hcph-protocol/commit/2a176c15d3bba5fc06f177b4b42af7f011de8c2f)) by Oscar Esteban (<https://github.com/oesteban>).
- Minimal improvements to clean-up ([d20edf3e87360d8dce1280c669edb6bc4559a3de](https://github.com/TheAxonLab/hcph-protocol/commit/d20edf3e87360d8dce1280c669edb6bc4559a3de)) by Oscar Esteban (<https://github.com/oesteban>).
- Add pictures and improve new exam description ([c02291f82d784bfa006c101cb20bce8c913851df](https://github.com/TheAxonLab/hcph-protocol/commit/c02291f82d784bfa006c101cb20bce8c913851df)) by Oscar Esteban (<https://github.com/oesteban>).
- Split data collection ([516c388cb1a38c699eb381b2f0586b617e16b73b](https://github.com/TheAxonLab/hcph-protocol/commit/516c388cb1a38c699eb381b2f0586b617e16b73b)) by Oscar Esteban (<https://github.com/oesteban>).
- Add GA video ([944a525880b2263f7c6b6b719fcf7f33f1fe4d3e](https://github.com/TheAxonLab/hcph-protocol/commit/944a525880b2263f7c6b6b719fcf7f33f1fe4d3e)) by Oscar Esteban (<https://github.com/oesteban>).
- Reorder misplaced steps, improve rendering ([3ede838775d3437c4fe377e47cf34a4d7e2e38f3](https://github.com/TheAxonLab/hcph-protocol/commit/3ede838775d3437c4fe377e47cf34a4d7e2e38f3)) by Oscar Esteban (<https://github.com/oesteban>).
- Ensuring it looks good when rendered ([07b0f04bf2298d818b97eb535885f9a4fe33ef02](https://github.com/TheAxonLab/hcph-protocol/commit/07b0f04bf2298d818b97eb535885f9a4fe33ef02)) by Oscar Esteban (<https://github.com/oesteban>)).

- Added some files, restructure and fix some items ([3fa2c85 \(https://github.com/TheAxonLab/hcph-protocol/commit/3fa2c85215c1881ed84cfa30c357f33847e84a07\)](https://github.com/TheAxonLab/hcph-protocol/commit/3fa2c85215c1881ed84cfa30c357f33847e84a07) by Oscar Esteban (<https://github.com/oesteban>)).
- Fix typos and overhaul of data collection ([00e3daf \(https://github.com/TheAxonLab/hcph-protocol/commit/00e3daf\)](https://github.com/TheAxonLab/hcph-protocol/commit/00e3daf) by Oscar Esteban (<https://github.com/oesteban>)).
- Add images of gas analyzer ([6032ed0 \(https://github.com/TheAxonLab/hcph-protocol/commit/6032ed01e4dfe354e8a2d3a59c6a6d5a957247f7\)](https://github.com/TheAxonLab/hcph-protocol/commit/6032ed01e4dfe354e8a2d3a59c6a6d5a957247f7) by Céline Provins (<https://github.com/celprov>)).
- Add info how to setup the respiration belt and the gas analyzer ([62bf6fd \(https://github.com/TheAxonLab/hcph-protocol/commit/62bf6fd2c7ab4a26396834432c752ef4cd436775\)](https://github.com/TheAxonLab/hcph-protocol/commit/62bf6fd2c7ab4a26396834432c752ef4cd436775) by Céline Provins (<https://github.com/celprov>)).
- Add info to setup BIOPAC ([3719eca \(https://github.com/TheAxonLab/hcph-protocol/commit/3719eca2529eaa681287c47edafc10f8a37b9850\)](https://github.com/TheAxonLab/hcph-protocol/commit/3719eca2529eaa681287c47edafc10f8a37b9850) by Céline Provins (<https://github.com/celprov>)).
- Add info to turn off computer ([3e66ec8 \(https://github.com/TheAxonLab/hcph-protocol/commit/3e66ec85861eab28338081da436aa0286a0fa9c8\)](https://github.com/TheAxonLab/hcph-protocol/commit/3e66ec85861eab28338081da436aa0286a0fa9c8) by Céline Provins (<https://github.com/celprov>)).
- Add info about plugging the coil after the exam has been open ([1d5b501 \(https://github.com/TheAxonLab/hcph-protocol/commit/1d5b501d7fd31b85f796ea24c44e15dd772ba1ba\)](https://github.com/TheAxonLab/hcph-protocol/commit/1d5b501d7fd31b85f796ea24c44e15dd772ba1ba) by Céline Provins (<https://github.com/celprov>)).
- Add info about how to save the magnitude image of the fmap ([d3efc7d \(https://github.com/TheAxonLab/hcph-protocol/commit/d3efc7dc2b6eed9e5dd8662fe545d100102f66cb\)](https://github.com/TheAxonLab/hcph-protocol/commit/d3efc7dc2b6eed9e5dd8662fe545d100102f66cb) by Céline Provins (<https://github.com/celprov>)).
- Add ack, edit/reorder some sections ([46e41fa \(https://github.com/TheAxonLab/hcph-protocol/commit/46e41fab015c6bd923a571f05fb69f916f9a10c2\)](https://github.com/TheAxonLab/hcph-protocol/commit/46e41fab015c6bd923a571f05fb69f916f9a10c2) by Oscar Esteban (<https://github.com/oesteban>)).
- First pass at data collection checklist ([2ab93f7 \(https://github.com/TheAxonLab/hcph-protocol/commit/2ab93f7e3e908f66a28ec124500c57853cf82e37\)](https://github.com/TheAxonLab/hcph-protocol/commit/2ab93f7e3e908f66a28ec124500c57853cf82e37) by Oscar Esteban (<https://github.com/oesteban>)).
- Update README ([3833e37 \(https://github.com/TheAxonLab/hcph-protocol/commit/3833e370c8d15e8263e34ae66d3a530dec13a2d7\)](https://github.com/TheAxonLab/hcph-protocol/commit/3833e370c8d15e8263e34ae66d3a530dec13a2d7) by Oscar Esteban (<https://github.com/oesteban>)).

Bug Fixes

- Add missing settings file ([0d4d3f8 \(https://github.com/TheAxonLab/hcph-protocol/commit/0d4d3f8ce7490657f0517595a71103996eb14615\)](https://github.com/TheAxonLab/hcph-protocol/commit/0d4d3f8ce7490657f0517595a71103996eb14615) by Oscar Esteban (<https://github.com/oesteban>)).
- [heudiconv heuristic] Identify phase and mag in func and fmap-epi ([e1e3170 \(https://github.com/TheAxonLab/hcph-protocol/commit/e1e3170d8da31a55d1a7b7cf1b53d9d7ed953844\)](https://github.com/TheAxonLab/hcph-protocol/commit/e1e3170d8da31a55d1a7b7cf1b53d9d7ed953844) by Oscar Esteban (<https://github.com/oesteban>)).

- [heudiconv heuristic] Robuster detection of phase/mag in GRE fieldmaps ([e65f0d2a6e26dcf3a96d21cce34d9febef727ec6](https://github.com/TheAxonLab/hcph-protocol/commit/e65f0d2a6e26dcf3a96d21cce34d9febef727ec6)) by Oscar Esteban (<https://github.com/oesteban>)).
- Wrong path of mathjax ([731dfdd89f49ef5980e7c3da9b3ea77f84e9a14](https://github.com/TheAxonLab/hcph-protocol/commit/731dfdd89f49ef5980e7c3da9b3ea77f84e9a14)) by Oscar Esteban (<https://github.com/oesteban>)).
- Reorder scanning protocol to match sequences order in the manuscript ([80ee8f4002cdd9ed003e9296b11355a2b18582ed](https://github.com/TheAxonLab/hcph-protocol/commit/80ee8f4002cdd9ed003e9296b11355a2b18582ed)) by Céline Provins (<https://github.com/celprov>)).
- Correct console parameter name for reconstruction ([dd1f3cf](https://github.com/TheAxonLab/hcph-protocol/commit/dd1f3cff78eb02521b7d73d91a3dc1770eea75f) (<https://github.com/TheAxonLab/hcph-protocol/commit/dd1f3cff78eb02521b7d73d91a3dc1770eea75f>) by Céline Provins (<https://github.com/celprov>)).
- Fix layout ([3facec988c160ffda362e71df55e6840b886d273](https://github.com/TheAxonLab/hcph-protocol/commit/3facec988c160ffda362e71df55e6840b886d273)) by Céline Provins (<https://github.com/celprov>)).
- Wrong link to psychopy git repo ([33ed5e5bc9610bb660f448550903e145da221389](https://github.com/TheAxonLab/hcph-protocol/commit/33ed5e5bc9610bb660f448550903e145da221389)) by Céline Provins (<https://github.com/celprov>)).
- Missing picture ([7eb7f42f37d064252f3ee2884d7d1017fc9db0ea](https://github.com/TheAxonLab/hcph-protocol/commit/7eb7f42f37d064252f3ee2884d7d1017fc9db0ea)) by Céline Provins (<https://github.com/celprov>)).
- Update RR figure 1 ([387722b35f7e93a0f67b5dadd32468d2e7e62fa2](https://github.com/TheAxonLab/hcph-protocol/commit/387722b35f7e93a0f67b5dadd32468d2e7e62fa2)) by Oscar Esteban (<https://github.com/oesteban>)).
- Add missing dependency ([976ae4cc269e1d5b82d9dcebf2087912379de9d3](https://github.com/TheAxonLab/hcph-protocol/commit/976ae4cc269e1d5b82d9dcebf2087912379de9d3)) by Oscar Esteban (<https://github.com/oesteban>)).
- Correct errors I introduced in [@helenelajous](https://github.com/helenelajous) (<https://github.com/helenelajous>)' PR ([3b656f27fe6185b9e1af0c0fc84528895b748d91](https://github.com/TheAxonLab/hcph-protocol/commit/3b656f27fe6185b9e1af0c0fc84528895b748d91)) by Oscar Esteban (<https://github.com/oesteban>)).
- [heudiconv heuristic] More sensible decision for phasediff fieldmaps ([3d9b73e73f6fb4735eb73bfbde084cf1346e9e8a](https://github.com/TheAxonLab/hcph-protocol/commit/3d9b73e73f6fb4735eb73bfbde084cf1346e9e8a)) by Oscar Esteban (<https://github.com/oesteban>)).
- [heudiconv heuristic] Set run when duplicates of a sequence are found ([504e2170dc92b607bcfd7d356d6bb5a02cb7f8ca](https://github.com/TheAxonLab/hcph-protocol/commit/504e2170dc92b607bcfd7d356d6bb5a02cb7f8ca)) by Oscar Esteban (<https://github.com/oesteban>)).
- [heudiconv heuristic] Overhaul of the reproin heuristic ([6576b321ec641c1eaea3e0800ea865a37ad8061a](https://github.com/TheAxonLab/hcph-protocol/commit/6576b321ec641c1eaea3e0800ea865a37ad8061a)) by Oscar Esteban (<https://github.com/oesteban>)).

- Minimal amends ([9e9d56f6d8cb0318b3ed382a0e31381f762fb311](https://github.com/TheAxonLab/hcph-protocol/commit/9e9d56f6d8cb0318b3ed382a0e31381f762fb311)) by Oscar Esteban (<https://github.com/oesteban>)).
- PACSMAN instructions ([b5623725f97e5832e1cb1bcb7da0c91c71cd5ed6](https://github.com/TheAxonLab/hcph-protocol/commit/b5623725f97e5832e1cb1bcb7da0c91c71cd5ed6)) by Oscar Esteban (<https://github.com/oesteban>)).
- PACSMAN csv file example ([e0a8f66725c2048235b7ea6a6357e5982890b53f](https://github.com/TheAxonLab/hcph-protocol/commit/e0a8f66725c2048235b7ea6a6357e5982890b53f)) by Oscar Esteban (<https://github.com/oesteban>)).
- Images with wrong paths, and names ([5260d62](https://github.com/TheAxonLab/hcph-protocol/commit/5260d62)) by Oscar Esteban (<https://github.com/oesteban>)).
- Miscellaneous stuff ([df5a300](https://github.com/TheAxonLab/hcph-protocol/commit/df5a300)) by Oscar Esteban (<https://github.com/oesteban>)).
- Update version of gha/checkout and fix path second time ([ccfc19c1a8da01f6d07ef4a58b3ac2cbd3bd0383](https://github.com/TheAxonLab/hcph-protocol/commit/cfcc19c1a8da01f6d07ef4a58b3ac2cbd3bd0383)) by Oscar Esteban (<https://github.com/oesteban>)).
- Still setting up path ([dfe542c96d3b1a064075715c5b7a09f98c29bc49](https://github.com/TheAxonLab/hcph-protocol/commit/dfe542c96d3b1a064075715c5b7a09f98c29bc49)) by Oscar Esteban (<https://github.com/oesteban>)).
- Roll-back the path option ([ac2661f25f768e27a0b71c6145ca9de2a1fdf333](https://github.com/TheAxonLab/hcph-protocol/commit/ac2661f25f768e27a0b71c6145ca9de2a1fdf333)) by Oscar Esteban (<https://github.com/oesteban>)).
- Checkout action ([1a149b2207ea72118e82e2f664431b5b8185870c](https://github.com/TheAxonLab/hcph-protocol/commit/1a149b2207ea72118e82e2f664431b5b8185870c)) by Oscar Esteban (<https://github.com/oesteban>)).
- Remove toc plugin ([38611744407fe9101edce0dfca812b930c2fbaf5](https://github.com/TheAxonLab/hcph-protocol/commit/38611744407fe9101edce0dfca812b930c2fbaf5)) by Oscar Esteban (<https://github.com/oesteban>)).

Maintenance and Continuous Integration

- Set --in-place editing of the changelog ([48f8acdab772c69d4a7cf1305562958292b4c163](https://github.com/TheAxonLab/hcph-protocol/commit/48f8acdab772c69d4a7cf1305562958292b4c163)) by Oscar Esteban (<https://github.com/oesteban>)).
- Refine changelog update with git-changelog ([e4ea298cd965c6e01953ded4f0868e4645899f](https://github.com/TheAxonLab/hcph-protocol/commit/e4ea298cd965c6e01953ded4f0868e4645899f)) by Oscar Esteban (<https://github.com/oesteban>)).
- Use git-changelog to update the changelog ([856e58a56f14861ce1bce6d9079d26b9e63ca539](https://github.com/TheAxonLab/hcph-protocol/commit/856e58a56f14861ce1bce6d9079d26b9e63ca539)) by Oscar Esteban (<https://github.com/oesteban>)).

- Remove old exemplary code ([2e5697c](https://github.com/TheAxonLab/hcph-protocol/commit/2e5697cb7c627422db6b5ff2a71c017f84ef216) (<https://github.com/TheAxonLab/hcph-protocol/commit/2e5697cb7c627422db6b5ff2a71c017f84ef216>) by Oscar Esteban (<https://github.com/oesteban>)).

Recruitment, Scheduling, and Screening

Recruitment and screening

Cohort I

Recruitment, screening and informed consent do not apply to Cohort I because the participant is the Principal Investigator himself.

Cohort III

Recruitment, screening and informed consent do not apply to Cohort III because the sessions have already been acquired.

Recruitment shortlist

- Distribute the [recruitment flyers](#) at CHUV, as well as on EPFL and UNIL campuses, both physically and electronically (e.g., e-mail lists).
- Insert any new potential participant who shows interest by calling ####-####-####, [SMS](#), email, etc. in [our recruits spreadsheet \(/redacted.html\)](#). Make sure you get an e-mail contact to send documents.

Recruits shortlist

- Remove all flyers and indicate that recruitment is not open anymore once the shortlist quotas have been reached (5 males and 5 females for Cohort II).

First contact

Important

- Write an email to them within the next 24h.
- Use [the email template](#) and make sure you attach the [MRI Safety and Screening Questionnaire](#) and the Informed Consent Form.
- Confirm the reception of the email AND the documents over the phone.

Phone call

Info

The study coordinator (█, Assistante doctorante) will call the potential participant after at least three days of having sent the information in the case of cohort II ([HRA, art. 16-3 \(https://www.fedlex.admin.ch/eli/cc/2013/642/en\)](https://www.fedlex.admin.ch/eli/cc/2013/642/en)).

- Use the [phone script](#) to drive the conversation and record participant responses to questions.
- If participant consents to the phone screen, conduct it and mark the results (screener date, if responded "yes" to any medical questions, whether or not passed screener) in the appropriate columns of the recruitment spreadsheet.
- Confirm whether the potential participant understood the [MRI Safety & Screening Questionnaire](#), and discuss with them any questions or potential reasons that may disqualify them to participate.

Carefully screen the subject

- In case of any doubts emerging from the [MRI](#) safety screening, indicate the potential participant that you will call them back within three days, after contacting the responsible physician.
 - Collect as much information as possible about their case.
 - Contact █ with all the information.
 - In case of negative assessment by the medical contact, the volunteer MUST NOT participate in the study.
 - Otherwise, call back the participant as soon as possible to confirm participation.
-
- Female participants will be informed and must acknowledge that they must take a pregnancy test before the first scanning session.
 - If the candidate participant does not pass the phone screen, then end the interview, informing them that they do not meet our inclusion criteria, and mark the screen fail in the recruitment spreadsheet.
 - Make sure that the participant's questions about the study are all addressed and answered.
 - Request the potential participant to confirm they are willing to continue.
 - Indicate in the shortlist of recruits that the participant is ready to schedule the first session.
 - Tell the participant that they will be called back to set up the first session.
 - Remind them that they can ask further questions at any time before the [MRI](#) scan session.

Templates

First contact email (FR)

Remember to attach the [MRI Safety and Screening Questionnaire](#) and the ICF.

Objet: Invitation à participer à une étude d'acquisition IRM du cerveau : informations et documents joints

Cher/Chère [nom],

Nous vous remercions vivement pour l'intérêt que vous portez à notre étude de recherche sur l'imagerie IRM du cerveau.

Notre équipe mène actuellement une étude visant à mieux comprendre les différentes sources de variabilité lors d'un examen IRM.

Nous recherchons des participants·tes âgés de 24 à 55 ans, en bonne santé et sans antécédents de maladies neurologiques. Les participants·tes doivent consentir à la publication de leurs données dans le cadre du projet. Des mesures de confidentialité sont rigoureusement mises en place pour garantir l'anonymat des données. Elles impliquent notamment la suppression de toute information permettant l'identification des participants, telles que la date de naissance ou le nom.

Participer à cette étude implique une présence à 12 séances d'acquisition IRM du cerveau, d'environ 1h30 chacune. Ceci représente un temps de participation total d'environ 18 heures. Vous recevrez une indemnité financière pour votre participation. Veuillez noter que si des découvertes fortuites concernant votre santé étaient faites au cours de l'expérience, vous consentez à en être informé·e.

Nous vous invitons à prendre connaissance des documents joints afin d'obtenir un aperçu de l'étude. Le premier document détaille les implications d'une participation à l'étude, l'organisation des séances d'acquisition et fournit un résumé des objectifs du projet. Le second document concerne les éventuelles contre-indications à passer un examen IRM. Veuillez le remplir soigneusement et nous le retourner.

Si après lecture des informations ci-dessus vous acceptez de participer, nous souhaiterions convenir d'un entretien téléphonique avec vous afin de récapituler les points importants de votre participation. Cet entretien nous permettra également de vérifier votre éligibilité à participer à l'étude et de répondre à toutes vos éventuelles questions. Nous vous prions de nous retourner votre réponse dans un délai de 3 jours ouvrables. Afin que nous puissions planifier l'entretien téléphonique, veuillez également nous indiquer les plages horaires dans lesquelles nous pourrions vous contacter.

Entre-temps, si vous avez des questions, n'hésitez pas à nous contacter par e-mail ou par téléphone au ####-####. Nous serons ravis de répondre à toutes vos questions.

Nous vous remercions encore une fois pour votre intérêt.

Cordialement,
Céline PROVINS
Assistante-doctorante

First contact call (FR)

First contact call script in French

Bonjour ici Céline Provins,

Je vous appelle concernant l'étude d'acquisition IRM du cerveau. Le but de cet appel est de vous répéter les éléments importants concernant le projet. Ensuite nous allons vérifier ensemble que vous êtes d'accord avec toutes les exigences pour participer à ce projet et nous allons vérifier que vous n'avez pas de contre-indications qui vous empêchent de passer un examen IRM. De plus, je suis aussi là pour répondre à toutes vos questions, donc n'hésitez pas à m'interrompre si vous ne comprenez pas quelque chose ou si vous avez des doutes.

Est-ce que vous avez des questions jusque là ?

Je vais maintenant vous présenter les éléments essentiels de votre participation à notre étude. La participation à ce projet comprend 12 séances d'environ 1h30 qui se dérouleront au CHUV. Chaque séance durera environ 1h30. Nous commencerons par remplir un bref questionnaire pour assurer la sécurité de la procédure, cela prendra environ 15 minutes ensuite, nous vous préparerons, nous vous expliquerons l'examen et nous nous assurerons que vous ne portez rien qui puisse causer des perturbations magnétiques. Nous vérifierons

également avec une liste de contrôle que toutes les mesures de sécurité sont prises et que vous n'avez pas d'éléments métalliques sur vous. Ensuite vous passerez environ 1h15 dans le scanner.

Dans chaque séance nous allons non seulement acquérir des images IRM mais nous allons aussi enregistrer des signaux physiologiques au moyen de quatres appareils supplémentaires. Ces appareils sont compatibles avec l'IRM et ils n'affectent pas votre santé.

Le premier appareil est une ceinture respiratoire pour suivre votre respiration. C'est simplement une ceinture autour de votre ventre ou autour de votre thorax qui mesure le déplacement de votre ventre.

Par la suite, nous installerons trois électrodes sur la partie supérieure de votre thorax. Ces électrodes seront fixées à l'aide d'un gel conducteur sur votre peau, permettant ainsi de mesurer vos pulsations cardiaques.

Le troisième appareil est une canule respiratoire pour mesurer la concentration de dioxyde de carbone expiré. Une canule respiratoire est un tube que certaines personnes âgées utilisent pour inhale de l'oxygène. La différence c'est que nous n'allons pas vous donner du gaz, mais simplement mesurer la quantité de dioxyde de carbone que vous expirez.

Le 4ème appareil est un appareil pour mesurer le mouvement de vos pupilles. Cet appareil ne sera pas fixé sur vous et n'a aucun effet ni sur votre santé ni sur votre confort. Durant toute la séance d'IRM, vous tiendrez un bouton alarme dans votre main, c'est-à-dire qu'à n'importe quel moment si vous avez un problème vous pouvez appuyer sur ce bouton d'alarme et nous interrompons l'examen immédiatement et venons vous chercher à l'intérieur du scanner pour voir avec vous ce qui ne va pas. Vous pouvez interrompre une session à tout moment sans explication.

Est-ce que vous avez des questions? Non, alors continuons.

Les risques liés à l'IRM sont les suivants.

l'IRM émet un fort champ magnétique, il est donc dangereux de rentrer dans la salle avec des objets à susceptibilité magnétique. C'est pourquoi plus tard nous allons minutieusement vérifier ensemble la liste du questionnaire de sécurité IRM. Toutefois en l'absence d'objet à susceptibilité magnétique, l'IRM est complètement sans danger car il n'utilise pas de rayonnement ionisant. Il n'y a pas de danger même si on fait beaucoup de séances.

Notez que le tunnel est assez étroit, ce qui pourrait occasionner une légère sensation de claustrophobie.

Si vous êtes une femme, je dois vous informer qu'avant la première session vous allez devoir faire un test de grossesse. C'est pour vérifier que vous n'êtes pas enceinte, car éthiquement nous n'avons pas le droit de scanner des femmes enceintes car les effets des IRM sur le fœtus n'ont pas encore été étudiés en détail. Avant chaque séance vous devrez également donner des informations sur vos règles comme le dernier jour des règles ainsi que la régularité de votre cycle. Ceci est important car le cycle menstruel a un effet sur le cerveau et pour la fiabilité de notre étude nous avons besoin ces informations. Néanmoins, veuillez noter que vous avez la possibilité de choisir de ne pas inclure les informations concernant vos cycles menstruels lorsque nous rendrons les données publiques.

Les sessions d'IRM seront planifiées en tenant compte de la disponibilité des équipements, de vos préférences et de votre emploi du temps. La participation maximale s'étend sur une période de 20 semaines consécutives, soit 5 mois. Cependant, dans l'idéal, les séances seront planifiées à des intervalles réguliers.

Est-ce que vous avez des questions jusque-là ?

Ok donc maintenant je veux juste vérifier avec vous que vous êtes d'accord avec toutes les exigences concernant la participation à ce projet. Est-ce que vous êtes âgé entre 24 et 55 ans ? Avez-vous été diagnostiquée(e) avec un trouble ou une maladie neurologique ? Consentez-vous à être informé(e) des découvertes fortuites relatives à votre santé ? En effet, par souci éthique, les images de la première session seront transmises à un radiologue qui les examinera attentivement. Si une anomalie venait à être détectée dans votre cerveau, vous seriez alors averti(e). Par la suite, un élément d'une grande importance est que vous devez donner votre accord pour la publication de vos données. Cependant, soyez assuré(e) que nous prendrons toutes les mesures nécessaires pour garantir la confidentialité de vos données avant toute publication.

Par exemple, nous allons enlever toute informations qui permettraient de vous reconnaître comme votre nom, votre date de naissance ou la date de l'examen afin de protéger votre confidentialité. Êtes-vous d'accord avec ce point? Un autre élément important est que la participation à cette étude implique de nombreuses sessions IRM. Comme je vous ai dit 12 sessions d'environ 1h30. Ainsi, je vous prie de prendre un moment pour réfléchir si votre engagement envers le projet n'est pas excessif ni susceptible de devenir pesant à mesure que le temps avance, et si vous disposez du temps nécessaire pour mener le projet à bien. Vous devez aussi accepter de nous informer si vous prenez des médicaments, si vous consommez de l'alcool ou de la drogue car ces substances ont un effet important sur le cerveau et nous avons besoin de savoir pour pouvoir quantifier ces effets.

Une autre contrainte c'est que vous devez éviter de boire du café 4h avant les séances car le café aussi est connu pour avoir des effets notables sur le cerveau.

Maintenant que nous avons confirmé que vous êtes d'accord avec toutes ces exigences, je vous rappelle que votre participation est entièrement libre et que vous pouvez vous retirer à tout moment sans explication. Cependant, il est primordial pour nous que les participants parviennent à accomplir les 12 sessions afin d'assurer l'intégralité de nos données. Dans cette optique, nous préférions que vous vous engagiez résolument à mener à terme les 12 sessions, en envisageant une interruption de votre participation uniquement en cas de circonstances urgentes ou imprévues.

Chaque séance sera rémunéré 45 francs plus les frais de transport.

Des questions ?

OK maintenant nous pouvons regarder ensemble le questionnaire de contrôle de sécurité et vérifier que vous avez répondu non à toutes les questions.

Avez-vous répondu oui à une des questions ? Non ok parfait.

Je veux juste revérifier avec vous que vous n'avez bien pas d'aide auditive.

Vous n'avez pas de gouttière dentaire, de prothèse dentaire, de fausses dents etc. Vous n'avez pas non plus de piercing de tatouage ou de maquillage permanent ni d'implant capillaire. Vous n'avez jamais été blessé par un objet métallique. Vous n'avez pas subi des opérations dans lesquelles il y aurait des métaux qui restent dans votre corps comme des clips chirurgicaux, des agrafes, des fixations vertébrale, un stimulateur de la moelle épinière, des extendeurs de tissu. Vous ne portez pas de valve cardiaque. Vous portez pas de biostimulateur, de pompe à médicament interne ou externe, de cathétér ou d'articulation artificielle.

C'est parfait, vous êtes éligible à participer.

Encore quelques instructions à suivre avant chaque la séance. Il faut retirer tous les bijoux, piercing compris, et tous les accessoires de cheveux. Veuillez aussi retirer vos prothèses dentaires, les fausses dents etc. Il faut également retirer les aides auditives et les lunettes. Si vous êtes un homme, veuillez s'il vous plaît vous raser la partie supérieure du torse car nous avons besoin de placer les électrodes à même la peau pour bien enregistrer le signal.

Voilà c'est toutes les informations que j'ai à vous partager. Est-ce que vous avez des questions?

En tout cas merci beaucoup pour votre participation! Si vous avez des questions, des doutes, n'hésitez pas à me rappeler à ce numéro et je vous rappelle dans quelques jours afin de fixer la première session.

Bonne journée.

Au revoir.

Scheduling

- Iteratively draw participants from the recruitment shortlist and call them back to set their first session.

Stop calling potential participants when the sample size has been achieved

Once the sample size is filled (e.g., 3M/3F for Cohort II), call the remainder of the participants in the shortlist to let them know that they have been moved into the wait list.

- The first session will always happen at MRI 1 (Prisma^{Fit}, █)

Scheduling of the Prisma^{Fit} system (█)

Contact █, MRI Operational Manager, for any doubts/problems regarding this system

- Open the █ scheduling system ([URL \(/redacted.html\)](#)) on a browser.
- With the participant on the phone, find a suitable, empty slot by scrolling the calendar.
- Click on the preferred slot, make sure that selected resource is █
- Select █ in the Operator dropdown menu.
- Select the adequate length for the session (120 minutes)
- Select *Research on healthy subjects* in the Type of Scan box.
- Select *true* in Technician Required if you are not a certified operator of the system.

Scheduling of the Vida^{Fit} system (█)

Contact █, Technical MRI Coordinator, for any doubts/problems regarding this system

- Open the █ scheduling system ([URL \(/redacted.html\)](#)) on a browser.
- With the participant on the phone, find a suitable, empty slot by scrolling the calendar.

Clinical scanner hours are very restricted

The study can only be executed on Fridays after 18h00

- Click on the preferred slot, make sure that selected resource is █
- Select █ in the Operator dropdown menu.
- Select the adequate length for the session (60 minutes)
- Select *Research on healthy subjects* in the Type of Scan box.

Select true in Technician Required.

Scheduling of the Vida system (■■■)

Only ■■■, Technical MRI Coordinator, can book this system.

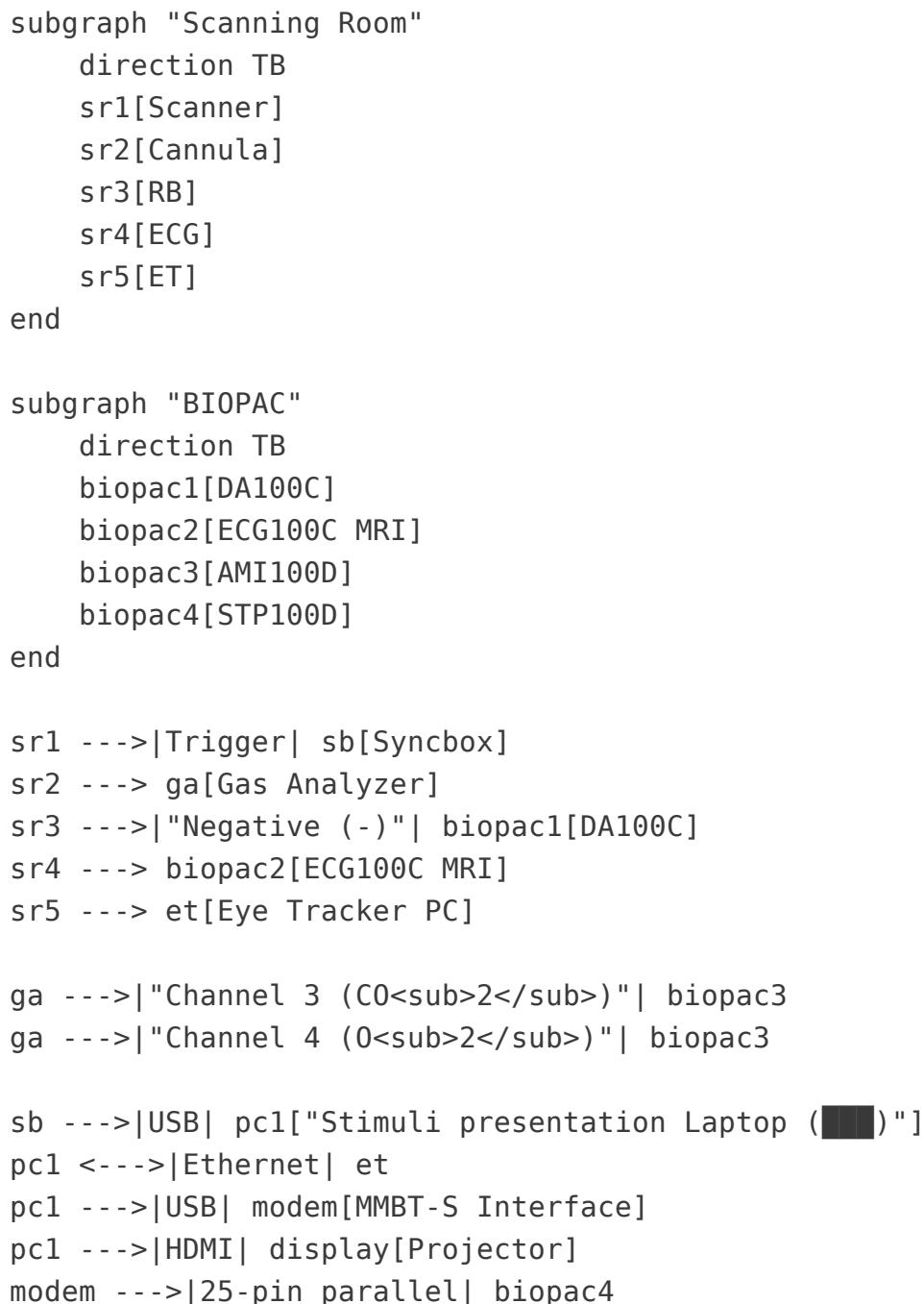
Data collection

Overall experimental settings

The goal of the experimental setting is to obtain several functional MRI tasks and a long diffusion MRI scan with synchronized physiological recordings, including gas contents with a gas analyzer (GA), eye tracking (ET; including the right eye position, pupil size, blinks, etc.), respiration tracking through a pneumatic respiration belt (RB), and finally MRI-compatible electrocardiogram (ECG).

The overall experimental setting can be summarized as follows:

flowchart TB



BIOPAC --->|Ethernet| pc2["Physio-recording Laptop (█)"]

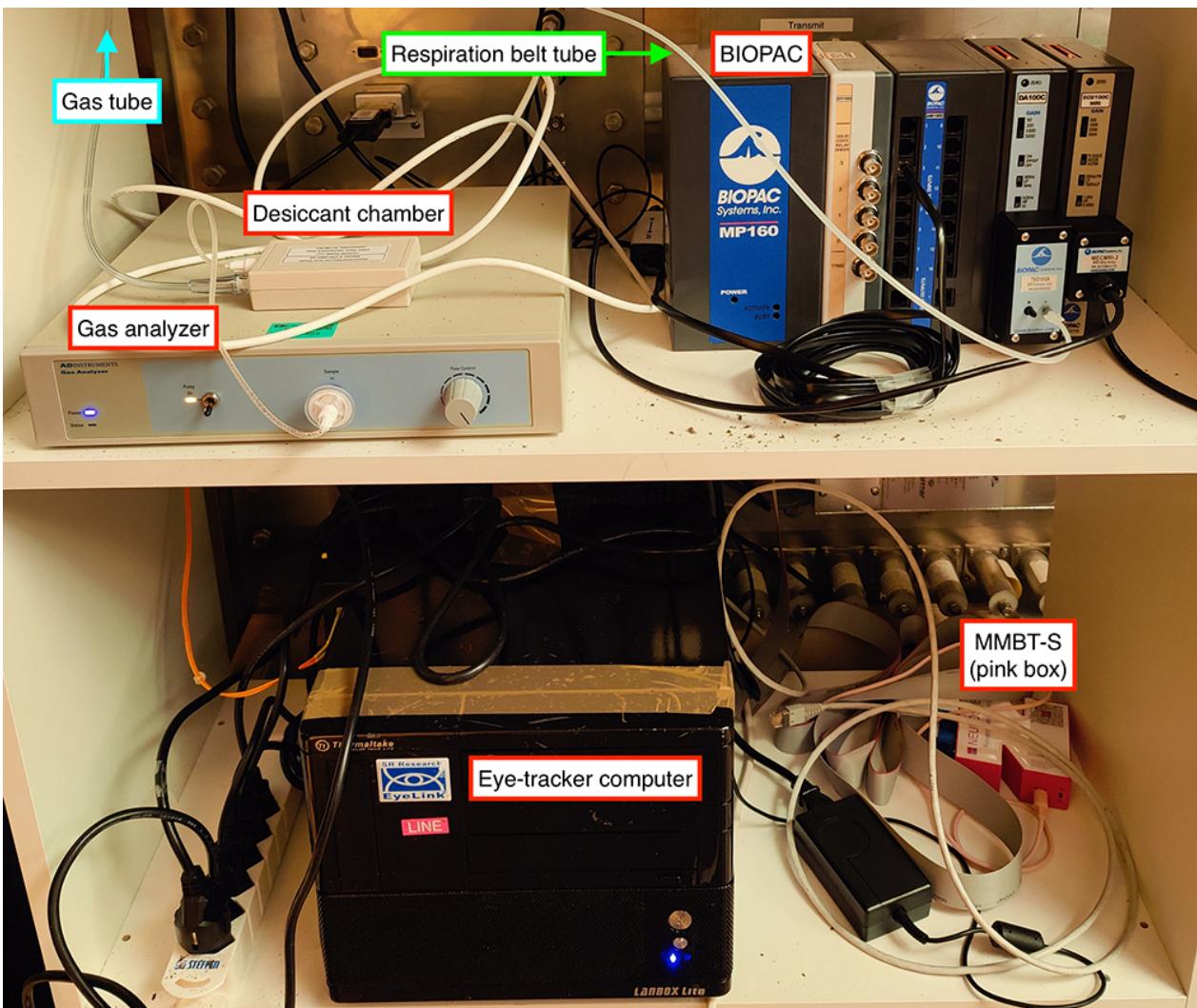
The above graph can be broken down as follows:

1. Signals generating from the Scanning Room. In addition to the MR imagery produced by the scanner, the participant will be wearing the RB, the ECG leads, a nasal cannula to retrieve the expired gases, and finally their right eye will be recorded with the infrared camera of the ET. All those probes and devices carry signals outside the Scanning Room either through cables or tubes, with the access panel as the interface. The access panel also has a connector carrying the trigger signals generated by MR schemes, which indicate important events in the MRI acquisition (typically, one trigger pulse is generated for each new *repetition time* —TR—, e.g., with every fMRI volume).
2. Syncbox. A *NordicLabs Syncbox* receives TTL (transistor-transistor logic) triggers from the scanner. This box can just forward the triggers converted into other formats and/or manipulate them (e.g., filter, generate, etc.).

3. Gas analyzer (GA). The GA is a device that continuously measures the amount of two gases (CO_2 and O_2) from a sample fed at the front of the device with a connected tube (this tube comes from inside of the Scanning Room and ends in the nasal cannula the participant is wearing, as shown in the graph).
4. BIOPAC. The BIOPAC is the main recording hub. It directly receives analogical signals from the Scanning Room (for the case of the RB and the ECG). Indirectly, it receives the analogical signal from the GA, and digital signals from the *Psychopy laptop* (■).
5. Eye tracker (ET). The ET is composed of two main elements: (i) inside the scanner's bore, we place an arm that holds an infrared lens and camera sensor on one side and an infrared lamp that illuminates the right eye of the subject through a special mirror to reflect the infrared spectrum; and (ii) a PC tower that receives the camera recordings, postprocess the images and calculates the final parameters of interest (position of the eye, pupil size, etc.). The ET is also connected to the *Psychopy laptop* (■), and communicates bi-directionally with it (e.g., to record logs or receive "messages" such as triggers or task events). The ET is NOT connected to the BIOPAC, with the implication that the ET data is not stored with the other physiological information.
6. Stimuli presentation laptop. The *Psychopy laptop* (■) has the *Psychopy* software installed and with it, the task programs are executed. This experiment consists of three tasks: breath-holding task (*BHT*), resting-state fMRI (*rest*), and a quality-control task (*QCT*). This laptop also stores the data recorded by the ET at the end of the experiment.
7. Physiology recording laptop. The *AcqKnowledge laptop* (■) runs the BIOPAC's *AcqKnowledge* software and with it, this computer records the signals and allows visualization of the data coming from the BIOPAC. All the inputs to the BIOPAC are multiplexed through into an Ethernet cable that is connected to this laptop.

Getting familiar with the instruments

Below is the overall setup of the instruments:

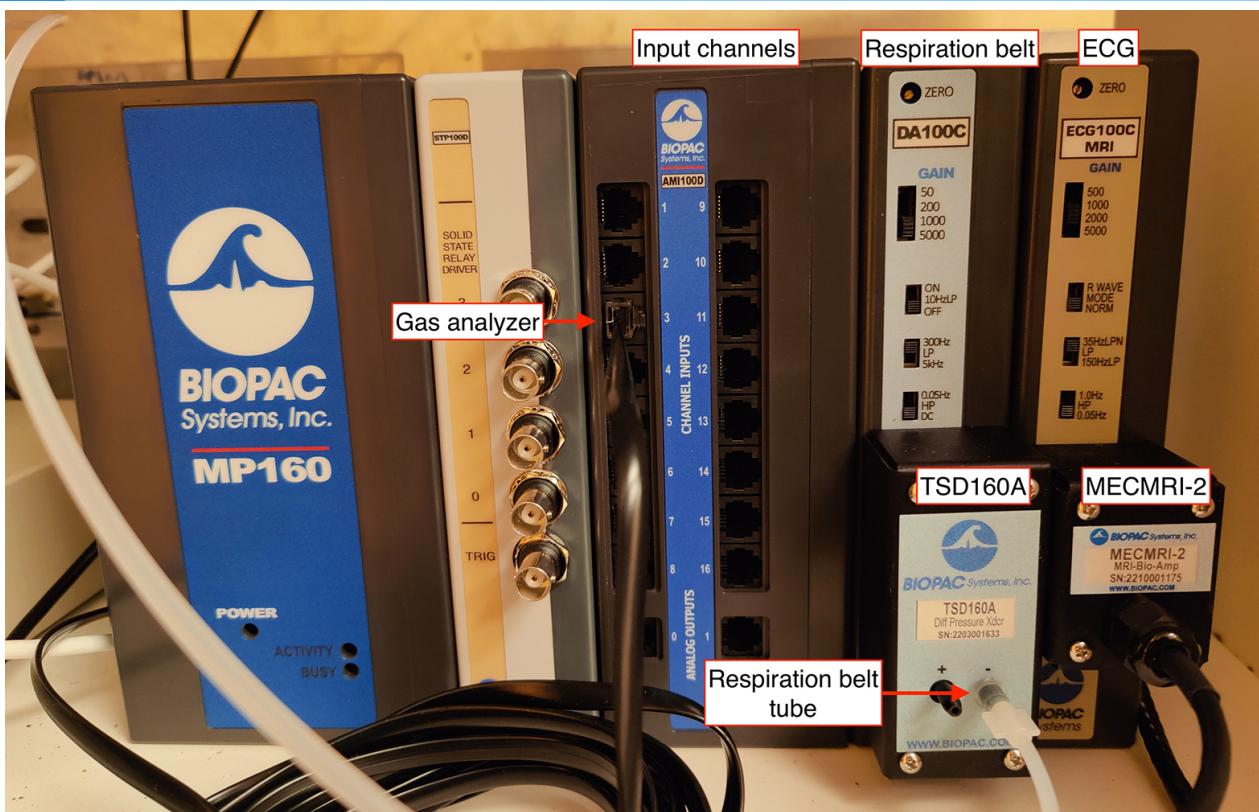


Emergency procedures

It is critical you fully understand and study the [emergency procedures to run an MRI scan at CHUV](#).

BIOPAC documentation and devices

Get familiar with the BIOPAC setup and read through the [hardware documentation \(\[https://www.biopac.com/wp-content/uploads/MP_Hardware_Guide.pdf\]\(https://www.biopac.com/wp-content/uploads/MP_Hardware_Guide.pdf\)\)](https://www.biopac.com/wp-content/uploads/MP_Hardware_Guide.pdf). The system is composed by the main unit (MP160; extreme left in the picture below), to which modules are attached depending on what signals are to be recorded.



Additional modules in our settings are (from left to right in the above picture):

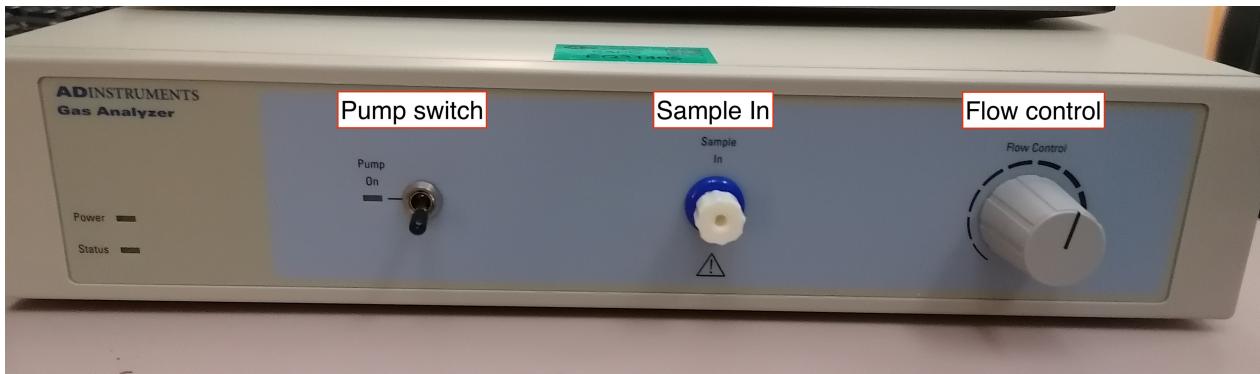
- The [SPT100D \(solid state relay driver unit\)](#) is used to input digital signals that must be recorded.
- The [AMI100C](#) unit can receive up to 16 analog signals.
- The [DA100C](#) unit records the signal coming from the respiration belt. This unit requires the pressure transducer [TSD160A](#) unit to be connected.
- The [ECG100C MRI](#) unit records the electrical signal coming from the heart via the [ECG](#). This unit requires the [MECMRI-2](#) unit on the [ECG100C](#) unit.

In addition to the main unit, we have a data modem to feed digital signals into the SPT100D. This modem is the [MMBT-S Trigger Interface Box adapter \(N-shaped, pink box\)](#):



AD Instruments ML206 Gas analyzer: documentation and basics

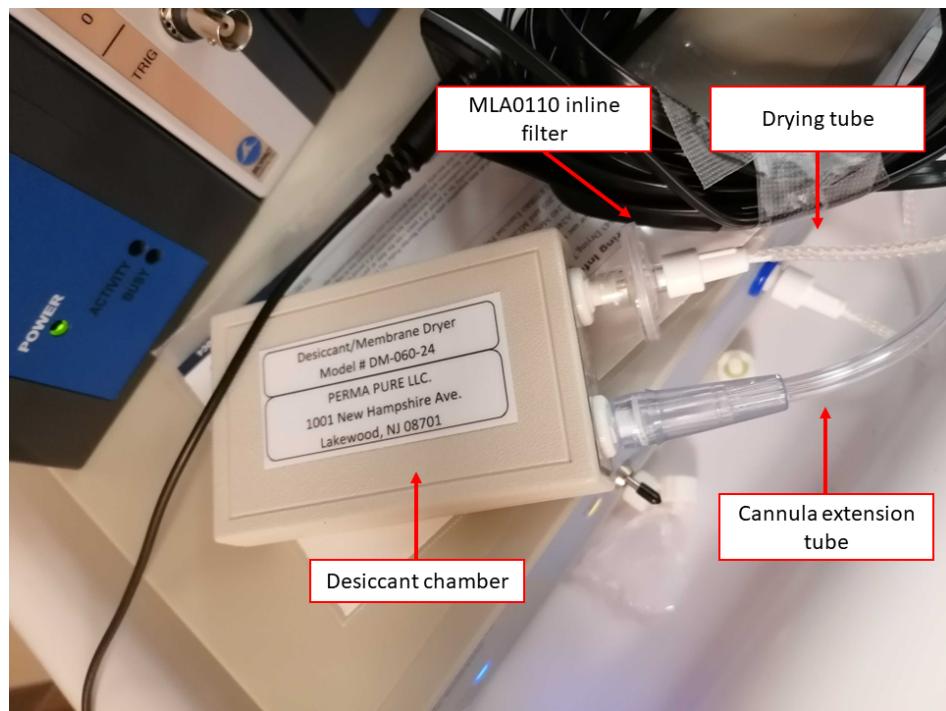
The front of the gas analyzer (GA) looks like this:



It is critical to familiarize with the [GA's manual](#) to learn about its correct utilization.

Make sure you understand the switching on and off procedures described in these SOPs

The input to the GA must be connected through a DM-060-24 desiccant chamber and a MLA0110 flow valve and a MLA0343 drying tube:



The MLA0343 drying tube and the DM-060-24 desiccant chamber MUST be replaced when their inside color turns into pink.

Finally, make sure to watch the following video:

<https://mkpdfs.comwes.euhttps://embed-ssl.wistia.com/deliveries/5e08ccab25ab45382329671a82dfe5123f6e840e/file.mp4> Your browser does not support the video. [Click here to download it](#)

EyeLink 1000 Plus eye tracker: documentation and basics

Get familiar with the setup and read through the [Eye Tracker Instruction Manual](#).

Thanks to Benedetta Franceschiello!

All the documentation about the ET is derived from Benedetta Franceschiello's user guide. We greatly appreciate her help with the device.

- The ET arm is an articulated support for the infrared camera and lens in one end and with an infrared lamp at the other end. The ET arm is installed inside the Scanning Room, inside the scanner's bore, standing on a transparent plexiglass panel tailored to the scanner's bed rail. Two lengthy cables (black for power and orange for signal) are passed through the access panel and connect the ET arm to the ET computer.
- The ET computer is a standard PC with customized software for the control of the ET.
- The infrared mirror is critical to be able to record the right eye of the participant, and is mounted covering the standard mirror of the coil.

Scanning protocols

The study will collect data with two different scanning protocols. Most of what is described in the present SOPs addresses the *Reliability Imaging Protocol* that will be acquired on the █ scanner.

Reliability Imaging Protocol (36 sessions \l(times\l) one scanner)	mm:ss	Standard Imaging Protocol (12 sessions \l(times\l) three scanners)	mm:ss
Head scout	00:14	Head scout	00:14
FoV Manual positioning	01:00	FoV Manual positioning	01:00
T1w (anatomical reference)	5:41	T1w (anatomical reference)	5:41
DWI (\(B_\text{0}\) field mapping)	00:54	EPI BOLD (\(B_\text{0}\) field mapping)	00:30
DWI (dMRI, structural connectivity)	33:52	BOLD (single-echo RSfMRI, eyes open)	20:09
GRE (\(B_\text{0}\) field mapping)	02:38	GRE (\(B_\text{0}\) field mapping)	03:08
BOLD (positive-control task fMRI)	03:07	BOLD (multi-echo RSfMRI, eyes open, only █)	10:09
EPI BOLD (\(B_\text{0}\) field mapping)	00:27	DWI (dMRI, structural connectivity)	27:31
BOLD (multi-echo RSfMRI, naturalistic movie)	20:09	DWI (\(B_\text{0}\) field mapping)	01:10
BOLD (breath-holding task fMRI)	06:00	T2w (anatomical reference)	08:24
T2w (anatomical reference)	05:10		
Total Acquisition Time	79:12	Total Acquisition Time	77:56

Stimulation program timings

The stimuli presentation laptop (█) will execute four experiments, which will allow the synchronization of all devices by sending the adequate signals at their predesignated times and also present visual stimuli with the scanner's projector. The lengths of the four *Psychopy* experiments should be:

- task-fixation_dwi → 33min 11s,
- task-qct_bold → 2min 38s,
- task-rest_bold → 20min 6s, and
- task-bht_bold → 5min 41s.

Preliminary work

Once, at the beginning of the project

Setting up the scanner protocol at the MR console

The pilot phase will conclude when the protocol is decided upon. Once finalized the protocol design, it will be *frozen* and it cannot be changed anymore.

- (Optional) Load an existing protocol
- Edit the protocol as needed

Follow Reproin conventions

When assigning names to the MR sequences in the protocol, make sure to follow the [Reproin conventions](https://dbic-handbook.readthedocs.io/en/latest/mri/reproin.html) (<https://dbic-handbook.readthedocs.io/en/latest/mri/reproin.html>) to maximally facilitate the conversion into BIDS.

- Update the *Number of measurements* in all `func-bold_task-*` sequences, according to the [previously recorded timings](#):

$$\text{\textbackslash}N_text{measurements} = L_t / text{TR}, quad t in \{text{bht}, text{qct}, text{rest}\},$$

where L_t is the length of a particular task t (either BHT, QCT, or resting state) in seconds as timed before, and $\text{text{TR}}$ is the repetition time of the BOLD sequence, in seconds.

- Save the protocol

Logging in as an advanced user is required before saving the protocol

As a good practice, always work as the standard user `janedoe`. However, you MUST change into *advanced user mode* before saving the protocol.

Simultaneously press the Tab + Delete + on the control-computer's keyboard:

Username: `superjanedoe`

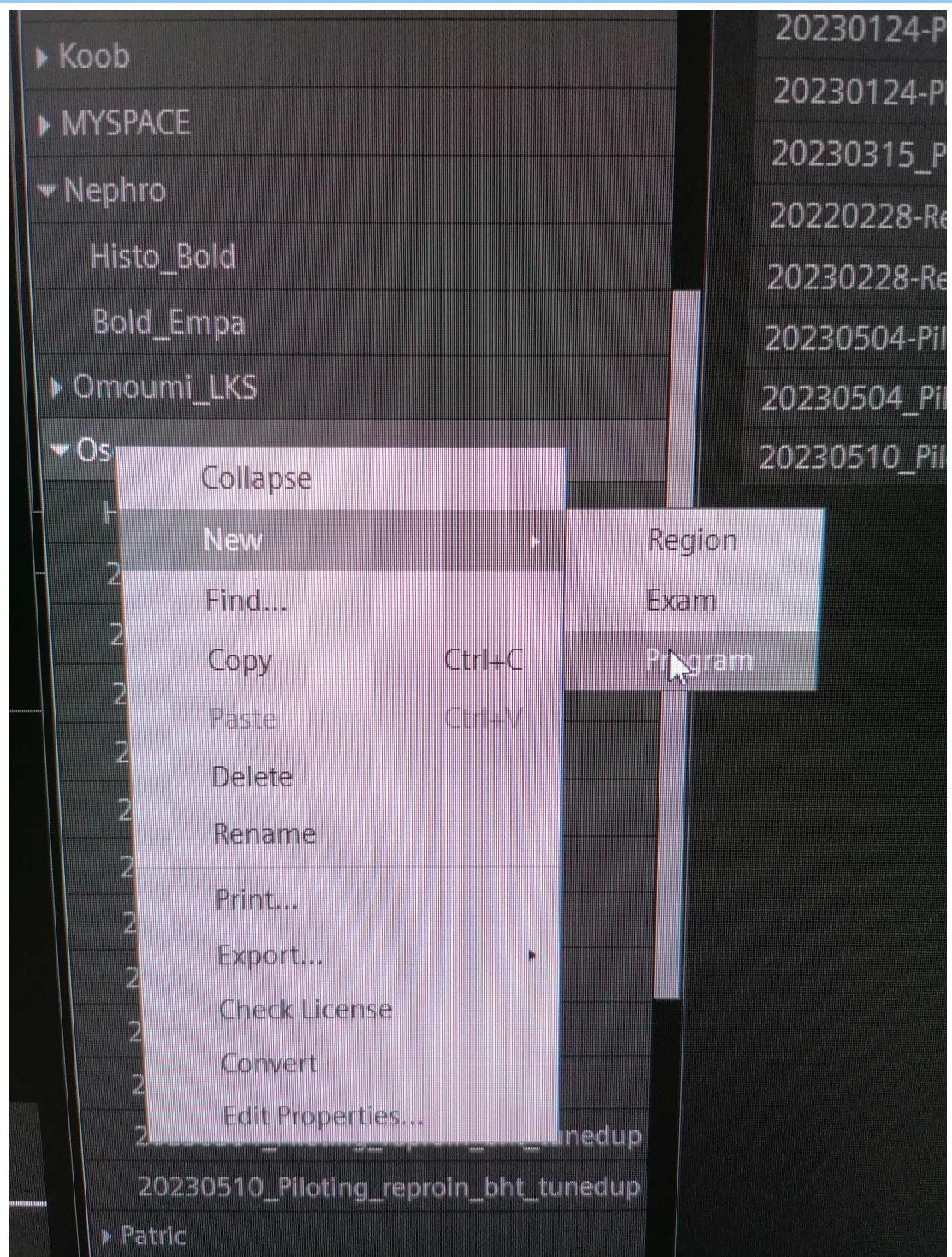
Password: *****

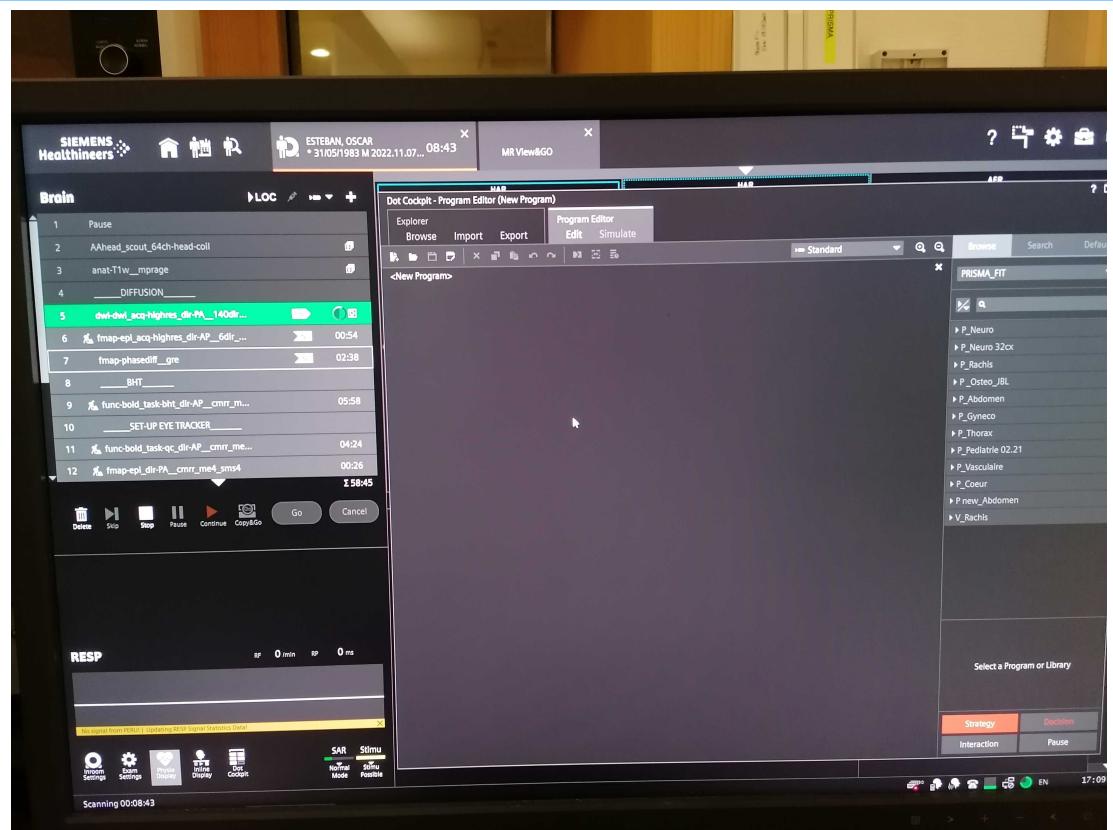
After three wrong password entries, access will be denied, and only a Siemens engineer will be able to unlock the MR scanner.

- Open the Dot-Cockpit window

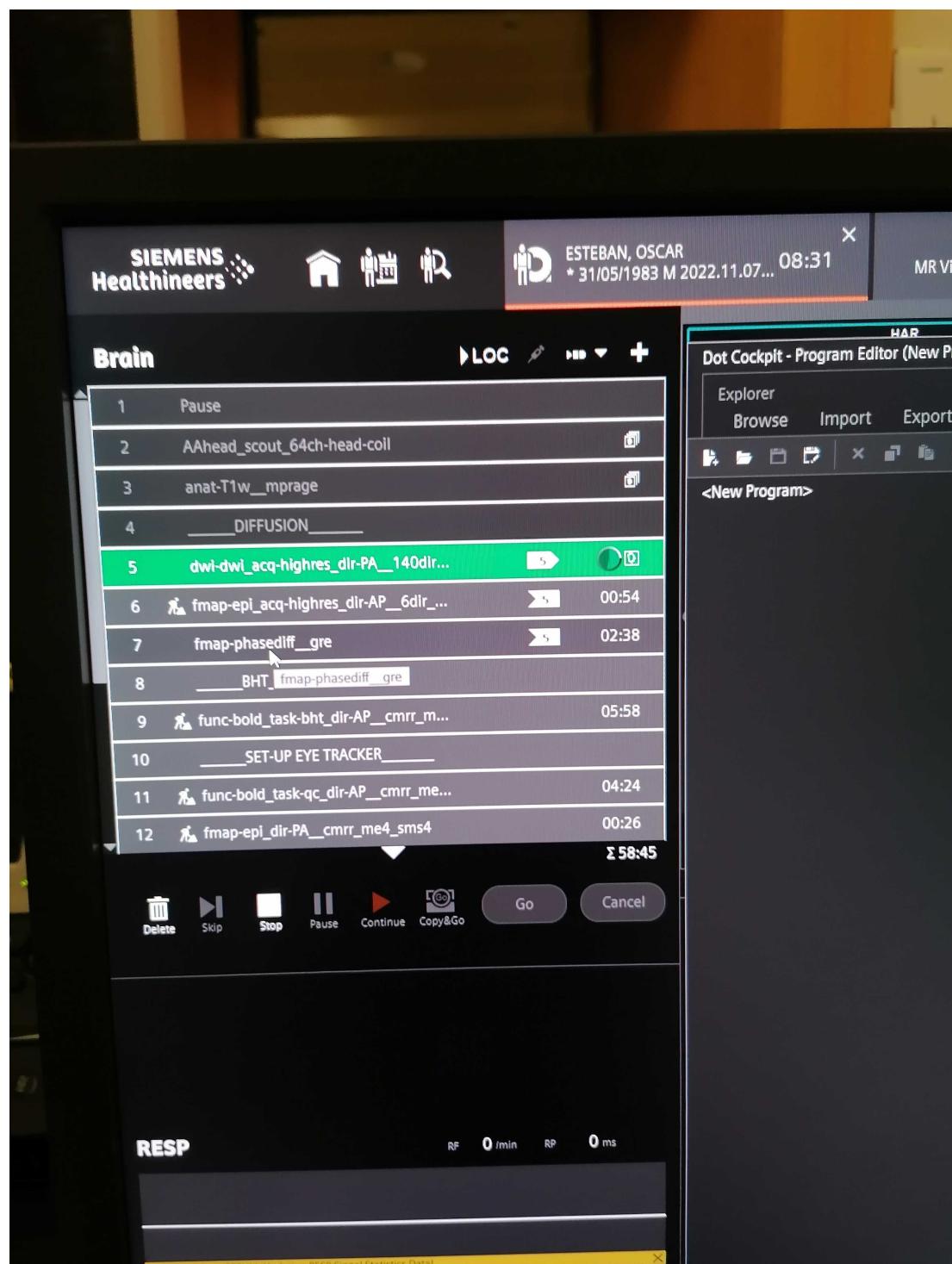


- In Browse, find the right folder to save the protocol in (RESEARCH ↴ Oscar).
- Right click on the folder and select New ↴ Program. This opens an empty page in the program editor

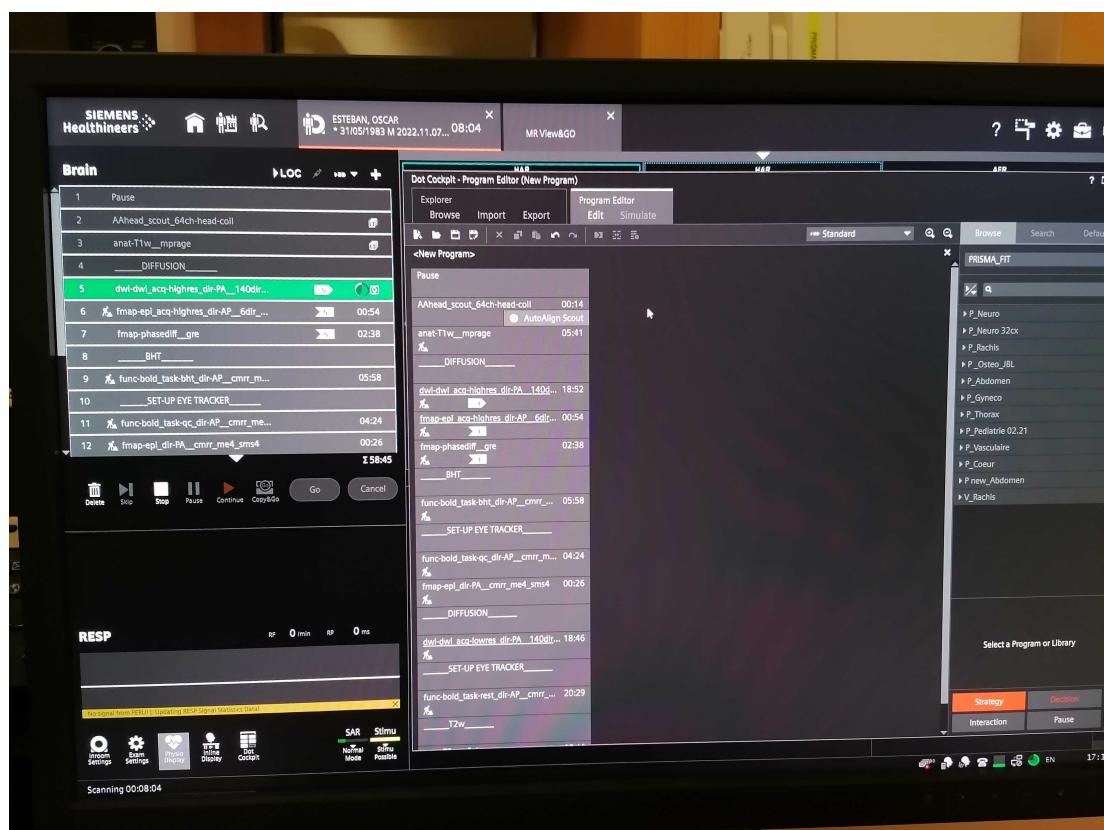




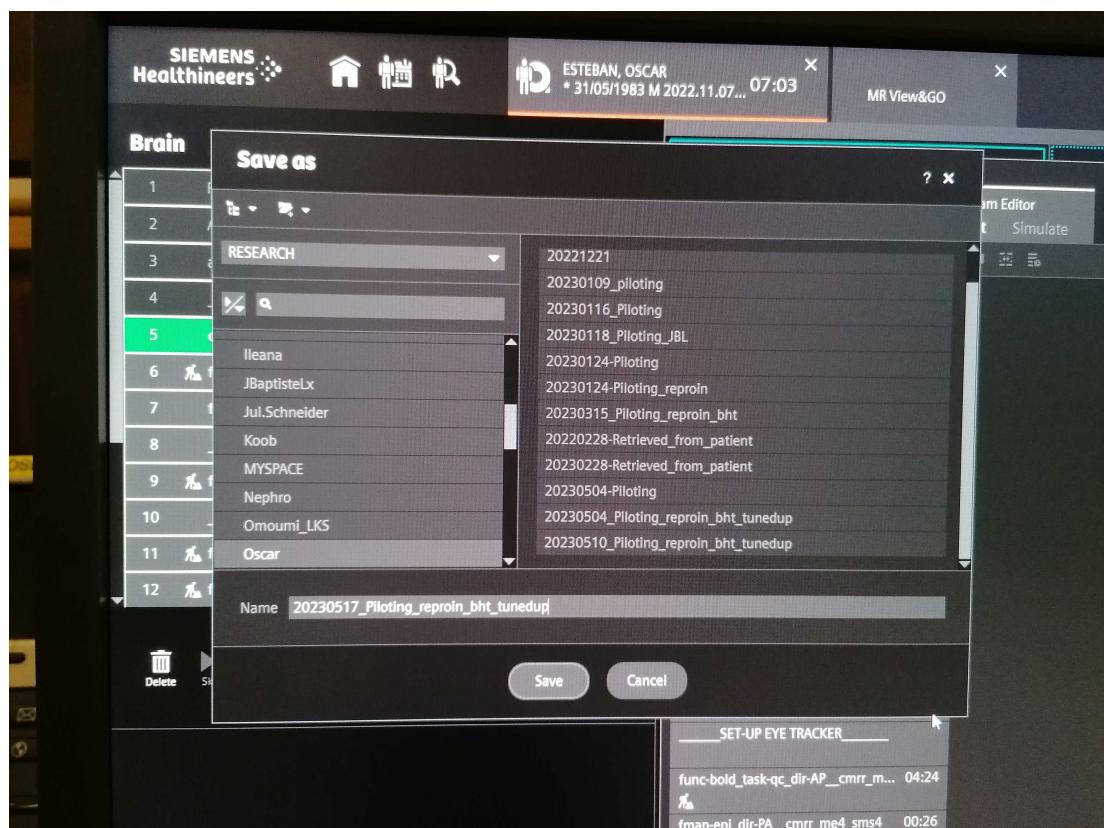
- Select all the sequences you want to run from the sequence list and click right to copy.



- Drag or paste the copied sequences in the program editor.



- Once finished, click on the floppy disk icon () in the upper left to save.
 Give the protocol a relevant name starting with the date of acquisition in the format YYYYMMDD and click Save.



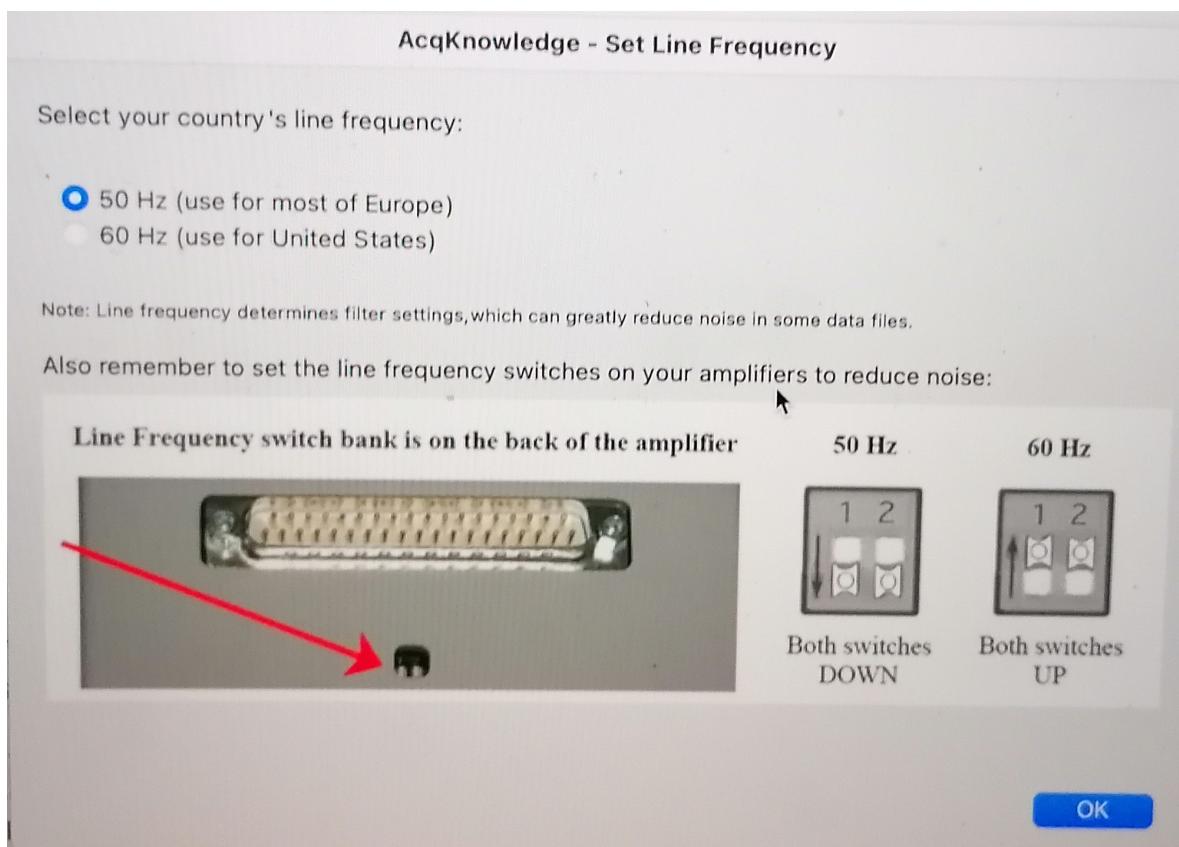
- If desired, the protocol details can also be downloaded as a pdf on a peripheral USB key.
 - Right-click on the protocol and select *Print*
 - Save the PDF in your USB key.
- Make sure you save a different protocol for each of the four PE directions (i.e., AP, PA, LR, RL).

Final protocol printouts

The final printouts are here: [HCPH_AP](#), [HCPH_PA](#), [HCPH_LR](#), and [HCPH_RL](#).

Install the BIOPAC

- Make sure you understand the components and settings of the BIOPAC, described in the [introduction section](#).
- Set up the line frequency switches on the back of the BIOPAC amplifier depending on your country frequency to reduce noise. Both switches should be DOWN if your country's line frequency is 50Hz. Both switches should be UP if your country's line frequency line is 60Hz.



- Plug the different units of the BIOPAC together if it has not been done yet.
- Ensure that the *Mode* switch of the [MMBT-S Trigger Interface Box adapter](#) (pink color box) is set on the P position.
- Install the BIOPAC recording software (*AcqKnowledge*).
- Create a template *graph file* ([EXP_BASE.gtl](#))

Creating the AcqKnowledge's template graph file

- Creating a graph file requires the BIOPAC system powered up and connected to the [REDACTED] computer.
- Add the RB module
 - Check the channel on top switch of the unit: the DA100C MUST be set on channel 1.
 - Under the tab *Analog*, click on *Add new module*.
 - Find the name of the BIOPAC unit corresponding to the DA100C.
 - Set the module settings (gain, filters, etc.) corresponding to those of the configuration switches in the front of the module.
 - When prompted to enter the calibration points, map the interval [-5, 0] to [0, 10]. You invert the sign of the interval for the interpretation to be more clear.
- Add the ECG module
 - Check the channel on top switch of the unit: the ECG100C MRI MUST be set on channel 2.
 - Under the tab *Analog*, click on *Add new module*.
 - Find the name of the BIOPAC unit corresponding to the ECG100C.
 - Set the module settings (gain, filters, etc.) corresponding to those of the configuration switches in the front of the module.
 - When prompted to enter [calibration?], for the ECG you should map the interval ?? to ??.
- Add the GA module
 - Confirm that the CO₂ output of the GA is connected through the ANISO filter to the channel 3 of the AMI100C module.
 - Under the tab *Analog*, click on *Add new module*.
 - Select *Custom* and then indicate it is connected to channel 3 by selecting *AMI/HLT - in3*.
 - When prompted to enter the calibration points, map the interval [0.03, 1.0] to [0, 10.0].
- Add the Digital inputs
 - Under the tab *Digital*, click on *Add new module*.
 - The parallel cable feeds into ports D8-D15.
 - Configure the sampling frequency
 - Configure the experiment length (at least 2.5 hours)
 - Configure whether you want to collect directly to hard disk and autosave settings
 - Save the experiment, making sure you choose a "graph template file" (with extension .gtl)

Install the gas analyzer (GA)

Preparing the *Stimuli presentation laptop* ([REDACTED])

The stimuli presentation laptop and any other box you want to use for debugging and development will require a few additional software packages to be available.

Installing *EyeLink* (eye tracker software)

The EyeLink software MUST be installed BEFORE Psychopy

- Log on [REDACTED] with the username [REDACTED] and password *****.
- Enable Canonical's universe repository with the following command:

```
sudo add-apt-repository universe  
sudo apt update
```

- Install and update the ca-certificates package:

```
sudo apt update  
sudo apt install ca-certificates
```

- Add the SR Research Software Repository signing key:

```
curl -sS https://apt.sr-research.com/SRResearch_key | gpg --dear
```

- Add the SR Research Software Repository as an *Aptitude* source:

```
sudo add-apt-repository 'deb [arch=amd64] https://apt.sr-researc
```

- Install the EyeLink Developers Kit:

```
sudo apt install eyelink-display-software
```

- Install the EyeLink Data Viewer:

```
sudo apt install eyelink-dataviewer
```

Installing our synchronization server

During the session, we run a synchronization server that acts as a hub for the signals (triggers, task events, etc.) that define the experiment. For the best experience, we *daemonize* the synchronization service (meaning, we make it a service of the operative system that runs in the background). To install it as a service, please follow [the documentation in the appendix](#)

- Locate the latest version of the synchronization service on your system. It is within the SOPs repository, at <path>/code/synchronization/forward-trigger-service.py.
- Install the necessary libraries **as root**:

```
sudo python3 -m pip install -r <path>/code/synchronization/requ
```

- Test the service is properly installed:

```
sudo python3 code/synchronization/forward-trigger-service.py --
```

Use the `--disable-mmbt-check` flag only if you do not plan to connect the MMBT-S trigger box

- Test operation with our test client:

Check the server's log file at `/var/log/forward-trigger-service.log`

Open a separate terminal on a separate window Then, open and follow the log file:

```
less +F /var/log/forward-trigger-service.log
```

Return to the original terminal, keeping the other window visible and execute:

```
python code/synchronization/forward-trigger-client.py
```

The log file should now have added two lines like:

```
2023-10-12 14:44:31.788 - INFO - Data received: <b'\x02'>
2023-10-12 14:44:31.788 - INFO - Forwarded <b'\x02'>
```

Testing the service without the MMBT-S connected

Testing the service without the MMBT-S trigger box connected requires emulating `/dev/ttyACM0`:

- Ensure socat and screen are installed (if not already):

```
sudo apt-get update
sudo apt-get install socat screen
```

- Create a virtual serial port and establish a symbolic link to `/dev/ttyACM0` using the following command:

```
sudo socat PTY,link=/tmp/virtual_serial_port PTY,link=/dev/ttyACM0,group=late:
```

- With screen, listen to the new virtual serial port:

```
screen /dev/ttyACM0
```

!!! tip "Alternatively, you can check the server's log file at `/var/log/forward-trigger-service.log`"

- Press s and verify that ^A appears in the screen terminal.

Prepare the *Psychopy* experiments

The appendix has some guides on [how to install *Psychopy*](#).

- Log on [REDACTED] with the username [REDACTED] and password *****.

Make sure to load the correct environment

- Deactivate conda (if active):

```
conda deactivate
```

- Load the new virtual environment:

```
source $HOME/psychopyenv/bin/activate
```

- Fork the *HCPh-fMRI-tasks* repository (<https://github.com/TheAxonLab/HCPh-fMRI-tasks/fork>) under your user on GitHub.
- Clone the *HCPh-fMRI-tasks* repository (<https://github.com/TheAxonLab/HCPh-fMRI-tasks>):

```
git clone git@github.com:<your-gh-username>/HCPh-fMRI-tasks.git
```

- Set-up the original repository as upstream remote:

```
git remote add upstream git@github.com:theaxonlab/HCPh-fMRI-tasks.git
```

- Open *Psychopy* and (optionally) a experiment file corresponding to a task by typing the following command in the terminal:

```
psychopy --no-splash -b task-qct_bold.psyexp
```

- For each task, check the following:

- task-qct_bold.psyexp* (quality-control task, QCT):
 - time it to [confirm the length](#), and
 - check the task runs properly.
- task-rest_bold.psyexp* (resting-state fMRI):
 - time it to confirm the length, and
 - check that the movie is played.
- task-bht_bold.psyexp* (breath-holding task, BHT):
 - time it to confirm the length, and
 - check the task runs properly.

- task-fixation_dwi.psyexp (fixation point during DWI):
 - time it to confirm the length, and
 - check the task runs properly.

Every two months

Calibrate the GA

A gas mixture bottle with a known CO₂ and O₂ concentrations is necessary

CO₂ concentration must be between 5% and 10%, while O₂ within 5% and 21%. A second reference mixture is necessary, and room air can be used, knowing that atmospheric contents by volume are 0.039 ±0.001% for CO₂ and 20.946 ±0.003% for O₂.

- Connect the GA to the BIOPAC as described in [this section](#).
- Connect the BIOPAC to the *Physiology recording laptop* (█) as described in [this section](#).
- Connect the AcqKnowledge License Key into a USB Port of the *Physiology recording laptop* (█).
- Open AcqKnowledge software on the *Physiology recording laptop* (█).
- Open the template *graph file* ([EXP_BASE.gtl](#))
- Edit the configuration of the inputs 3 (connected to the CO₂ output of the GA) and 4 (connected to the O₂ output of the GA). Lower and upper calibration points can be set by sampling the input a number of times with the *AcqKnowledge* utility.
- Overwrite the template *graph file* EXP_BASE.gtl.

Before each session

Instructions of operations to be performed before the participant arrival, before EACH session (i.e., DAY OF SCAN)

Three days before 1st session

- Verify that as part of the [recruitment and screening procedure](#), you have sent a copy of the [MRI Safety and screening form \(EN|FR\)](#) to the participant over email and confirm reception by checking the 'First contact email sent' column in [our recruits spreadsheet \(/redacted.html\)](#).
- Verify also that you confirmed that the participant has read and understood the document, and in particular, you double-checked that they do not have any [MRI contraindications](#), by checking the 'Phone interview done' and 'Participant volunteer and eligible' column in [our recruits spreadsheet \(/redacted.html\)](#).
- If the phone call interview was more than three days before the first session, call the participant again to reconfirm the following information:
 - Remind the participant that any jewelry should be removed prior to the scan.
 - Indicate that they MUST shave the upper area of their chest where the [ECG electrodes](#) will be placed, if there is hair. The [ECG electrodes](#) MUST directly contact the skin.
 - Confirm clothing:
 - if allowed to wear street clothes, remind the participant to avoid clothing with metal or that would be uncomfortable to lie in for the duration of the scan; otherwise
 - remark the participant they will be given a gown and they will need to change before every session.
 - Repeat at what time and where will you meet the participant.
 - Verify that the participant has your phone number #####-#####-##### to call you in case he gets lost.
 - FEMALE PARTICIPANTS ONLY: Remind the participant that pregnant women cannot undergo our [MRI protocols](#). Therefore, they will take a pregnancy test (which we will have prepared) before the first session.
- If participant has indicated nervousness or history of claustrophobia, organize a session to use the mock scanner.

Three days before EVERY session

We MUST verify that █ correctly runs all *Psychopy* experiments.

- Connect a secondary screen to the [HDMI](#) input of the computer

- Switch it on and log in into the common user (password: *****).
- Open a terminal

Shortcut + t

- Update the [HCPH-fMRI-tasks](https://github.com/TheAxonLab/HCPH-fMRI-tasks) repository (<https://github.com/TheAxonLab/HCPH-fMRI-tasks>) on []:

```
cd ~/workspace/HCPH-fMRI-tasks
git fetch upstream
git checkout master
git rebase upstream/master
```

The following two commands are executed with sudo

The console will request the common user password (*****).

- Spin up a mock MMBT-S device listening on /dev/ttyACM0:

```
sudo socat PTY,link=/tmp/virtual_serial_port PTY,link=/dev/tty/
```

- Manually spin up the trigger-forwarding service:

```
sudo python3 code/synchronization/forward-trigger-service.py --
```

Make sure to load the correct environment

- Deactivate conda (if active):

```
conda deactivate
```

- Load the new virtual environment:

```
source $HOME/psychopyenv/bin/activate
```

- Run the compiled tasks with *Python* directly.
- Load in the different experiments and check for proper functioning and timing:
 - dMRI (only fixation):

```
python task-fixation_dwi.py
```

- QCT:

```
python task-qct_bold.py
```

- RSfMRI

```
python task-rest_bold.py
```

- BHT:

```
python task-bht_bold.py
```

All of the above command lines SHOULD open a modal dialog asking you for the number of trial (automatically calculated, DO NOT modify) and the session number.

The following steps MUST be executed in this order

- [] Drag and drop the modal dialog into the scanner's projector screen.
- [] Update the session number with the corresponding number.

- Check the correct session number is set (use the default 9999 for testing) and hit *OK*.

The OK button MUST be clicked with this modal dialog on the secondary screen

Otherwise, the wrong screen will be selected by *Psychopy*

Updating *Ubuntu* or *Psychopy* is not recommended in the proximity of data collection

However, you should make sure you are on *Ubuntu* 22.04 LTS, *Python* 3.10, and *Psychopy* 2023.2.3.

One day before the session

- Print the informed consent form (first session only)
- Print the MRI safety screener (EN|FR).
- Print a receipt form for each participant that will get scanned.

Day of scan, BEFORE the participant arrives

Boot the scanner up if it is shut down

Please wait for all systems to finalize their boot-up (about 10 minutes), even if only the satellite station is to be used.



- Turn the key of the System ON/OFF Station Box into the *open lock* position ()
- Push the blue button with the sun symbol and the SYSTEM ON label above, which is found right above the key

Documentation and secondary instruments

- Prepare [the informed consent form](#) (first session only)
- Prepare an [MRI safety screener \(EN|FR\)](#)
- Prepare a pen and a receipt form that the participant will sign when they are given the compensation
- Check you have the AcqKnowledge software [USB license key](#)
- Prepare a pregnancy test (Only female participants on their first session)
- Prepare a thermometer
- Prepare a blood pressure meter
- Prepare scrubs and [MR-compatible glasses](#) if applicable
- Prepare a pack of sterile cotton gauze, a bottle of medical alcohol, the *Nuprep* skin preparation gel (white/blue tubes), and three new electrodes.

nuprep-tube

Start a new session log form

Collect comments and annotations about the session using GitHub issues. A laptop should be available to fill the issue.

- Click this link (https://github.com/TheAxonLab/hcph-sops/issues/new?assignees=acionca&labels=scan&projects=&template=scan-session.yml&title=%5BSCAN%5D+sub-001_ses-yyy), or alternatively
- manually open a GitHub Issue at the [SOPs repository](#) (<https://github.com/TheAxonLab/hcph-sops>):

 - Under the section **Issues**, click on New issue
 - This should lead you to a page that looks like this



- Click on Get started on the issue template Scan session.
- Modify the title of the issue by replacing yyyy with the session index. If you don't remember the session index of today, check the [session index table](#).
- Verify that your phone is on ringing mode so the participants can reach you.
- Check the time regularly to be on time to meet with the participant at the predefined location

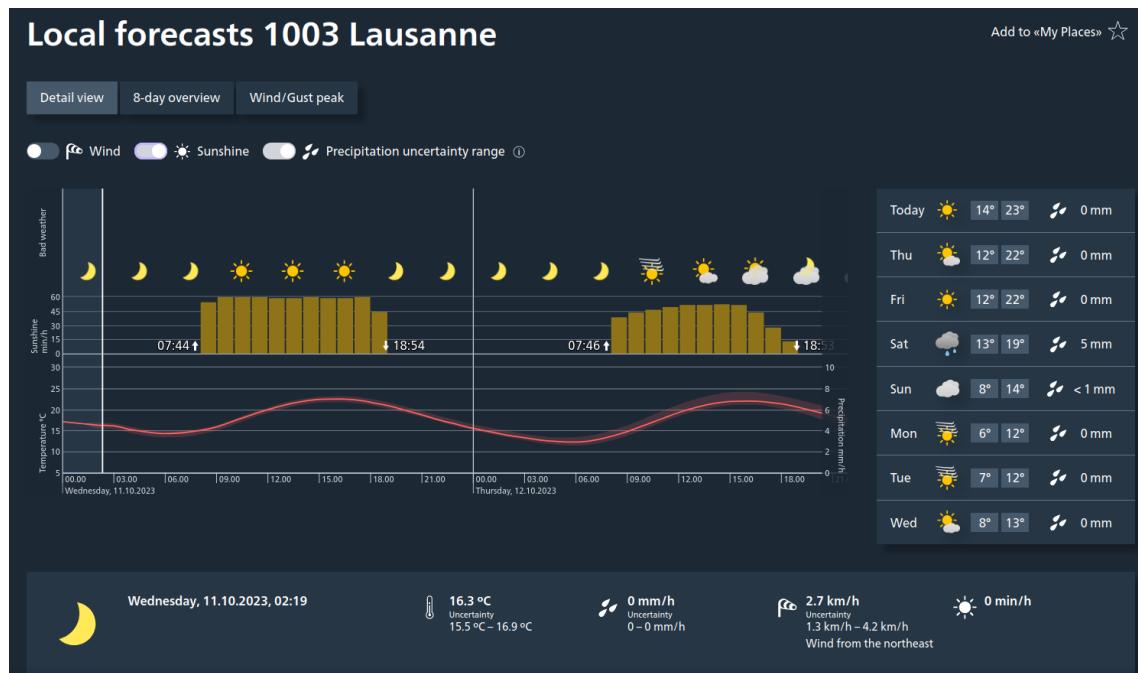
Start a new session log for the collection of covariates

- Click this link (https://github.com/<gh_user>/<name>/issues/new?assignees=acionca&labels=mood&projects=&template=mood-questionnaire.yml&title=%5BMOOD%5D+sub-001_ses-yyy), or alternatively
- manually open a GitHub Issue at the [questionnaire repository](#) (https://github.com/<gh_user>/<name>):

 - Under the section **Issues**, click on New issue
 - Fill the date of the scan as well as the **PE** for this session (accessible in the [schedule](#))
 - Fill in weather details of the scanning day based [MeteoSwiss](https://www.meteoswiss.admin.ch/local-forecasts/lausanne/1003.html#forecast-tab=detail-view) (<https://www.meteoswiss.admin.ch/local-forecasts/lausanne/1003.html#forecast-tab=detail-view>) in 1003 Lausanne.
 - Report the maximum and minimum temperature in degrees celsius.
 - Report the wind speed at the time of scanning in km/h.
 - Report the precipitation type and amount (in mm).
 - Report the outside atmospheric pressure (in hPa) and relative humidity (in %).
 - Report the hours of daylight (rounded to the number of hours).

How to find the precipitation information on MeteoSwiss

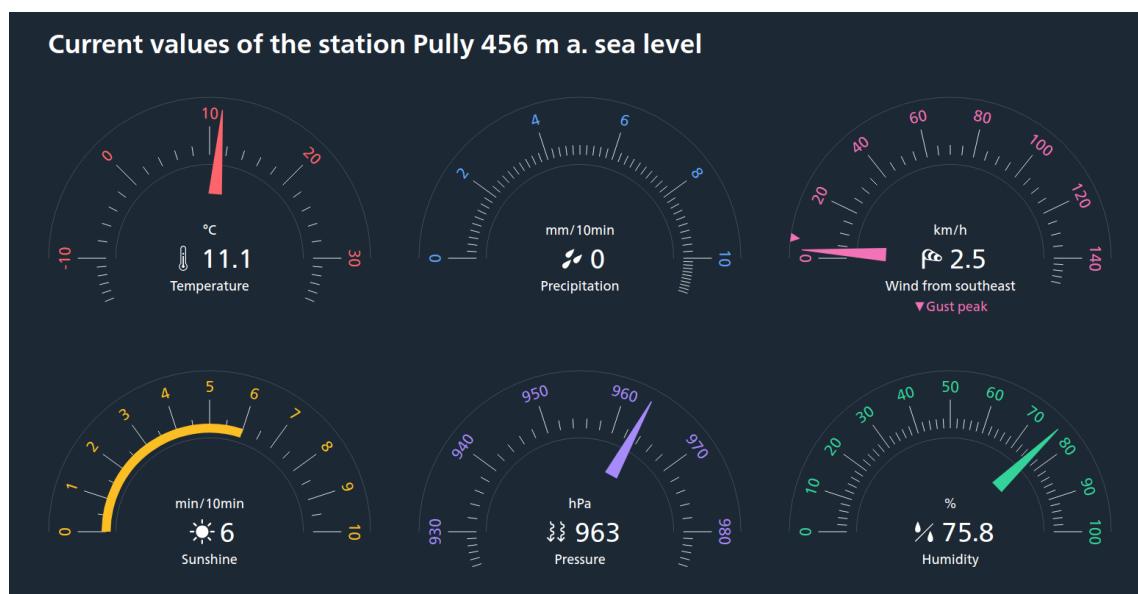
Here is what the MeteoSwiss interface looks like on a computer.



In the screenshot above, the information to be reported would be:

- Minimum outside temperature for the day of the scan (°C): 14°C
- Maximum outside temperature for the day of the scan (°C): 23°C
- Wind speed (km/h): 2.7 km/h
- Precipitation (mm): 0mm
- Hours of daylight (h): 11h (18:54-07:44=11:10h roundup)

Scrolling down, you will find additional measurement values that look like:



Here the relevant additional information is:

- Current outside atmospheric pressure (hPa): 963 hPa
- Current outside relative humidity (%): 75.8%

- Fill in the details related to the MR and scanner room.

- Report the MR room temperature (°C) and relative humidity (%)

Location of the MR room thermometer

The thermometer in the MR room can be found on the left of the operator window when inside the scanner room (see below).



- Report MR helium level (%)

- In the top bar of the MR console, click on System>Control.
- In the window that just opened, click on the section MR Scanner.
- Report Helium Fill Level in percentage.

Basic preparations in the scanning room

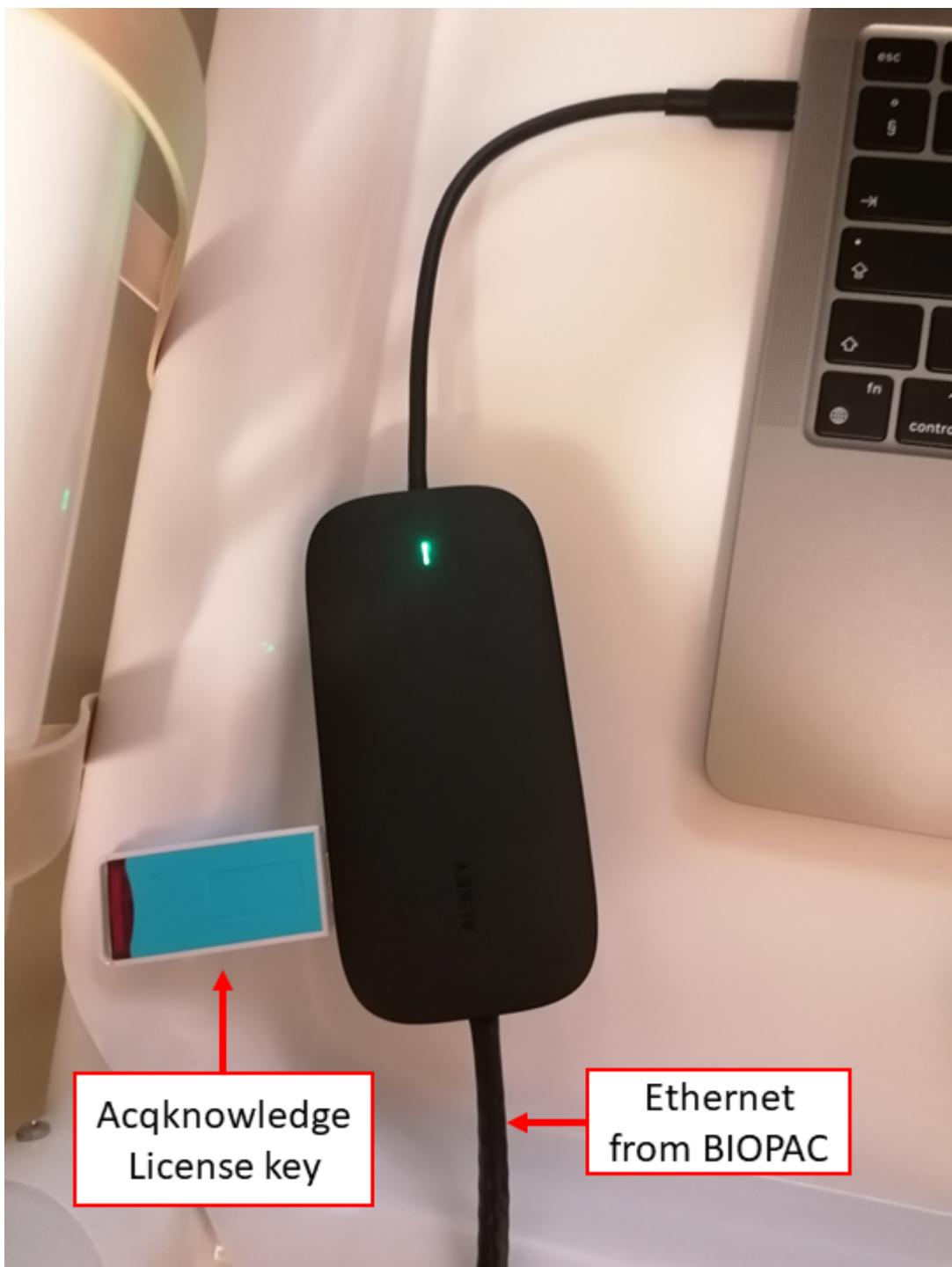
- If any head coil from the last exam is still plugged, remove it:
 - If it is the 64-channel coil, you can just temporarily move it into the scanner's bore.
 - Otherwise, store it on the shelf where the other coils are and bring the 64-channel one in the proximity of the bed (e.g., inside the scanner's bore). Make sure to remove other coil's fitting element.
- Remove the spine coil by lifting the corresponding latch, then sliding it toward the head of the bed, lift it from the bed, and place it on the floor ensuring it is not obstructing any passage or unstable.
- Place the two back padding elements filling the spine coil socket.
- Cover the MRI bed with a sheet.
- Place the 64-channel head-and-neck coil into its socket at the head end of the bed.
- Completely remove the light inside of the scanner and the ventilation of the scanning room using [the scanner's interface](#).

Remove the light and ventilation to facilitate the best performance of the ET

Setting up the BIOPAC system and physiological recording sensors

- Ensure you have the AcqKnowledge software [USB](#) license key. Plug the [USB](#) key to the multiport adapter for Mac and plug that adapter to the computer  as shown in the

picture below. It needs to stay plugged at all times during the acquisition.



- Open the *AcqKnowledge* software
- Initiate an *Amphetamin* session to avoid the computer to go to sleep/lock the screen:
 - Click on the pill icon on the Mac's status bar
 - Select *New session* ↳ *While is running* ↳ *Acqknowledge*.
- Plug the power cord of the BIOPAC and of the GA into suitable power sockets.

- Plug in the Ethernet (the plug is on the back side of the BIOPAC) to the multiport adapter connected to the computer [REDACTED].



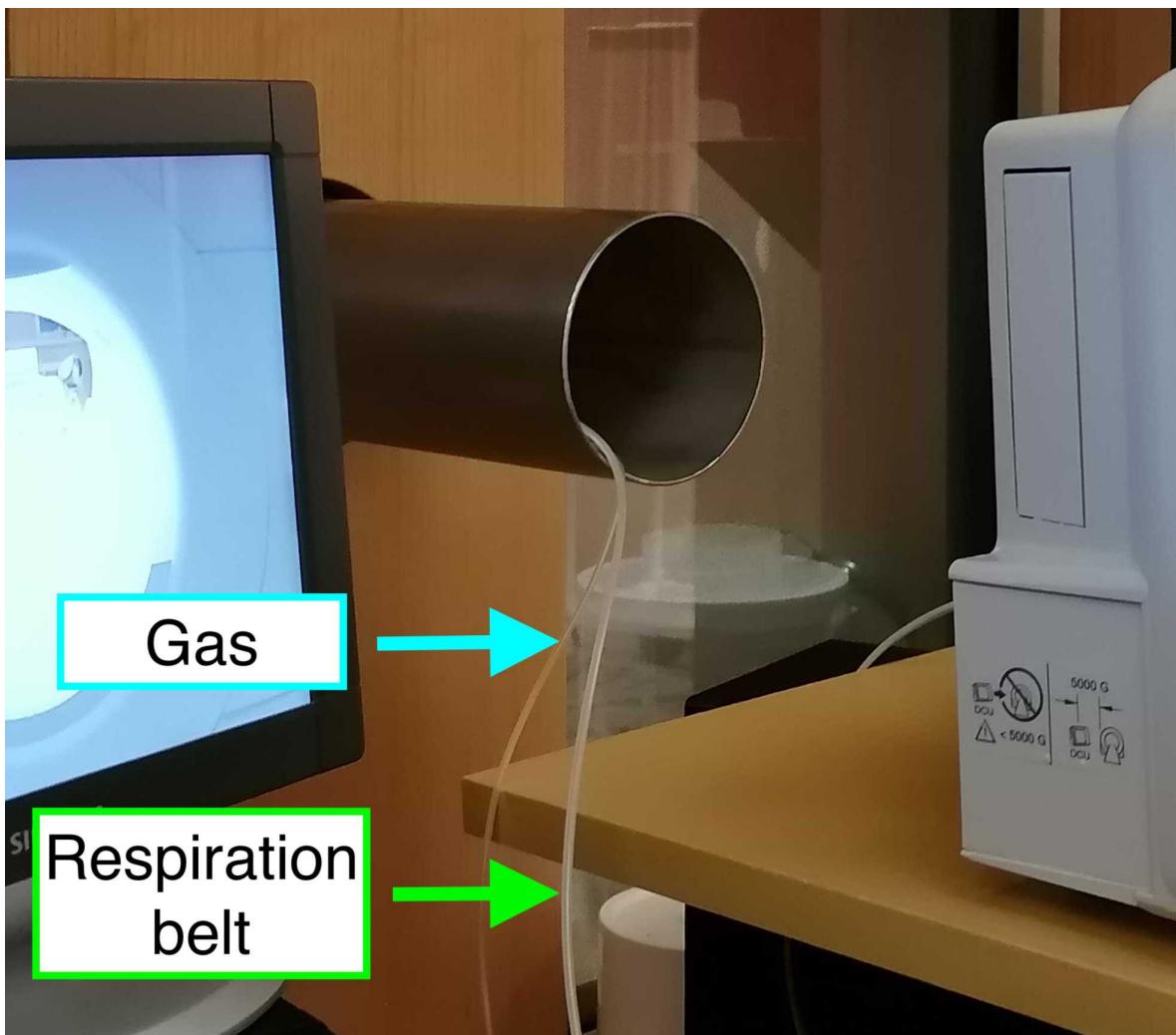
- Connect the parallel cable to the 25-pin socket at the back of the SPT100D of the BIOPAC and to the parallel port of the MMBT-S Trigger Interface Box adapter (N-shaped pink box).





- Plug the power cords of the BIOPAC and the GA into suitable power sockets.
- Go inside the scanning room, unscrew the wood cap that covers the hole in front of the MR.
- Check that the extension tube for the nasal cannula does not contain any bubbles.

- Delicately pass the extension tube that will be connected to the nasal cannula and the extension tube from the respiration-belt (RB) through the front access tube.



- Connect the distal end of the extension tube to the cannula and leave the cannula on the bed ready for the participant. To connect the extension tube to the cannula, you need to insert with force the end into the cannula.

Ensure that the length of the tubing inside the MR room is sufficient so that it can lie on the floor.

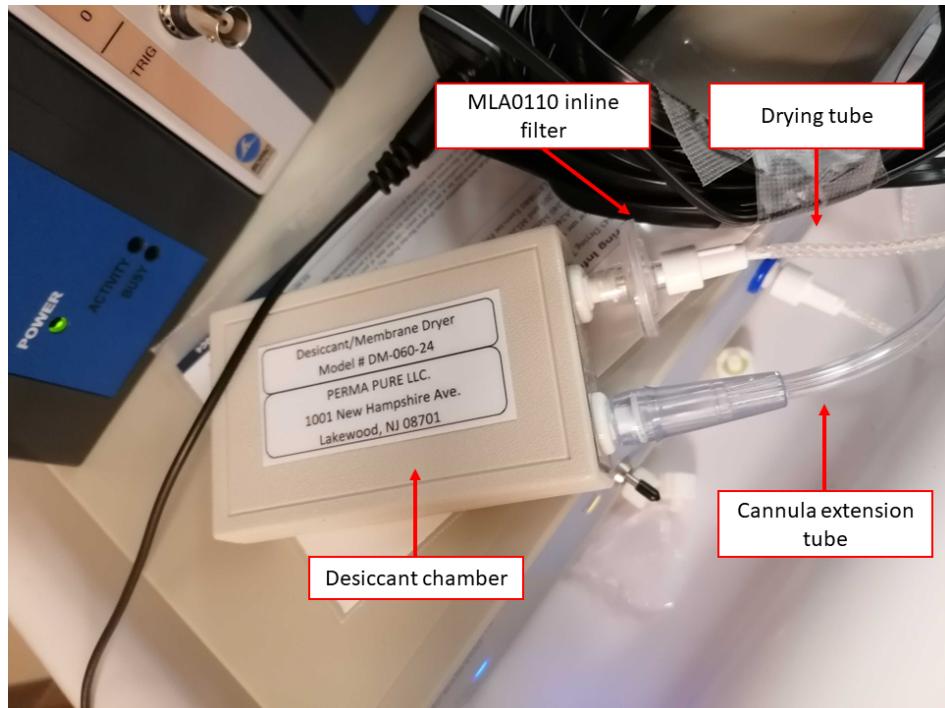
When the tubing is hanging, pressure waves may alter the recorded gas concentration.

- Connect the distal end of the RB tube to the RB and leave it on the bed.

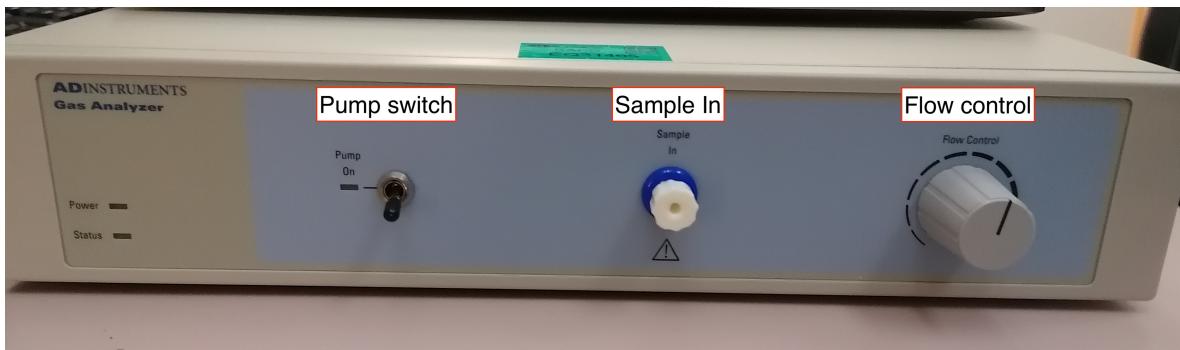


- Go back to the control room and connect the proximal end of the cannula extension tube to one plug of the desiccant chamber (which one is not important). Connect the MLA0110 inline filter to the other plug of the desiccant chamber. Connect the MLA0343 drying tube to the MLA0110 inline filter.

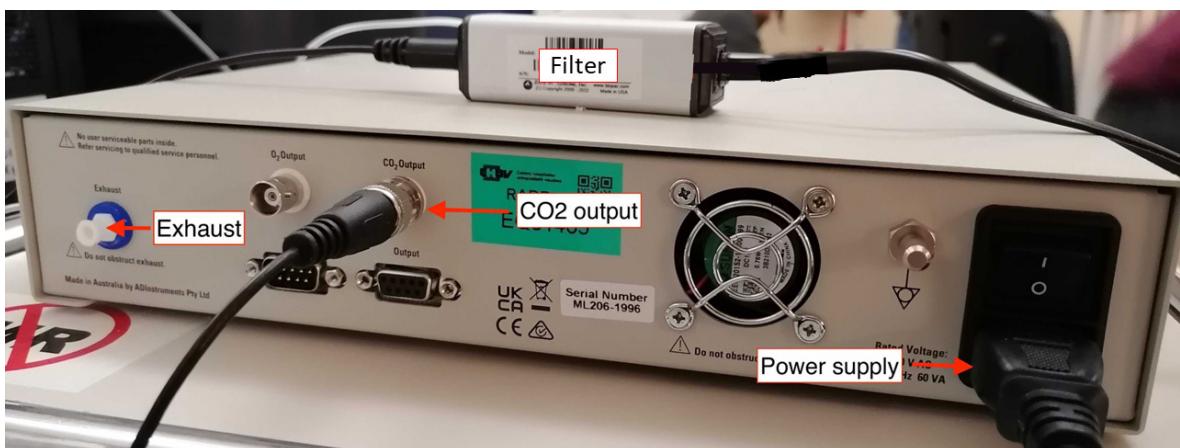
Make sure that the inside color of the drying tube and the desiccant chamber have not turned pink. They must be replaced if it is the case.



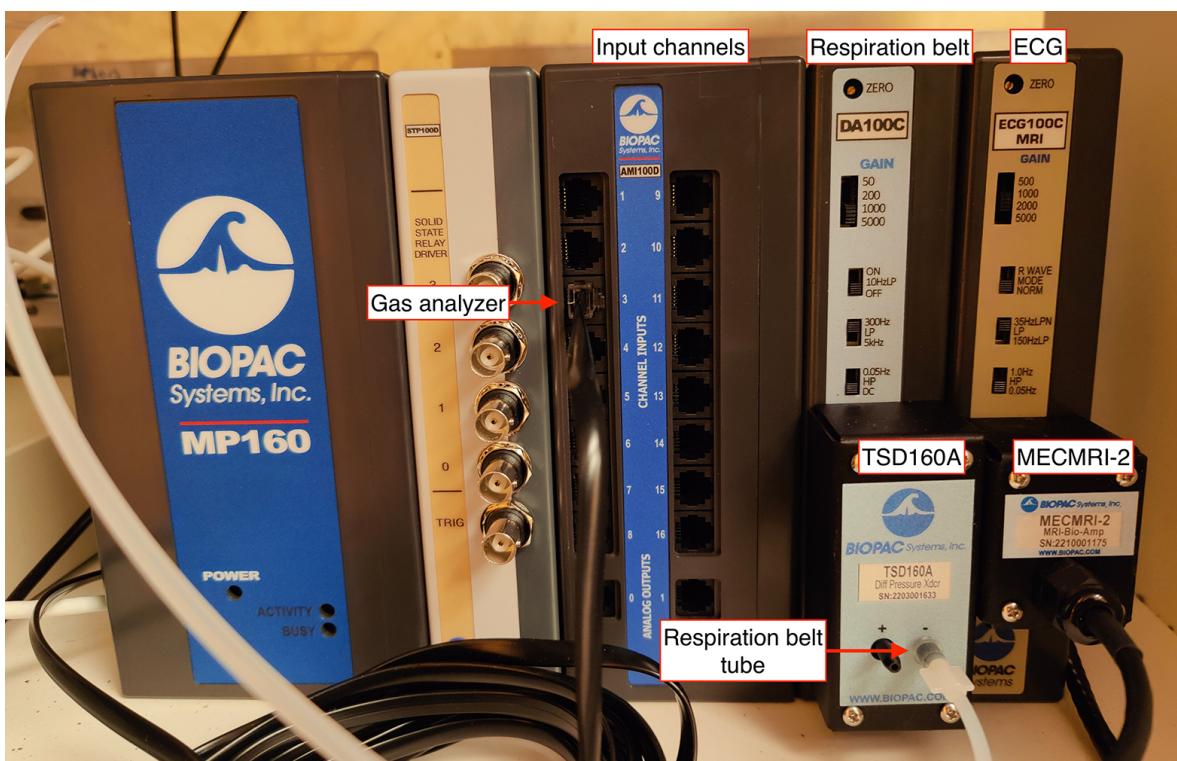
- Remove the cap of the gas input (Sample In, front panel of the GA) and connect the MLA0110 inline filter to it. The inline filter MUST be replaced after some ten sessions.



- Connect the coaxial end of the BNC-BNC cable to the CO₂ output in the back of the GA and connect the other end (jack plug) into the input end of the INISO/A filter.



- Connect one end (RJ-11 to RJ-11) to the output of the INISO/A filter, and the other into channel 3 of the AMI100D BIOPAC module.



- Check that the RB (DA100C) and ECG (ECG100C MRI) channels are set to channel 1 and channel 2.

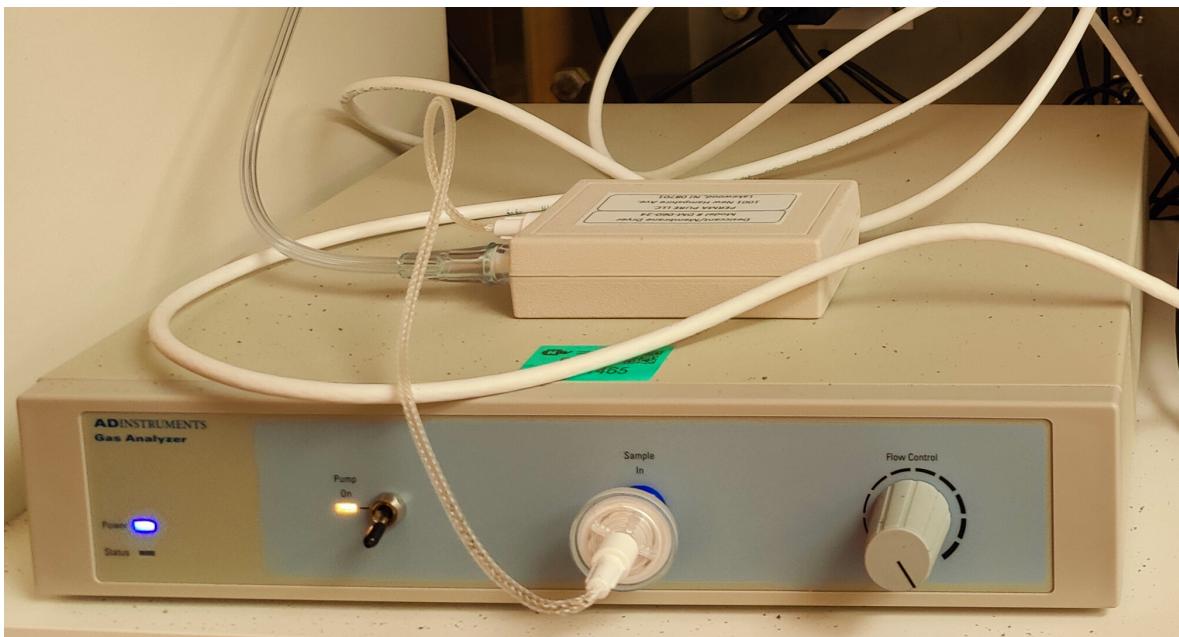


Important

- Check that the exhaust pipe (back of the GA) is free of obstruction. An obstructed exhaust can damage the device!



- Check that the cap on Sample In is removed and that the MLA0110 inline filter is connected to it. The pump switch MUST BE OFF when the cap is on and when switching on the GA. Turn the GA on using the on/off switch located at the front of the GA. The GA MUST be ON for 20-30 min to warm-up before measuring.



- Check that the flow control wheel (front of the GA) is set to the maximum.
- Connect the proximal end of the RB tube to the TSD160A BIOPAC unit, using the plug marked negative (- symbol).
- Connect the cable from the RJ-45 output of the syncbox to the first filter (BNC connector; has a label "External signal") in the cupboard covering the access panel to the Faraday cage. The cable might be stored in the lower left cupboard of office [REDACTED]. Make sure you will have access to the cable with sufficient time ahead. [INSERT PICTURE]
- Connect the syncbox to the Biopac via the white trigger cable. [TOCHECK]

Setting up the projector

- Go to room [REDACTED], where the projector is installed.

- Switch the projector ON by hitting the power button, located on its right side.
- Verify the aim of the projector's beam by looking through the tube into the Scanning Room.

The projector's position SHALL NOT be modified unless it is evidently off

Only in the case that the projector beam is not correctly targeting the projection screen inside the Scanning Room, which is possible if someone accidentally altered the configuration, you may adjust its position as follows:

- Adjust the projector tilt to center the projection if it does not properly aim the panel inside the scanner's bore. E.g., change the height of the paper pile that supports it (see images, FENS papers).



The tube is the part through which you should check the beam alignment.

- Verify the projection corresponds to the *Psychopy* laptop (██████) screen.
- Before you exit room █████, go to the next step.

Setting up the eye-tracker (ET) computer

- The eye-tracker (ET) computer is kept on its designated rolling table, which is stored under the projector in room █████. Behind the rolling table, there is a transparent panel (the *plexiglas* in the following) where the ET arm will stand inside the scanner bore.
- Verify that the screen, the cables, as well as the ET computer are fixated onto the rolling table with scotch tape.
- Bring the rolling table out of the projector room (██████) into the control room. Be very attentive during the displacement and lift the front wheels when passing steps or cables. The plexiglas panel can also be brought to the scanning room at this time, if done with care.
- Place the rolling table next to the access closet.
- Connect the Ethernet cable from the ET computer into the Ethernet plug of the *Psychopy* laptop (██████).
- Connect the power strip attached to the rolling table on to the closest power plug (likely, a power strip coming across the corridor).

Setting up the ET arm

- Go to room █ and bring the blue box labeled *Eye-Tracker only for fMRI* into the scanning room. This box contains the ET arm with the camera and infrared lamp mounted on it, lenses, and the special infrared mirror. The box should be found in the first cabinet on the left section of the cupboard.
- Take the MR-compatible lens out of the lenses box.



The appropriate lens is found in a correspondingly labeled bag (left) and it is the only one with two gold

(right).

- Install the MR-compatible lens, after removing any other present lens. If other lens is present, put it back into its plastic bag inside the lenses box after unscrewing and removal.

The lens MUST be handled with care

1. The lens MUST be installed in the Control Room, BEFORE taking the ET arm inside the Scanner Room.
2. One of your hands MUST be under the lens at all times while screwing/unscrewing it, to avoid accidentally dropping a lens.

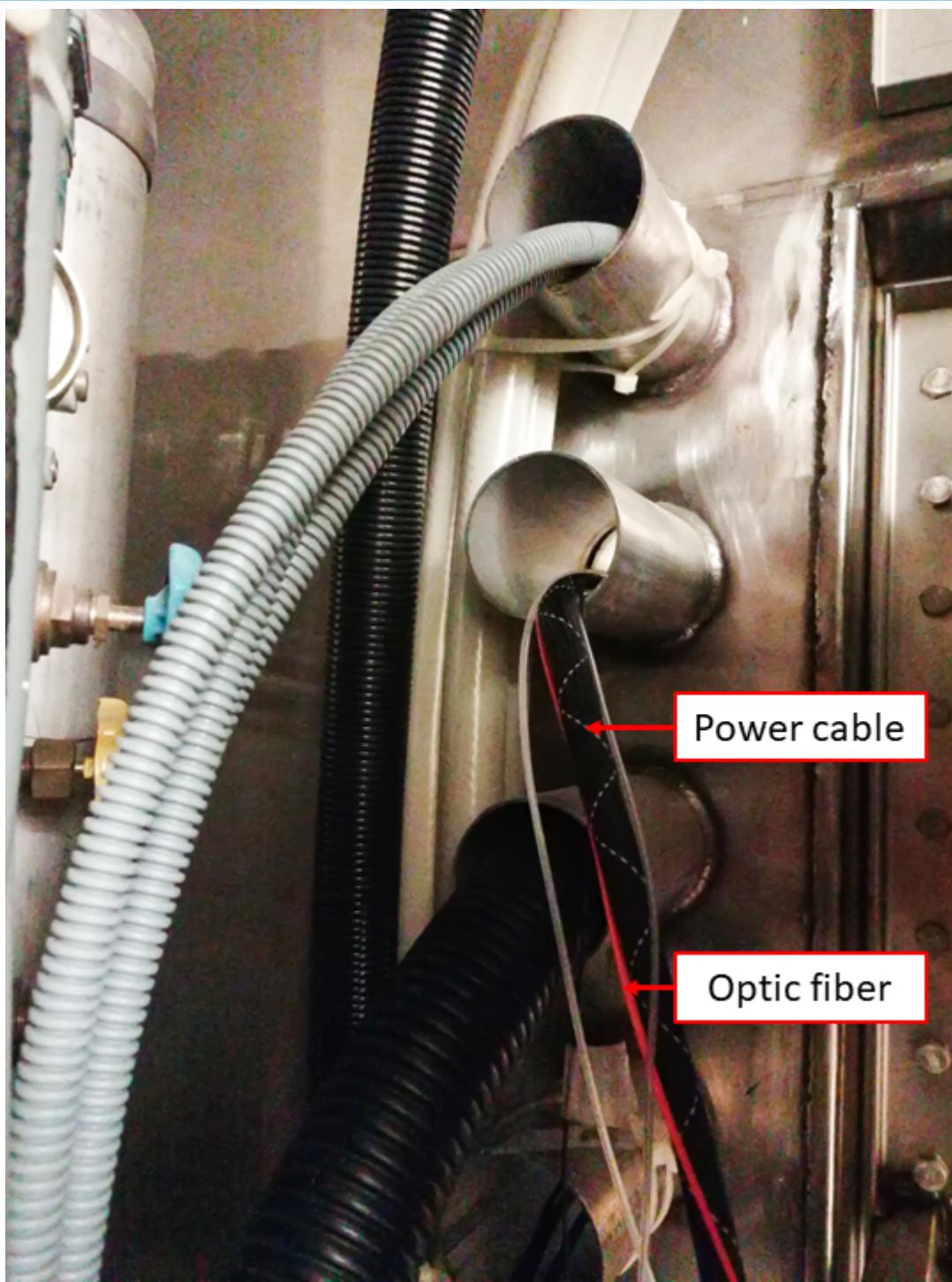


3. Screws holding the lens MUST be properly tightened at this point because the vibration of the scanner may loosen them and the screw(s) may drop during the session.

- Open the door of the access cupboard.
- With the help of someone else, pass the optic fiber (orange wire) and the power cable (the one with a fabric sheet) through the access point.

This operation requires two people

One person will feed the cables from the control room interface of the access cupboard. The other person will gently pull the two cables from inside. Both people will lift the cable to avoid its abrasion with the edges of the metallic cylinder, which is the passage between exterior and interior of the scanner room. Once the sliding of the cable is finished, leave the extremities inside the scanner room in the left-top corner, far from the scanner because they are magnetic.



Since someone will enter the Scanning Room to receive the cables, this is a perfect moment for the helper from inside to take the plexiglass panel with them when entering the Scanning Room.

INSIDE the scanner room

- Take the ET arm inside the Scanning Room (check that the plexiglass panel is already inside the Scanning Room, and bring it inside with you if not).
- Place the plexiglass standing panel inside the scanner bore: a sign notes the top side that faces up. The plastic feet must face down to avoid the panel to slide. To ensure the

repeatable positioning of the ET, place the end of the plexiglass such that its edge aligns with the edge of the illuminated MRI rails.

- Place the ET arm on top of the plexiglass panel with the two posterior feet of the ET arm aligned within the two corner signs made of scotch tape.

Hold the ET arm FIRMLY, because the magnetic field imposes some resistance.

- Connect the cables (two plugs for the black, one plug for the orange).



- Take the half-circle one-direction screen from the table behind the scanner and put it on the back of the scanner, behind the ET system (don't push the plexiglass yet)



Placing the infrared mirror

- Detach the standard mirror's frame from the head coil, if it is placed there. Remove unnecessary items from the scanning bed, and prepare the mirror to attach the infrared mirror of the ET at a later step.
- Prepare two long strips of scotch tape and leave them in a convenient place to attach the ET mirror later. E.g., attach the corner of each strip to the back part of the mirror frame.
- Go back to the control room and take the infrared mirror out of the «fMRI usage» box. **DO NOT EXTRACT THE MIRROR OUT FROM ITS BOX YET**. The mirror's box is labeled as *RELIQUIA DI SAN GENNARO* (https://it.wikipedia.org/wiki/San_Gennaro#La_reliquia) to emphasize that THIS IS THE MOST DELICATE PART, BECAUSE THE MIRROR CANNOT BE REPLACED NOR CLEANED. This mirror is EXTREMELY EXPENSIVE.



- Get two gloves (e.g., from the box hanging at the entrance of the scanner room), then approach the scanner bed. Put the gloves on, and DON'T TOUCH ANYTHING. You MUST have the standard mirror dismounted and in front of you at this point. WITH THE GLOVES proceed to extract the infra-red mirror from its box, being extremely careful. YOU CAN ONLY TOUCH THE MIRROR WITH GLOVES, because it cannot be cleaned up. Watch out for FINGERPRINTS and once taken out of its box, IMMEDIATELY PROCEED TO ATTACH IT to the standard coil mirror. The mirror MUST NOT be placed anywhere else if not in its box.
- WITH YOUR GLOVES ON, attach the ET mirror to the standard coil mirror (the larger mirror that points toward projector's screen at the back of the scanning room) using the scotch tape strips you prepared before. Put it more or less in the center, although **this position may need to be adjusted** (being careful and with the same precautions explained before). Do not touch the surface of the ET mirror.



The infrared mirror MUST be airtight attached

It is critical that there is no air gap between the infrared mirror and the standard mirror. Also, make sure the scotch tape is firmly glued to the standard mirror because the infrared mirror will be hanging when placed on the coil and may loosen up creating a gap with the standard mirror.

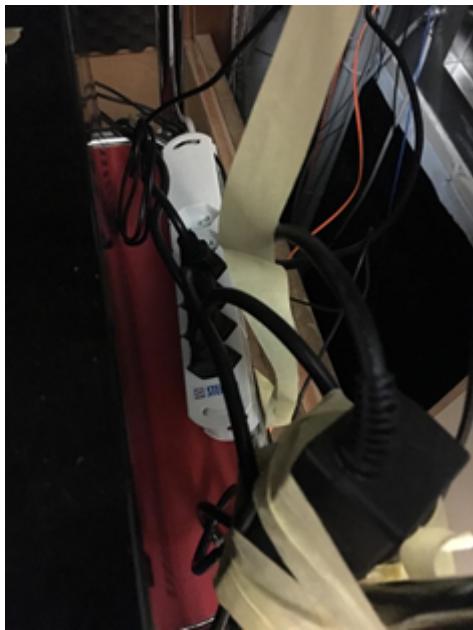
Suggestion

Since we are going to track the right eye only, it is useful to displace the infrared mirror to the right from the participant's standpoint and cut the scotch tape narrower to occlude less surface of the mirrors on the right side.

- Place the mirror frame back on the head coil. As always, DO NOT TOUCH THE MIRROR.

Back OUTSIDE THE SCANNER ROOM (control room)

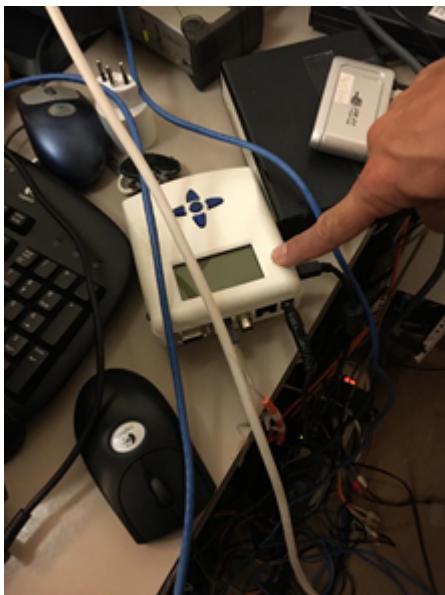
- Plug in the Power strip containing the ET Power Cable, the PC-tower power, etc



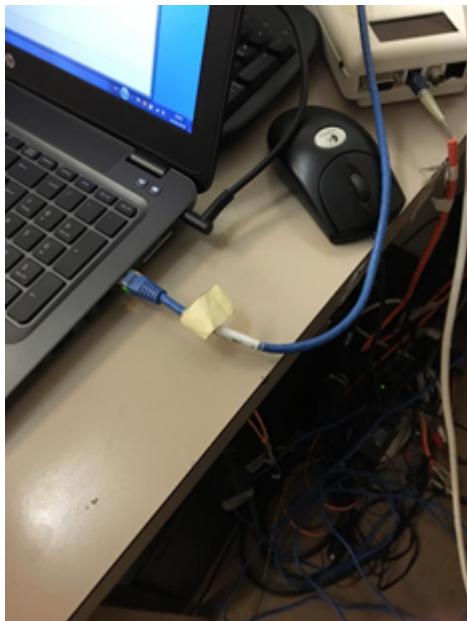
- Switch on the ET PC-tower. Select "Eyelink" when given the option of which operating system to launch.



- This is the sync box of the scanner, allowing a synchronization of the triggers between the scanner sequence and the ET recordings.



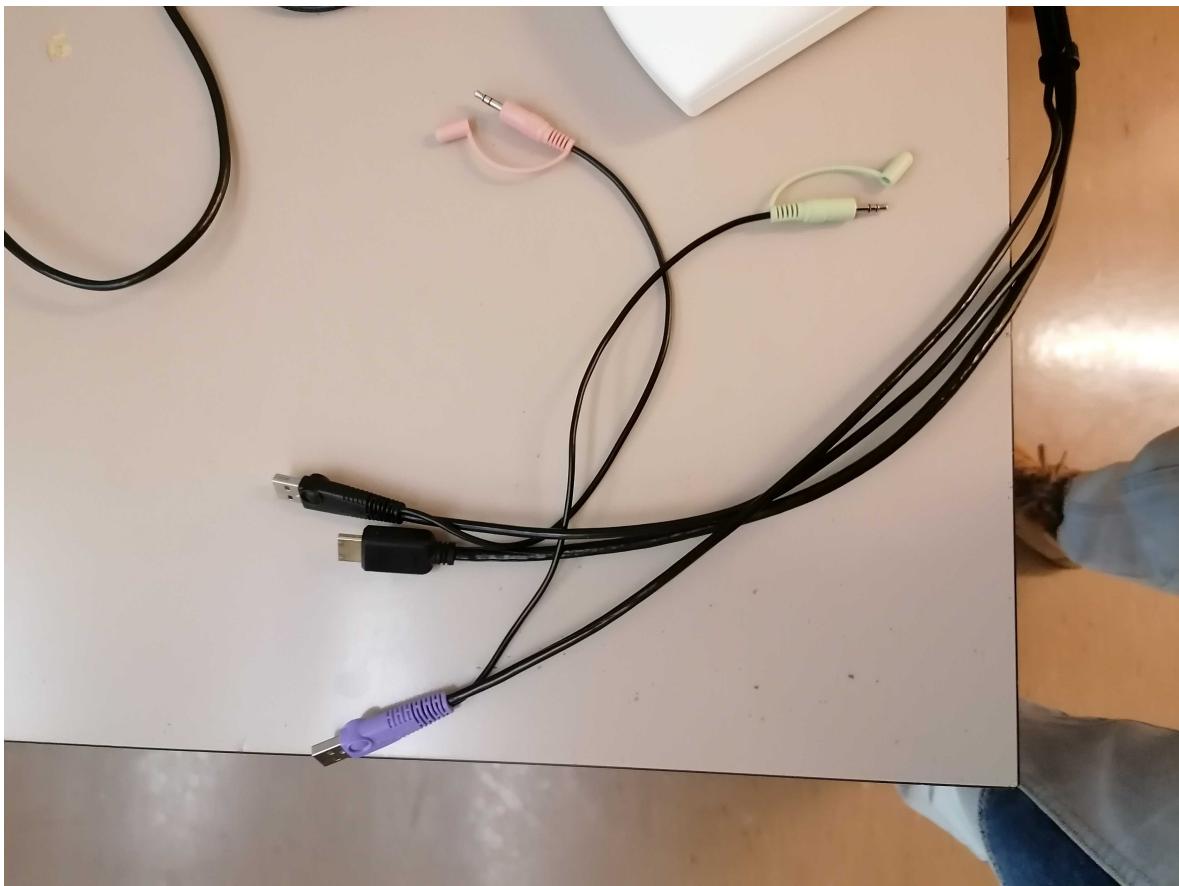
- Switch on █ and log-in with the username █ and password *****.
- Connect to the E.T to the █ laptop with the ethernet cable (blue color).



- Connect the sync box to the laptop with the USB cable. It is normally plugged into the █, it must be re-plugged in after usage.



- Connect the [REDACTED] laptop to the screen switch box (see picture below) with the corresponding **HDMI** cable. This should project your screen on the screen of CHUV's tower [REDACTED].



If the monitor does not automatically switch the source of the screen, you can use the button below to switch it.

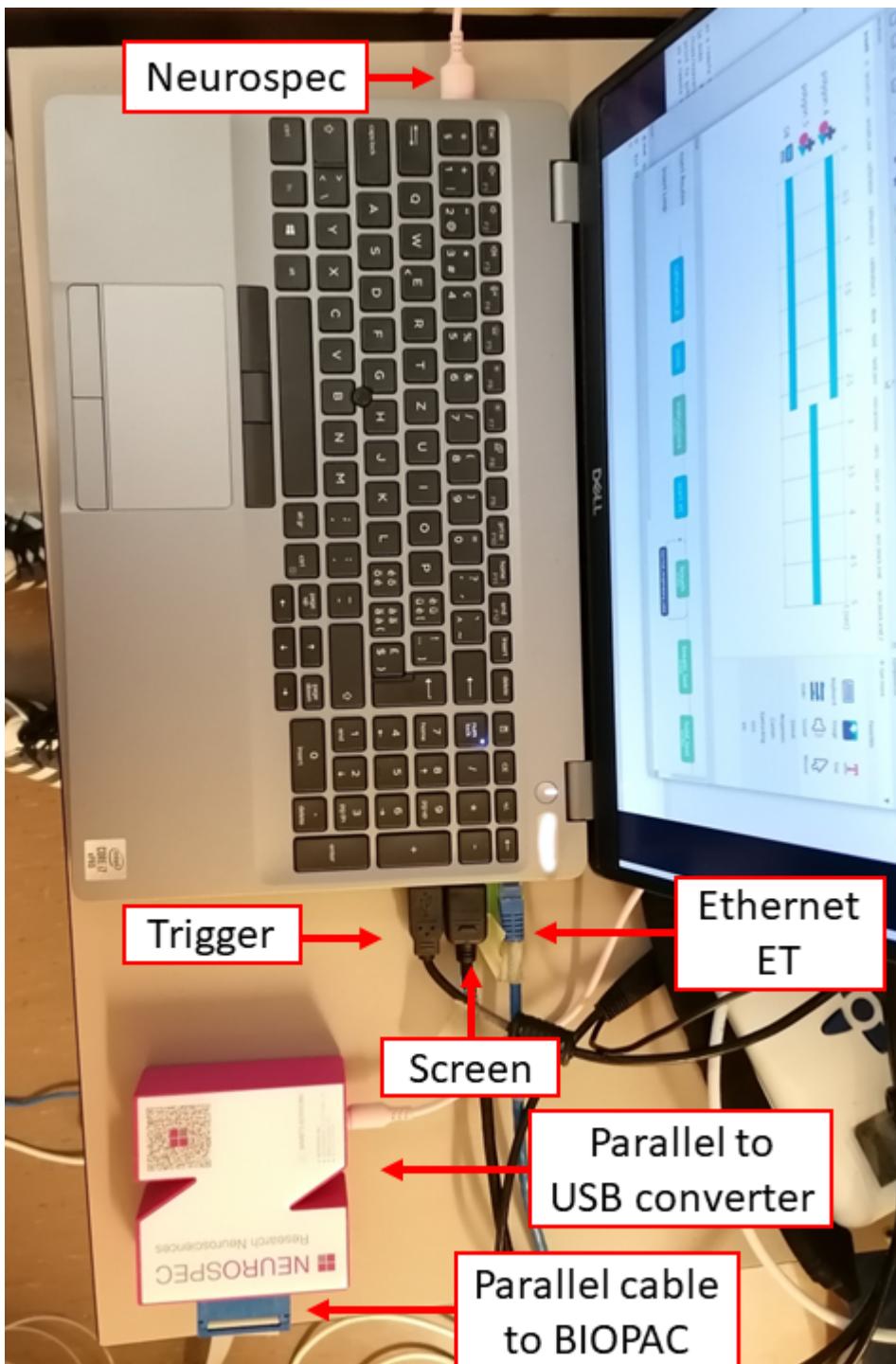


- Connect the MMBT-S Trigger Interface Box adapter (pink USB cable) to one of the USB ports of the laptop.



The MMBT-S Trigger Interface MUST be connected to the laptop AFTER the trigger USB cable coming from the SyncBox.

- Your laptop connections should now look like this.



- Configure the display settings of the laptop to mirror outputs and set a resolution of 800x600 for both screens. That step and that exact resolution is crucial for the eye-tracker calibration to work.
- Configure the display settings of the laptop to mirror outputs and set a resolution of 800x600 for both screens.
- Double check that the IP address corresponding to the ethernet interface of the **█** laptop is correct. You can either run `ifconfig -a` or use the GUI. Make sure the IP/mask is 100.1.1.2/24, and the protocol is IP version 4. Execute `ping 100.1.1.1` to see if the **ET** is responding to echoes.

- Check that the service to synchronize the triggers is up with `sudo systemctl status forward-trigger`.

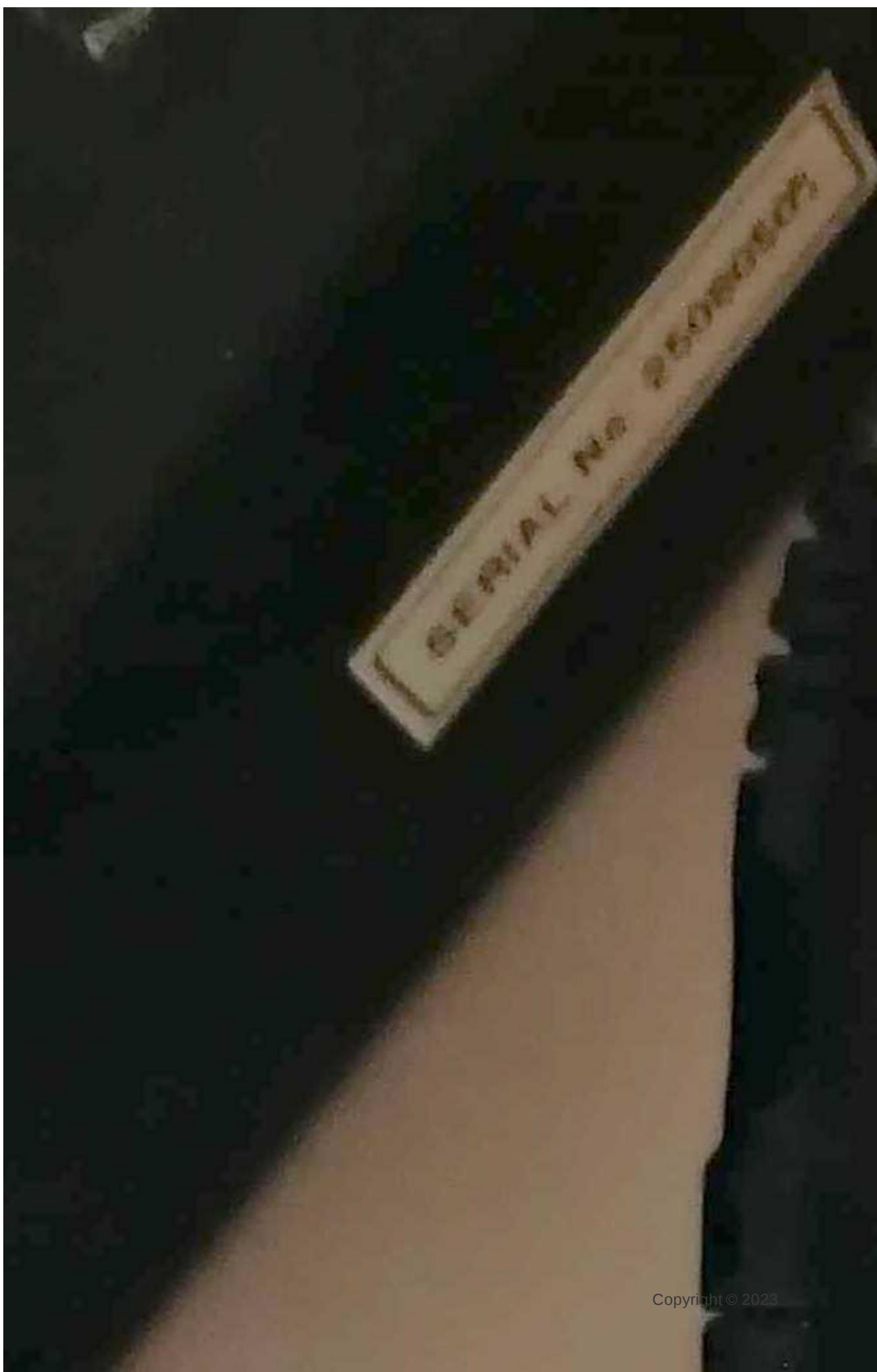
If the service is down, manually force its start

- Run `sudo systemctl start forward-trigger`
- Recheck the status with `sudo systemctl status forward-trigger`.

These commands are executed with sudo

The console will prompt you for the common user password: *****

- Check that you can send trigger events manually:
 - Enter the Synchronization mode by selecting it and pushing the enter button .
 - Hit the down arrow button until you find Send triggerpulse
 - Push the enter button every time you want to send an s character.
 - Check that the [REDACTED] laptop types those triggers (e.g., on an open editor receiving keypresses, or the shell prompt).
 - Check that the BIOPAC is properly registering the trigger too. Every trigger sent should be seen in the *AcqKnowledge* GUI.
- Start the syncbox session:
 - Push the up arrow button until you find Start Session
 - Push the enter button and the syncbox will be now waiting for the scanner's trigger signal to forward it.



Final checks inside the scanning room

- Prepare padding: under-knee padding, neck padding, inflatable head-padding.
 - Wrap a sanitary cover around each padding.
 - The head padding should be chosen and adjusted to each participant depending on their head size so that their nose is only 1-2mm away from the anterior part of the coil. The anterior part of the head coil will be tight around the participant's nose, so ensure they are nonetheless comfortable.
- Prepare a blanket.
- Prepare a new pair of earplugs.
- Check the RB, ECG, and nasal cannula are prepared.

Preparing the participant

Procedures for when the participant has arrived

It is critical to stay alert and anticipate any potential risk to the participant to avert them. This is particularly important for the first session.

Preparation of the participant in the CONTROL ROOM

Participant reception

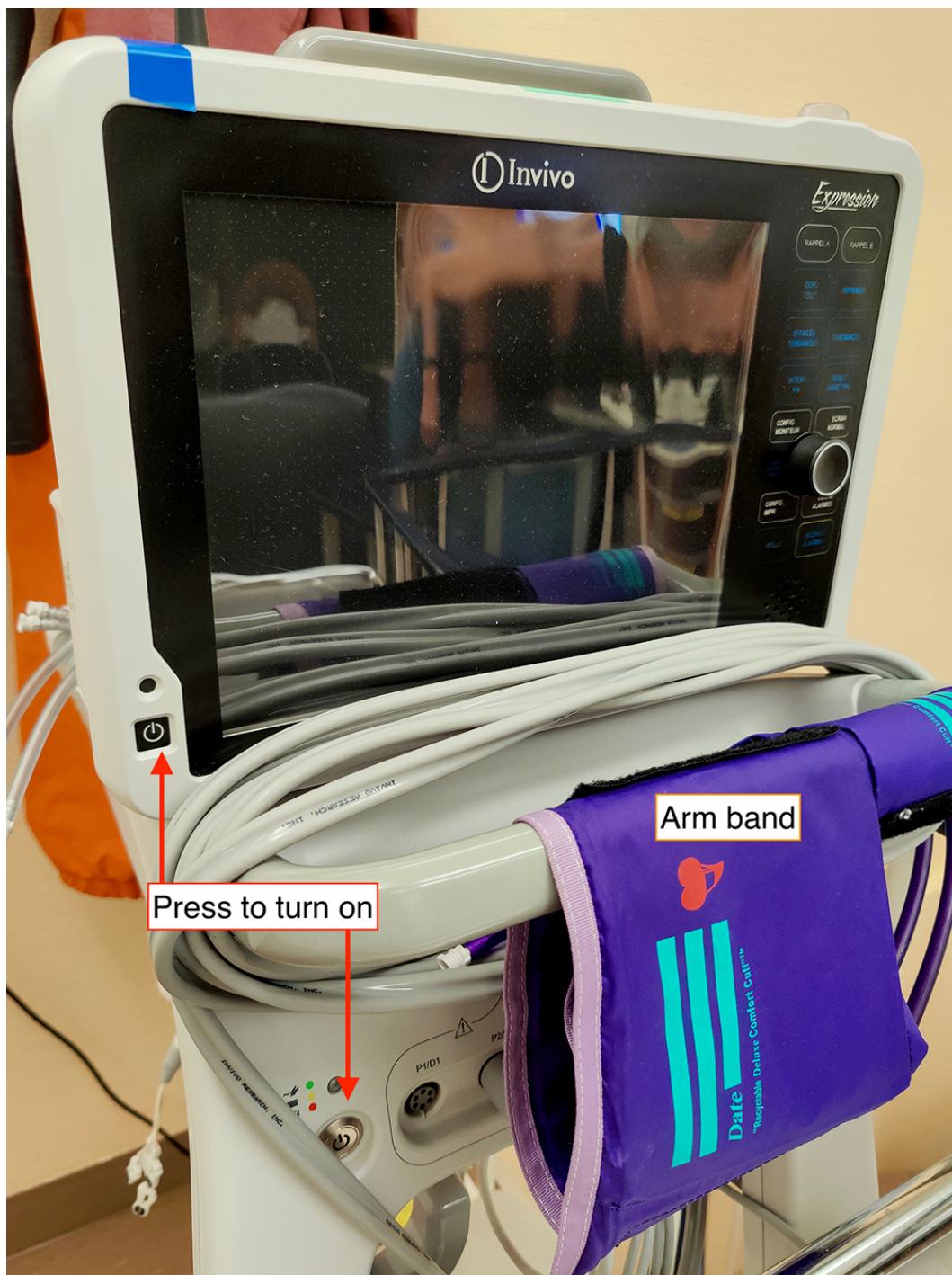
- Meet the participant at an easily locatable place (e.g., the reception desk of the Radiology Unit) and show them the way into the control room. **Allow sufficient time before the experiment for the preparation (min. 30 minutes).**
- Show the participant the scanning room and explain to them how the device is controlled from outside.
- Ask the participant to fill out the consent form and MRI safety screener, and verbally confirm responses, paying attention to frequently forgotten devices and implants, like orthodontia.

DO NOT subject the participant to any risk

- In case of any doubts emerging from the MRI safety screening, contact █ immediately at ####-####-####. **DO NOT PROCEED if the medical contact cannot be reached.**
 - In case of discovering any previously undisclosed contraindication, the volunteer MUST NOT participate in the study.
-
- Ask the participant to fill out the Before scan part of the covariates collection on the issue you opened [earlier](#).

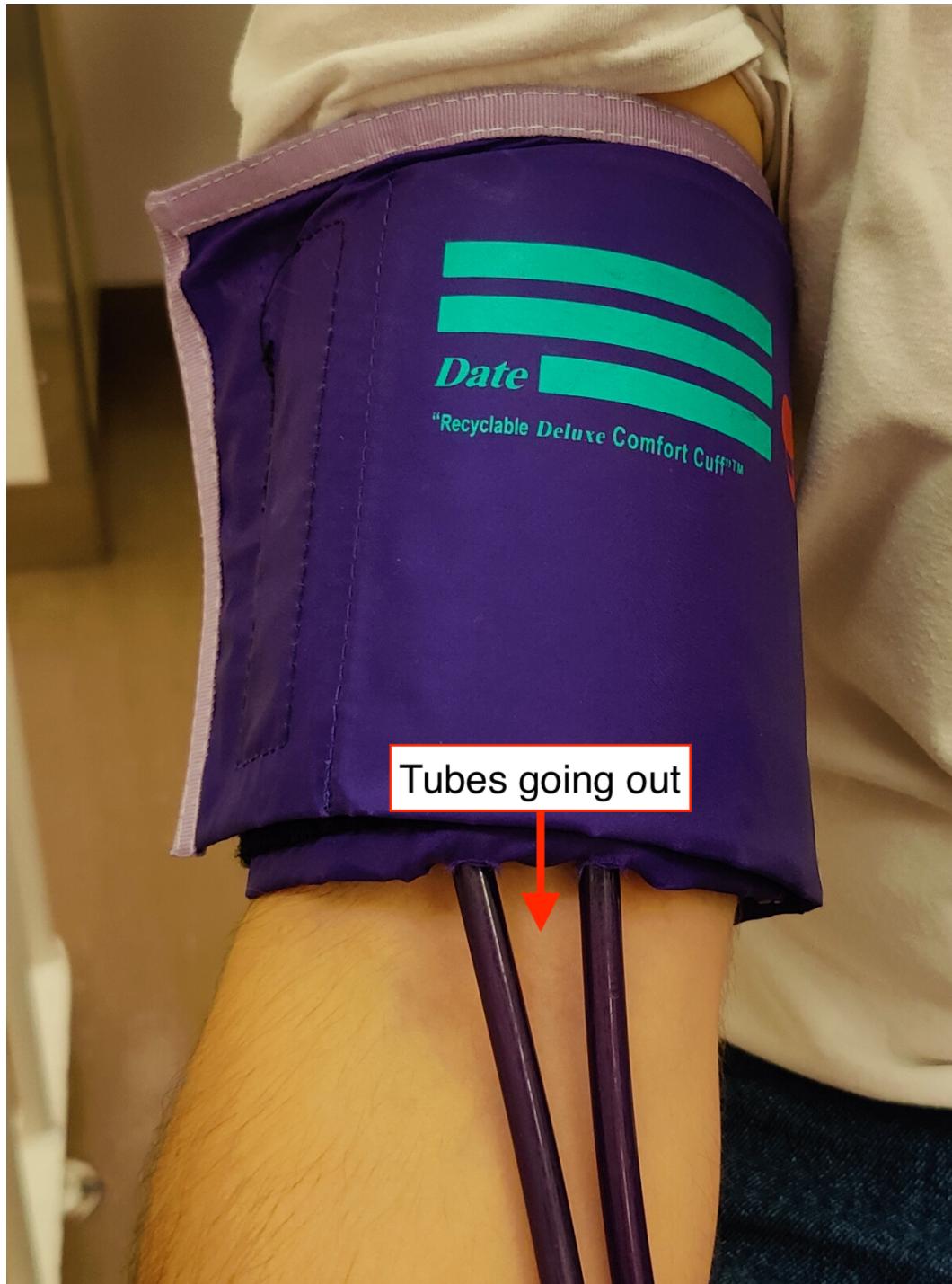
Measuring blood pressure

- Turn the blood pressure machine on.



- Carefully place the arm band on the patient's right arm.

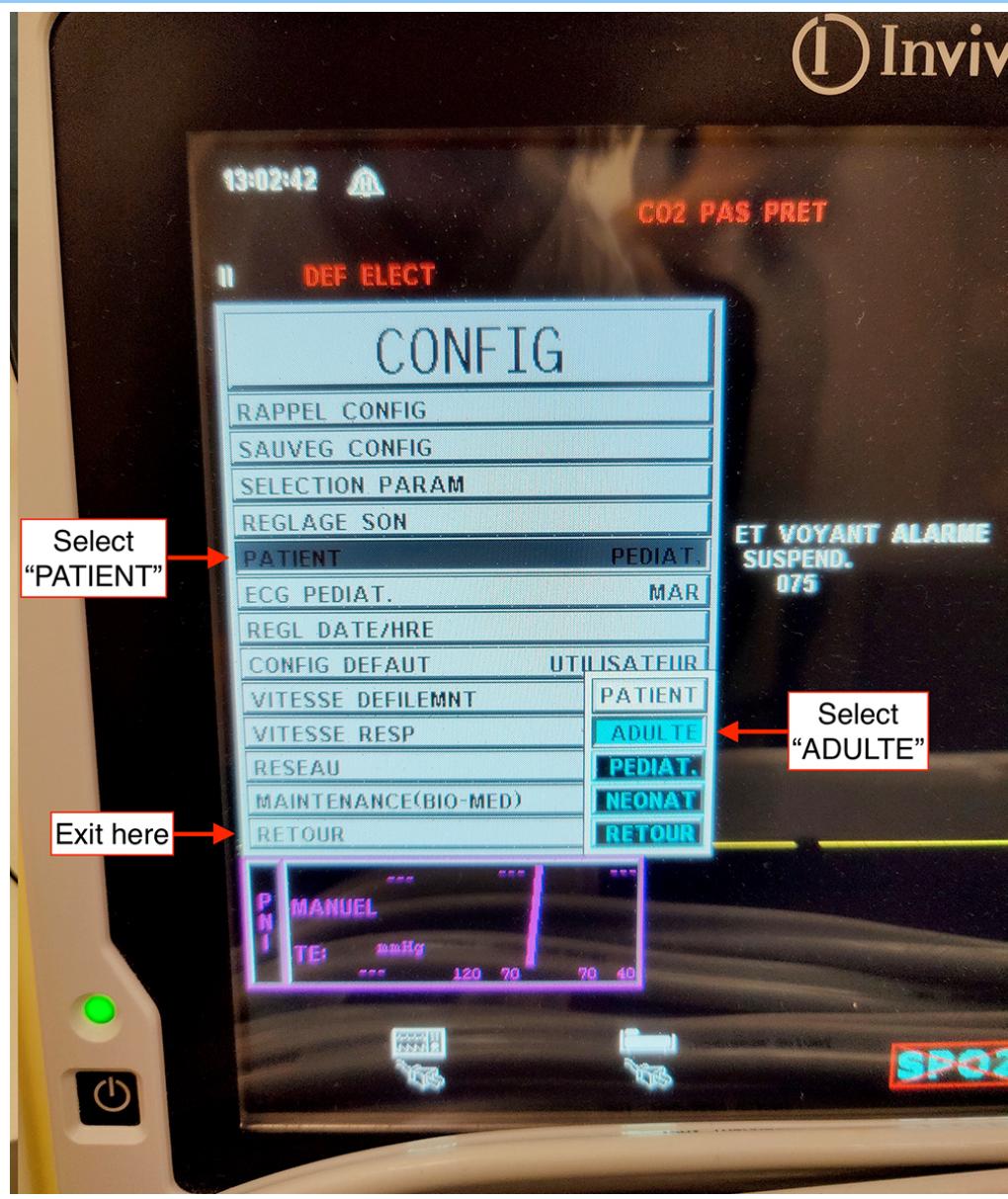
- Make sure the tubes are placed correctly (see below).



- Check that the adult preset is loaded (if not, load it).

Load a new preset

- Press CONFIG MONITEUR to open the options.
- Scroll using the wheel and select by pressing it.
- Enter to PATIENT, and select ADULTE.
- Exit by pressing the wheel on RETOUR.



- Measure the blood pressure by pressing the DEBUT ARRET button.



- Remind the participant to use the bathroom at this moment if they need (████).

Only female participants, only the first session

- Remind the participant that for their safety, pregnant women cannot participate:

Hey [NAME], I have to remind you that pregnant women cannot participate for their safety. To be absolutely sure that you are not scanned while being pregnant, the ethical review board requests us that you take a pregnancy test before the first session. Here you have a test, and this is the urine sample cup. I'm going to show you the bathroom now so that you can do the test with the necessary privacy.

- Provide the participant with a pregnancy test and a urine sample cup.
- Go over the instructions with them.
- Accompany them to the bathroom (situated at █████), and ask whether there is anything else they anticipate they will need.
- If the test is positive, the person CANNOT PARTICIPATE in the study. You MUST be understanding of the situation as most likely the person will not be aware of the circumstance.

- Instruct the participant on how to use the alarm button:

Alarm button should be used when needed

During the duration of the exam, you'll have an alarm button on your hand. You can use it at any moment. We will first talk with you to check everything is fine, and we will stop the session whenever you need to stop the experiment. There is no need for you to endure uncomfortable experiences or anxiety (for instance, if you feel claustrophobic)

Describing the development of the session

- Describe the participant how the session will develop, with special attention to tasks. In the first session, show the task while explaining them for clarity. Let them interrupt you to ask for clarifications and answer all the questions that may arise.

Script for the first session

We are going to acquire three types of images. The first type is anatomical imaging that we use to study the morphology of the brain. The second type is diffusion MRI, which we use to infer the pathways of major fiber bundles showing how the different regions of the brain may be interconnected. Finally, we collect functional MRI, which we use to understand how the brain activates as a response to stimuli we will present to you. During the whole duration of the exam, please do not create closed loops by crossing your legs or holding your hands together. It is possible that your peripheral nerves get stimulated at some points, so you will feel twitching of muscles, for instance, of your pectorals. Do not panic, it is okay, but if it feels too uncomfortable, please squeeze the alarm button.

For the anatomical and the diffusion MRI we just ask you to relax and try to stay as still and comfortable as possible. Like a photographic camera, the largest problem making analyses difficult is motion. As opposed to a photo camera, the imaging of the brain happens very slow so there is a lot of opportunity for involuntary movements (e.g., when you blink or you take a deeper breath) or semi-voluntary (e.g., you need to swallow).

The functional MRI is a bit more entertaining, as we will ask you to engage in different behavioral activities. The first functional block is what we call a positive-control task, that will tell us little about your brain but will help us determine if there are confounding signals intermixed with your data. In this positive-control task, you will be shown a fixation point with the shape of a circle. Whenever you see that fixation point, please focus your gaze at the center of it. At points the fixation point will browse around the screen. When that happens, please follow it with your eyes taking care of not moving your head with the eye movement. Other times it will be fixed on the center, and have a blank gray background or a flickering or grating circular area behind it. The last element of this block will show the words LEFT or RIGHT. When either appears, please tap your thumb on each of the your other four fingers of the hand designated by the word, sequentially with all fingers and reversing the direction at the extremes (your pointer and your pinkie). This positive-control task has a length of 2min 38s. During this task, please leave the alarm button on your tummy, where you can recover it when it finishes.

Then there is a long block of 20min 6s that we call *resting state*. During this block, all you have to do is stay still and look at the movie. Please do not close your eyes.

Finally, a breath-holding task will help us understand the signals elicited by your breathing that are detected by the scanner. This block has a length of 5min 41s. You will watch five repeats of the same block. Each block will show you a colored rectangle in the middle. The green rectangle means *breathe in*, the yellow rectangle means *breathe out*, and the red rectangle means *hold your breath*. The last two green and yellow rectangle will be shown on a lighter green and orange color respectively to signal you that a hold will follow immediately after the breathe-out. The red rectangle will turn pink to indicate that you will soon be able to breathe-out any remaining air in your lungs and breathe in again. Please remember to breathe out after the breath-hold. When no rectangle is presented, you can breathe as it feels more comfortable to you. The first of the blocks is a mock. That will be reminded to you at the beginning of the task on the screen. During the mock block, please look at the stimuli on the screen but keep your habitual breathing pace disregarding the task instructions. At the end of this mock block, a message will remind you to follow the task instructions from that moment on. You must adapt your breathing to the pace indicated by the color-changing rectangle in the center of the screen for the remaining four repetitions of the block.

Is everything clear to you? Do you have any questions?

Script for the following sessions

As you probably remember, we acquire three types of images. For two of them you just stay still in the scanner, but we will also require your collaboration for the third, which is functional MRI. During the whole duration of the exam, please do not create closed loops by crossing your legs or holding your hands

together. Also, remember to breathe through your nose, not through your mouth, so the expired CO₂ can be measured with the cannula. It is possible that your peripheral nerves get stimulated at some points, so you will feel twitching of muscles, for instance, of your pectorals. Do not panic, it is okay, but if it feels too uncomfortable, please squeeze the alarm button.

Let's quickly recap the functional MRI tasks. The first is the positive-control task, you will be shown a fixation point with the shape of a circle that you must follow with your gaze wherever it goes and then the words LEFT or RIGHT while which you tap your fingers like this (remind to them). During this task, please leave the alarm button on your tummy, where you can recover it when it finishes.

Then there is a long block of about 20 minutes that we call *resting state*, where you will be watching a movie. During this block, all you have to do is stay still and please do not close your eyes.

Finally, the breath-holding task where you will watch five repeats of the same block with colored rectangles in the middle. The green rectangle means *breathe in*, the yellow rectangle means *breathe out*, and the red rectangle means *hold your breath*. The last two green and yellow rectangle will be shown on a lighter green and orange color respectively to signal you that a hold will follow immediately after the breathe-out. The red rectangle will turn pink to indicate that you will soon be able to breathe-out any remaining air in your lungs and breathe in again. Please remember to breathe out after the breath-hold. When no rectangle is presented, you can breathe as it feels more comfortable to you. The first of the blocks is a mock. That will be reminded to you at the beginning of the task on the screen. During the mock block, please look at the stimuli on the screen but keep your habitual breathing pace disregarding the task instructions. At the end of this mock block, a message will remind you to follow the task instructions from that moment on. You must adapt your breathing to the pace indicated by the color-changing rectangle in the center of the screen for the remaining four repetitions of the block.

Is everything clear to you? Do you have any questions?

Finalizing the preparation

- Offer the participant a box to deposit everything they have in their pockets and all jewelry/ hair accessories, and indicate the clothing to enter the scanning room:

Dress code inside the scanner if they need to CHANGE INTO SCRUBS

Before we continue, we need to make sure we do not introduce any dangerous object in the magnet room.

Here you will find a changing room [SHOW THEM THE CHANGING ROOM]. I have prepared some scrubs for you. Please remove all your clothes and leave them in the changing room. Please keep your underwear on [if a woman, ask whether their undergarment DOES NOT contain any large metallic part such as shaping guides, and request their removal if they do].

Dress code inside the scanner if they CAN WEAR THEIR CLOTHES

Before we continue, we need to make sure we do not introduce any dangerous object in the magnet room.

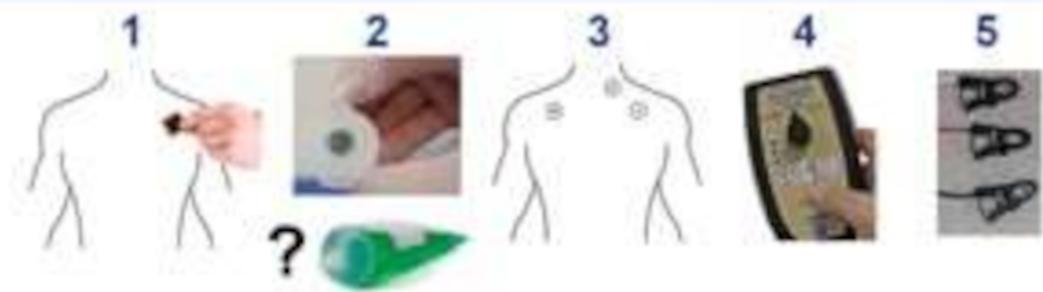
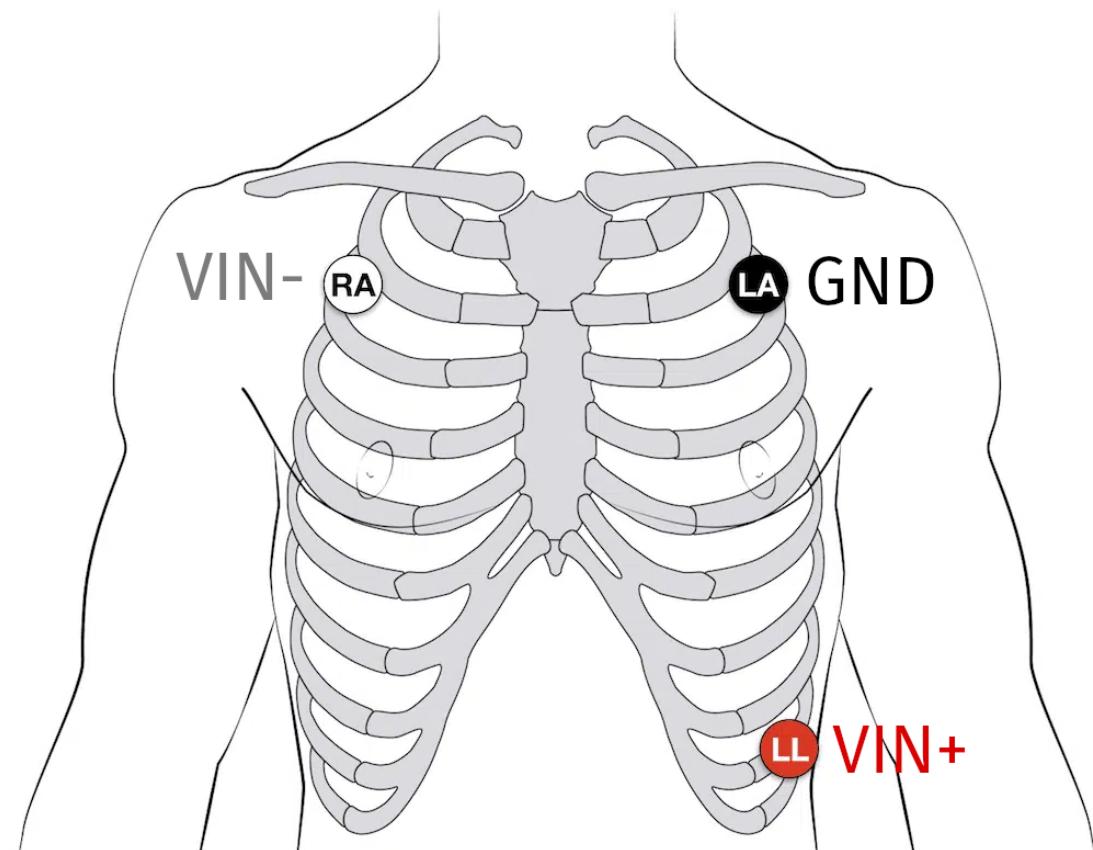
Please deposit here all your belongings, your belt, your glasses, your jewelry and any accessories, piercings, etc. that you have on you. If a woman, ask whether their undergarment DOES NOT contain any large metallic part such as shaping guides, and request their removal in the changing room.

- Help the participant to prepare their skin and place the ECG electrodes:

Ask the participant if they have atopic skin or other skin problems

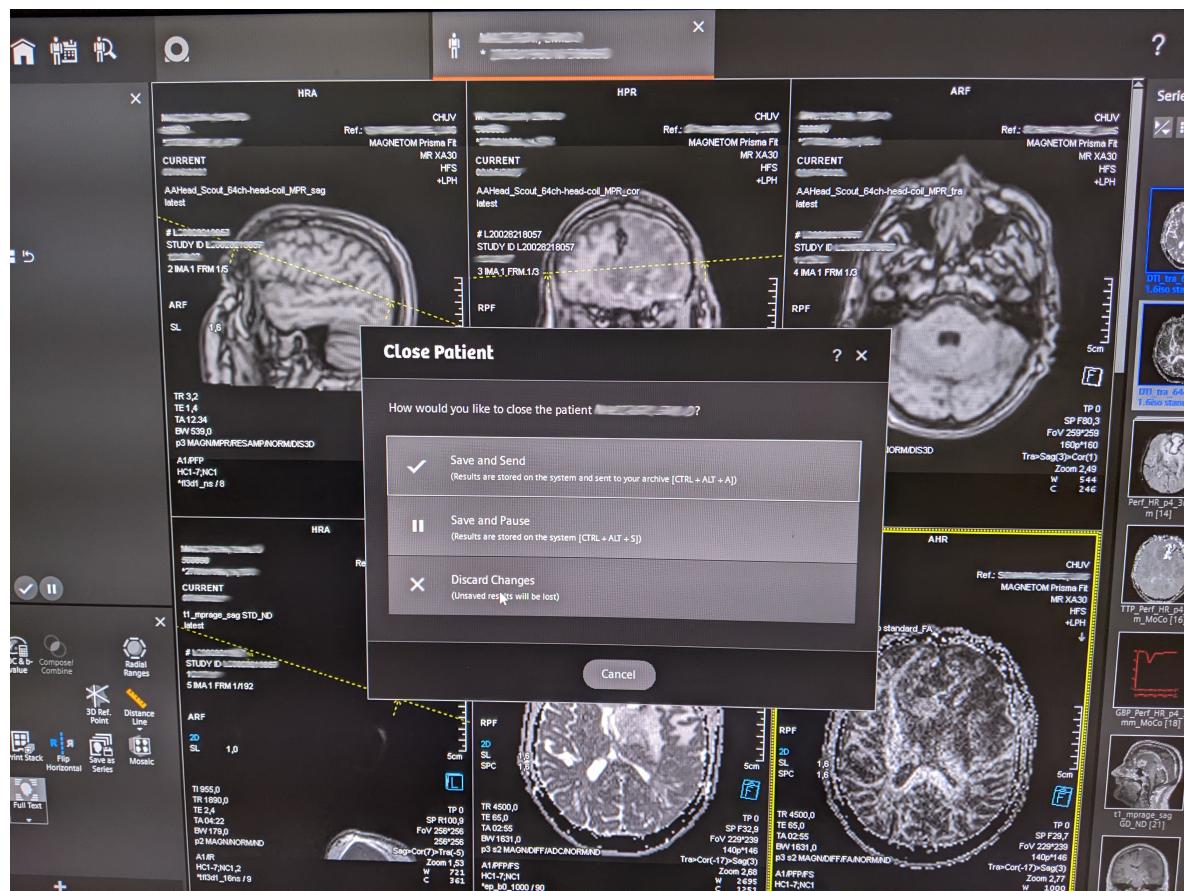
If the participant reports having skin issues, be careful with the following process and do not unnecessarily irritate their skin (e.g., skip the alcohol cleaning and perhaps the abrasion with the preparation gel)

- Open the sterile cotton gauze pads package, take one and moisten it with alcohol.
- Clean the skin around the three areas with the alcohol-soaked pad with circular movements.
- Get a second cotton gauze pad and put some *Nuprep* preparation gel and gently abrade the skin by rubbing it onto the skin with four or five circular movements.
- Remove gel excess with a clean cotton gauze.
- Remove the protective film from the electrode.
- Stick the electrode on the participant's skin by starting in one side and ironing the rest of the electrode. This procedure ensures that no air is trapped between the electrode and your skin and that no wrinkles form at the edges. Repeat for the three electrodes.

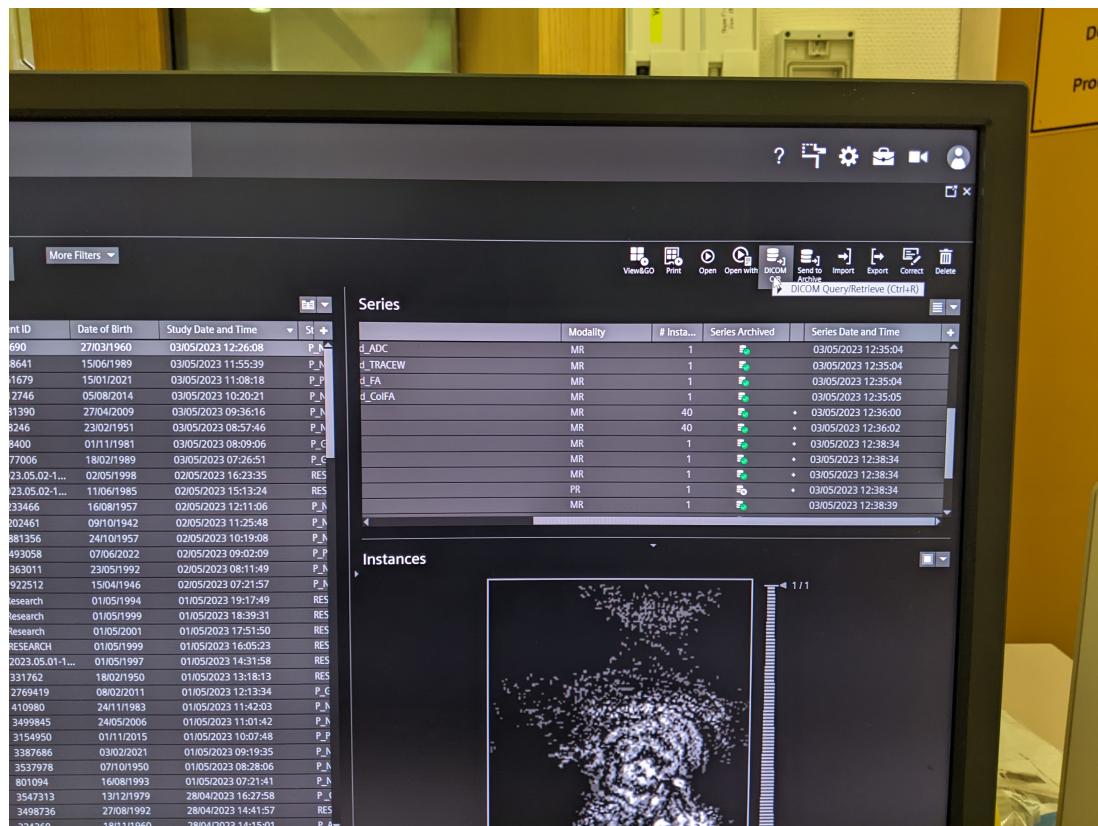


Preparation of the scanning protocol (control console)

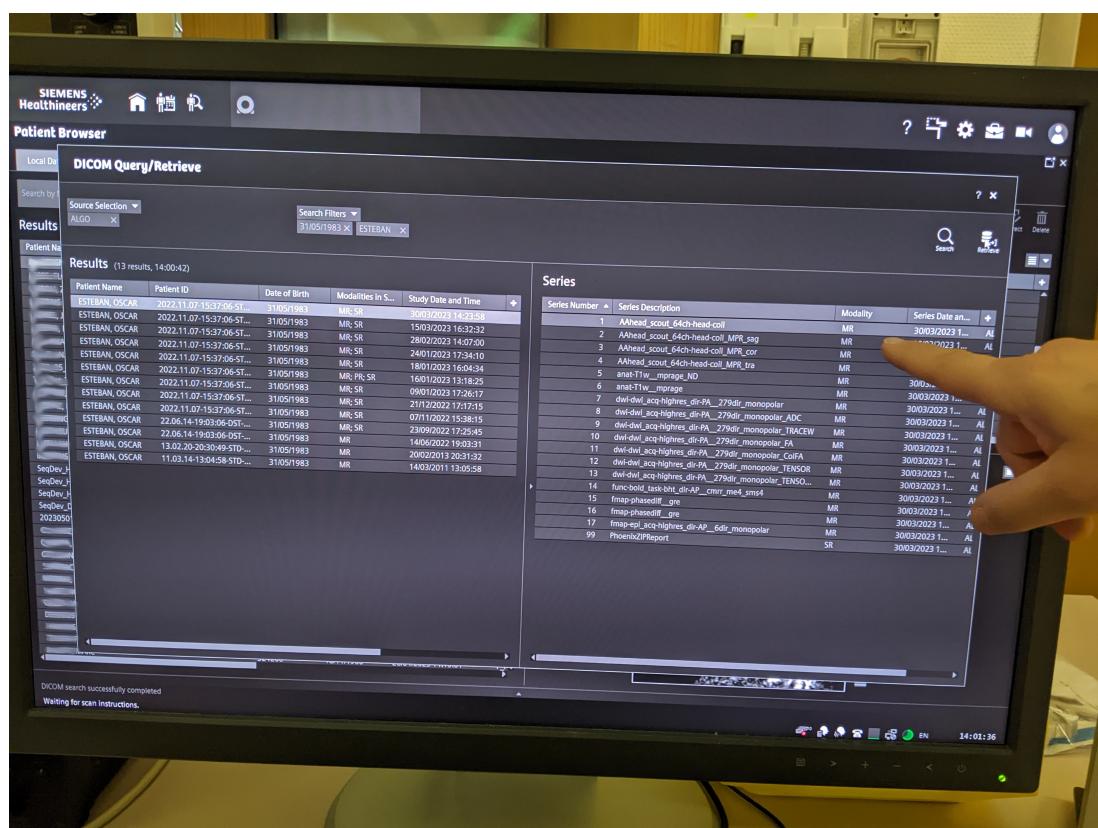
- Close open patients discarding changes.



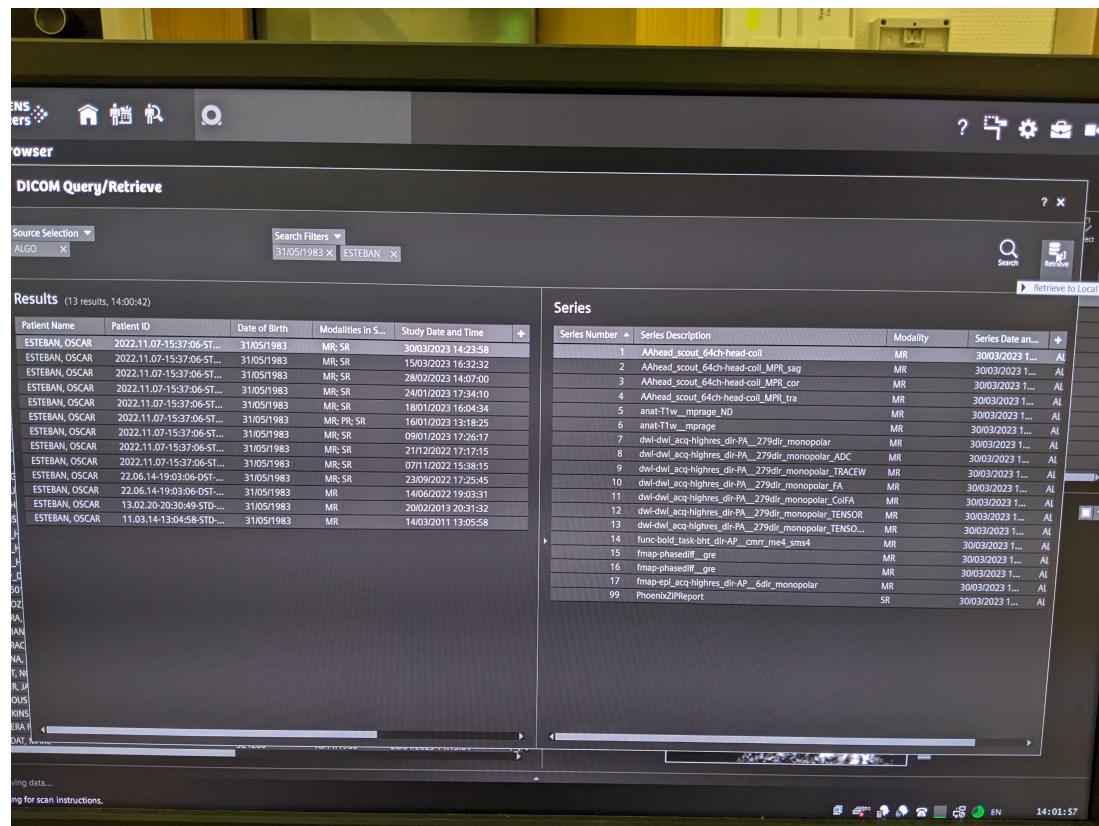
- Search for the participant by clicking on the "Patient Browser" in the top left corner. If the participant is not shown (because it is archived and hence not locally found):
 - Click on the *DICOM Q/R* button on the top-right area.



- Introduce some unambiguous search criteria:

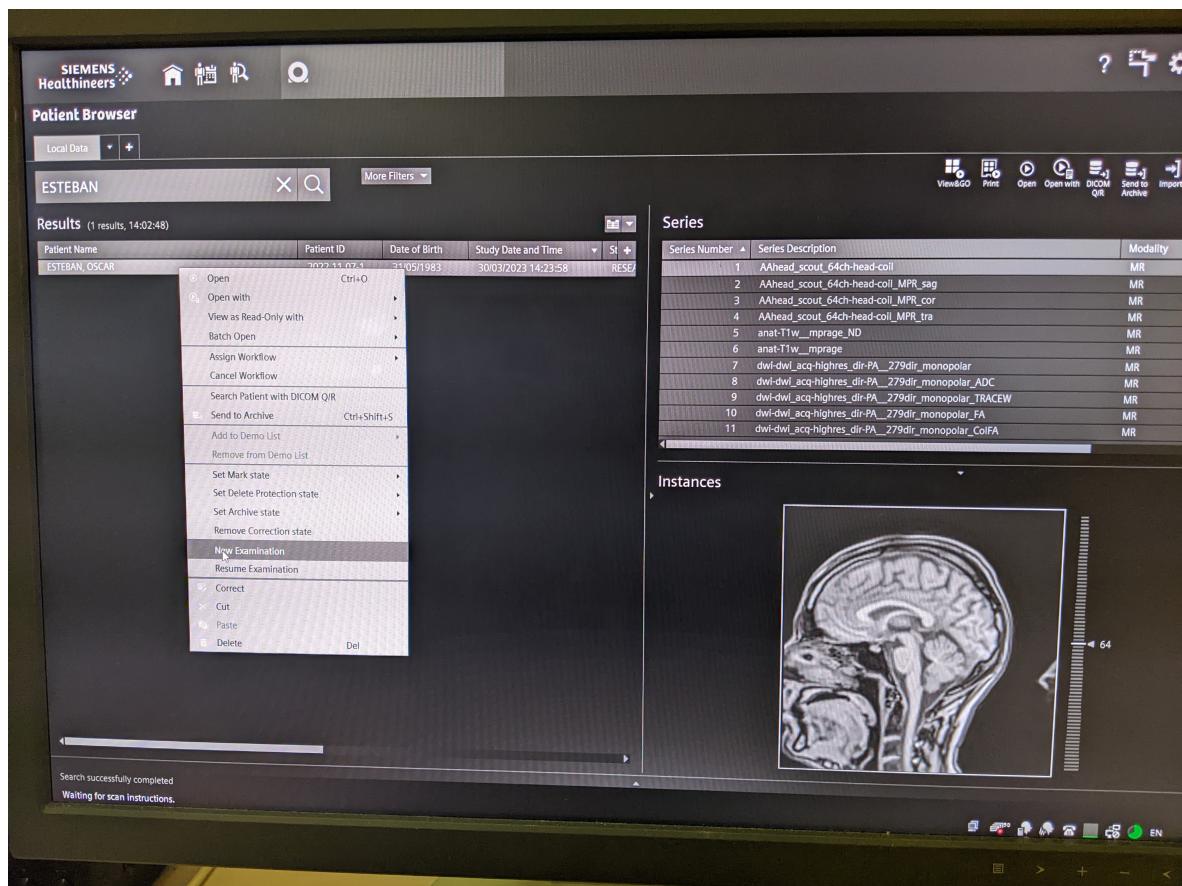


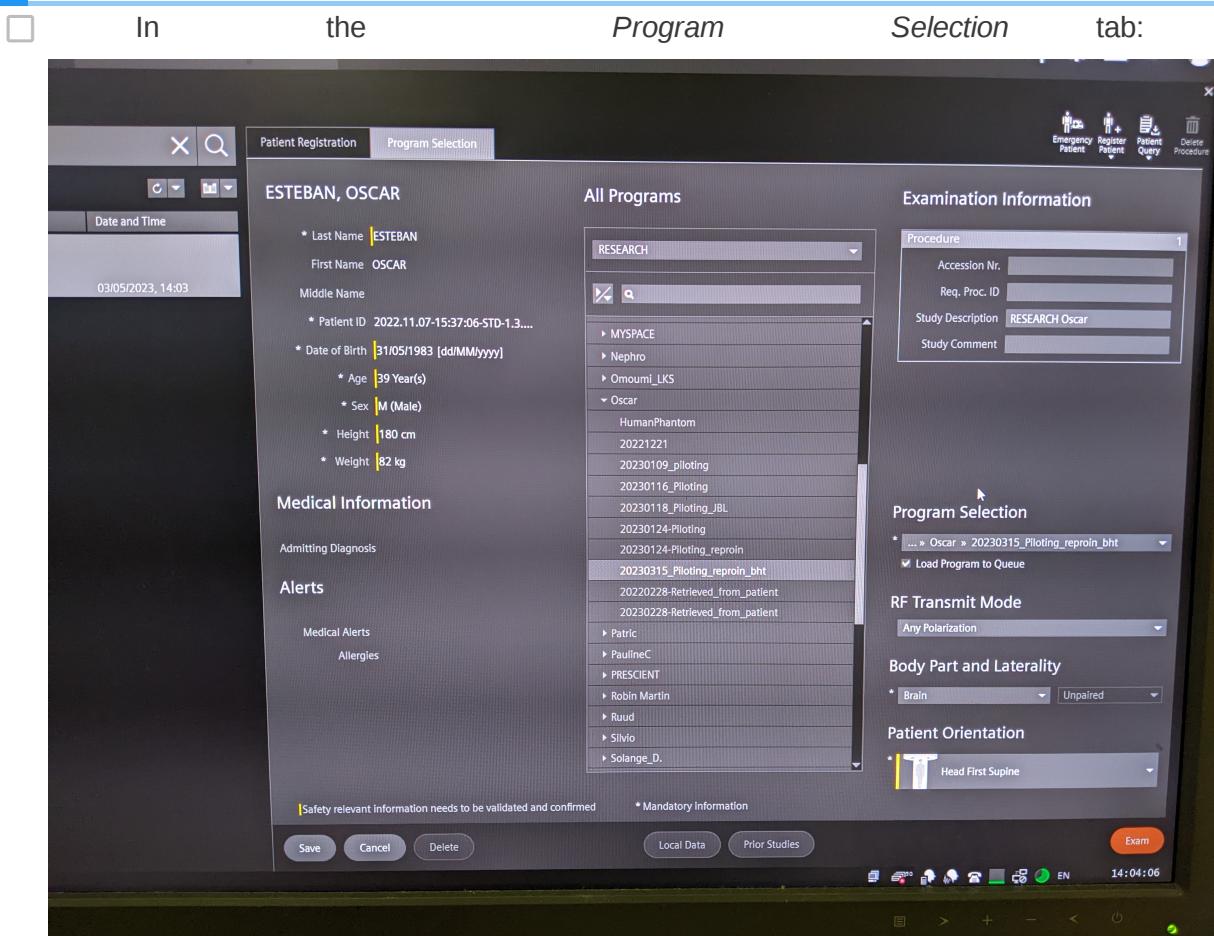
- Select the subject (left column) or the sequence (right column) you want to retrieve and hit *Retrieve*. Be careful, you probably want to retrieve a subject, that means make sure you have selected a row on the left column:



- Go back to the "Patient Browser" and check that the patient now shows up in the local search.
- Check the head coil is not plugged before initiating a "New examination" to ensure good SNR of the localizer sequence.

- Right click and select "New examination".





- Enter the weight and height of the participant.
- Select the right protocol under *RESEARCH* ↴ *Oscar*.
- Select *Brain* as the organ.
- Select the *Position* as "Head First Supine".
- Before you hit Exam, you can edit general patient's data by changing to the *Patient Registration* tab if you need to edit general information about the patient.
- Click the Exam button (red background, rightmost-bottom).

- Load the adequate protocol, making sure of loading the right phase-encoding (PE) direction corresponding to the session.

Session schedule

Today is **2023-10-25 17:05**:

session day	PE
1	2023-10-20 LR
2	2023-10-20 LR
3	2023-10-21 LR
4	2023-10-21 RL
5	2023-10-22 PA
6	2023-10-22 PA

session day	PE
7	2023-10-23 LR
8	2023-10-23 RL
9	2023-10-24 AP
10	2023-10-24 RL
11	2023-10-25 AP
12	2023-10-25 PA
13	2023-10-26 PA
14	2023-10-26 LR
15	2023-10-27 AP
16	2023-10-27 RL
17	2023-10-28 PA
18	2023-10-28 LR
19	2023-10-29 PA
20	2023-10-29 RL
21	2023-10-30 RL
22	2023-10-30 AP
23	2023-10-31 AP
24	2023-10-31 AP
25	2023-11-01 RL
26	2023-11-01 PA
27	2023-11-02 AP
28	2023-11-02 RL
29	2023-11-03 PA
30	2023-11-03 AP
31	2023-11-04 PA
32	2023-11-04 AP
33	2023-11-05 LR
34	2023-11-05 LR
35	2023-11-06 LR
36	2023-11-06 RL

Installing the participant in the SCANNING ROOM

Thanks to Stephanie Bogaert, MSc, Pieter Vandemaele, MSc and Pim Pullens, PhD

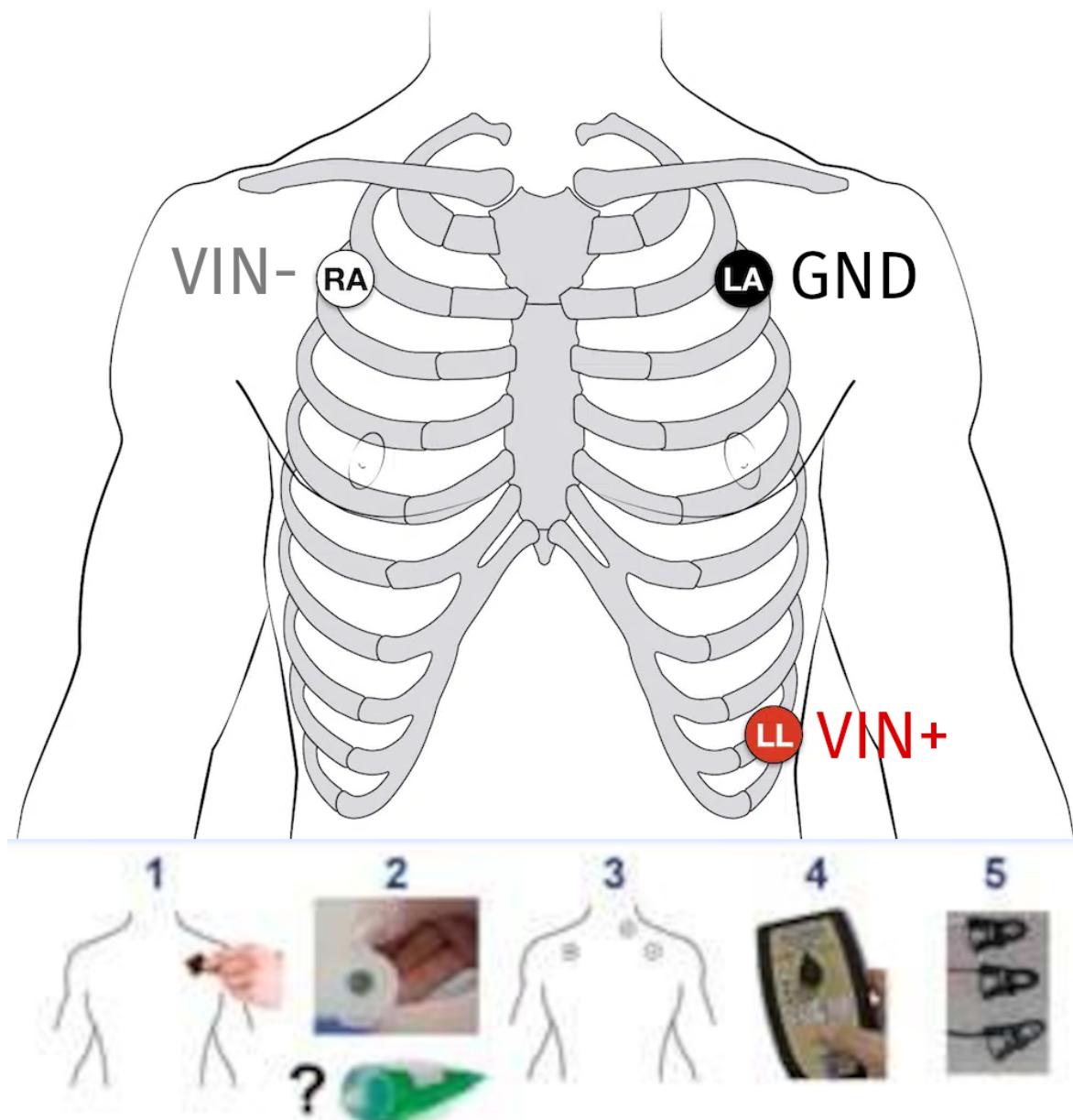
Some of the pictures in this section have been extracted from the Ghent Institute for functional and Metabolic Imaging [MRI](#) [User](#) [2019](#) (<http://gifmi.ugent.be/drupal/system/files/documents/>)

GfMRI_MRI%20user%20manual_BASIC_SiemensPrisma_EN.pdf written by Stephanie Bogaert, MSc, Pieter Vandemaele, MSc and Pim Pullens, PhD. We express our gratitude that they put together such a comprehensive guide.

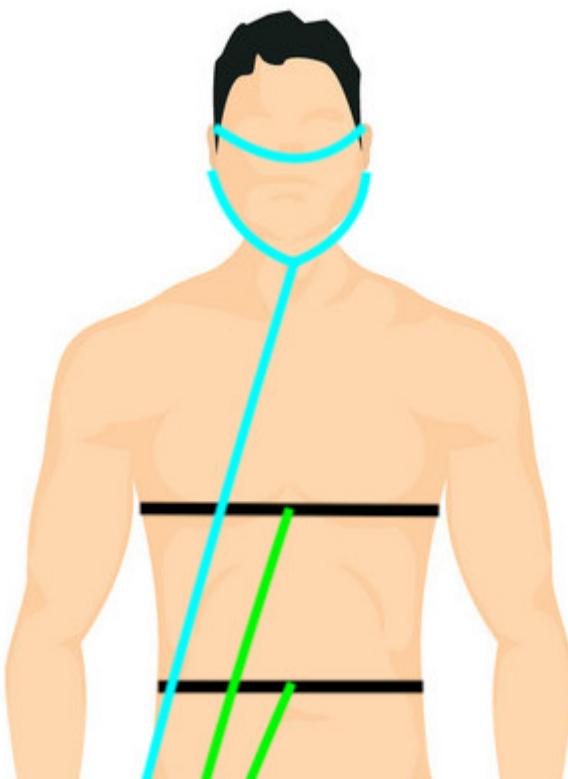
- Have the participant remove their shoes at the entrance of the scanning room.
- Show the alarm button to the participant and explain how they may use it.
- Give to the participant the emergency button. Make the participant try it, so they can see it works. To switch off the alarm, there's a button on the scanner (circular, both on the left and on the right of the hole)
- Give them the ear-plugs to protect their hearing during acquisition, allow time for them to place them.
- Instruct the participant to lay on the MRI bed.

Connecting physiological recording sensors and probes

- Connect the ECG leads to the three electrodes. The electrodes MUST be connected following the color scheme shown in the picture below.



- Install the RB below the participant's chest and connect it to the tube as shown in the picture below. The RB measures the stretching induced by breathing, so it MUST surround the chest or stomach comfortably. Positioning the RB higher (chest) or lower (stomach) depends on the individual's preferential respiration mode (chest breathing or diaphragmatic, respectively).
- Place the nasal cannula in the nose of the participant making sure the two protrusions are aligned with the nostrils of the participant. Place the tube behind the ears and tighten under the chin for comfort and stability by sliding the ring as shown in the picture below.



- When completely laying down on the bed, tightly fasten the RB and check with the participant whether they are too uncomfortable.
- Check the *AcqKnowledge* signal visualization of the adjustment of the RB, and make sure that the signal is not saturating (when the RB is too tight) or too weak (when the RB is too loose).

Two-people protocol to check the RB settings.

This check requires two experimenters, one INSIDE (IN) the scanning room and one more outside (OUT)

- OUT indicates they are ready to start the check by signaling a THUMBS-UP WITH BOTH HANDS through the Scanning Room window .
- IN MUST confirm they understand returning the THUMBS-UP WITH ONE HAND .
- IN finalizes the setting of the RB if necessary and asks the participant to breathe normally.
- Once the participant is lying down on the bed and breathing normally, and the check can be carried out, IN MUST signal they are ready by sending a THUMBS-UP WITH BOTH HANDS through the window.
- OUT MUST acknowledge the understanding, return a THUMBS-UP WITH BOTH HANDS , and check the *AcqKnowledge* screen.
- OUT checks for signs of saturation and insufficient dynamic range. These issues manifest as plateaus and excessively flat lines (respectively) in the *AcqKnowledge* visualization of the RB signal.
- OUT provides feedback to the inside room as follows:
 - If the RB must be tightened up, pointer finger going up ;
 - if the RB must be loosened up, pointer finger going down ;
 - if OUT needs to check again, they show two hands , checks the *AcqKnowledge* again and signs another instruction; and
 - if the check is finished, OUT signs a THUMBS-UP WITH BOTH HANDS .

- IN MUST acknowledge all the commands with THUMBS-UP WITH ONE HAND if understood. If not understood, they can request with a PRAYING gesture .

- Solicit feedback on participant's comfort while positioning them on the scanner bed and suggest ergonomic positioning of their arms to avoid discomfort.

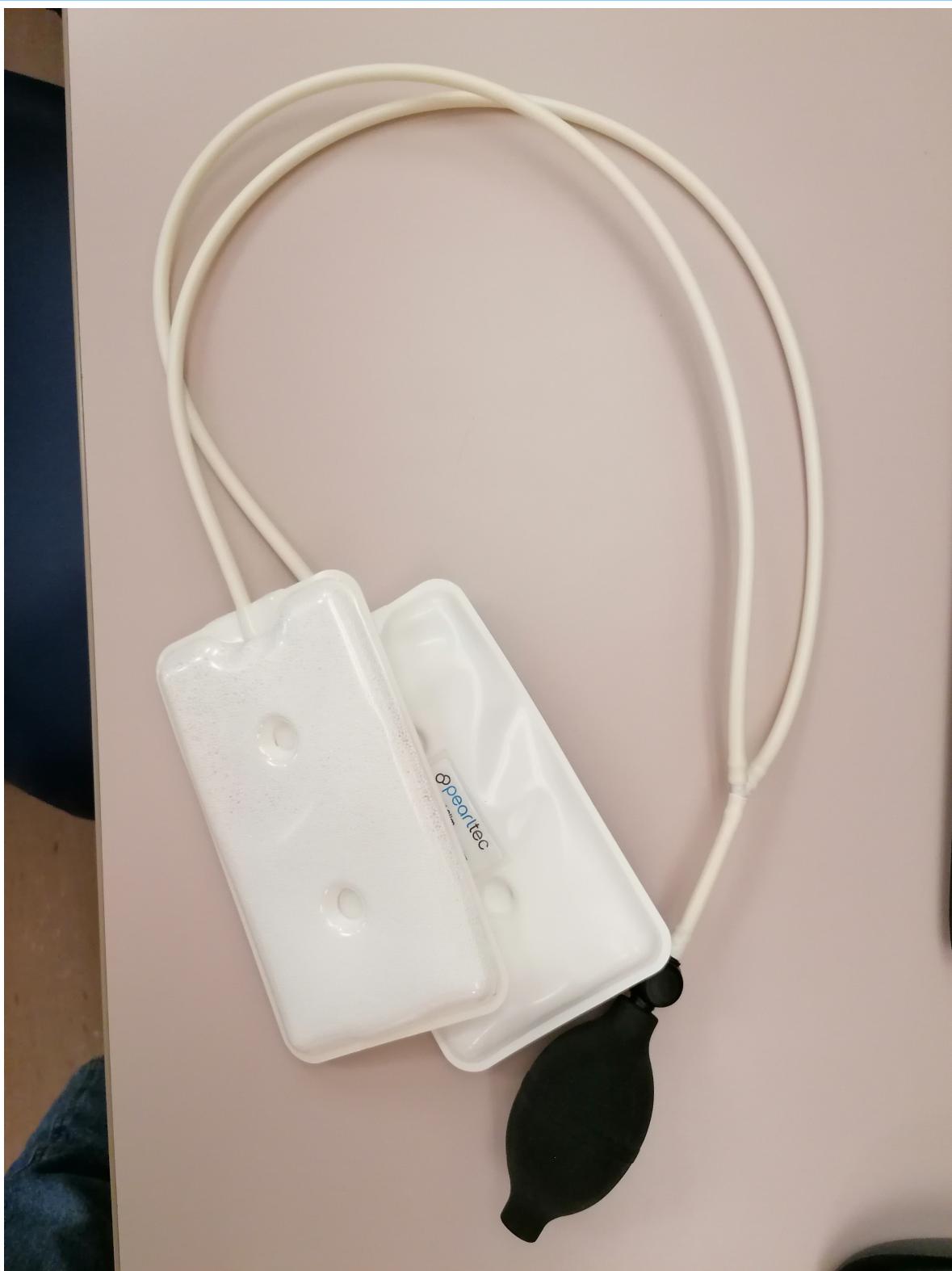
Accommodating the participant's head in the coil

- Adjust the participant inside. With the paddings, their head position MUST be adjusted and elevated so that the nose and the forehead of the participant are both close to the upper coil. This procedure ensures the ET has the clearest possible view of eye.
- This part must be repeated taking out and putting back the upper part of the head-coil, adjusting the pillow at every step, until the head is fixed and the nose and forehead of the participant almost touch the coil. In case of need, ask the participant to rotate their head like when saying yes until reaching an adequate position, place any remaining paddings.





- Take the side paddings and fit them between each ear and the coil. If using the inflatable padding, pump air into them without making the participant uncomfortable (check with them).



- Cut a long strip of medical auto-adhesive band and stick it at each side of the lower block of the head coil, across the participant's forehead and stick it to the participant's forehead. Indicate the participant that this band will tell them when they moved and help them recover the original position.

- Place the top block of the coil and check that the participants' front touches or is really close to the coil. Now the nose can also be a bit far from the coil. Tell the participant to relax the neck, so the nose should go a bit up and touch the coil.
- Connect the coil's cable to the corresponding socket on the table.
- Check that both the posterior and anterior parts of the head-and-neck coil are now detected by the scanner. To do so, ensure their names ("Head Neck 64 Posterior", and "Head Neck 64 Anterior", respectively) appear on the scanner's monitor screen.
- Place rectangular paddings at each side of the chest and help the participant accommodate their elbows on them.
- Cover them with a blanket if necessary, and remind them of not closing loops with their body:

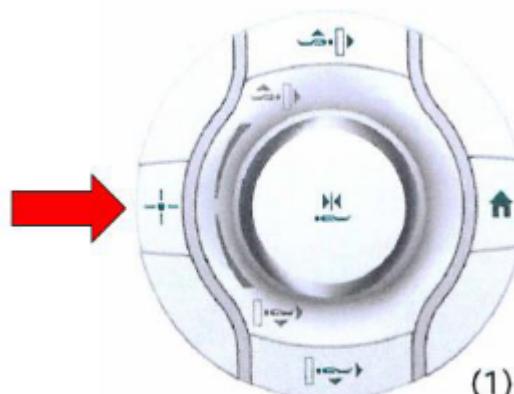
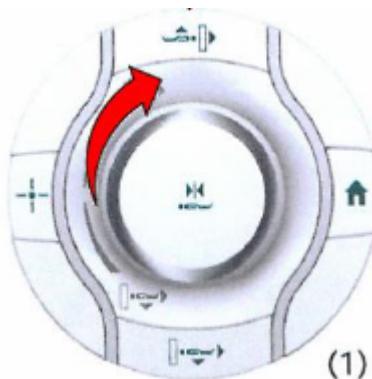
Ask the participant if they are feeling cold

Hey [NAME], are you feeling cold? Do you want a blanket?

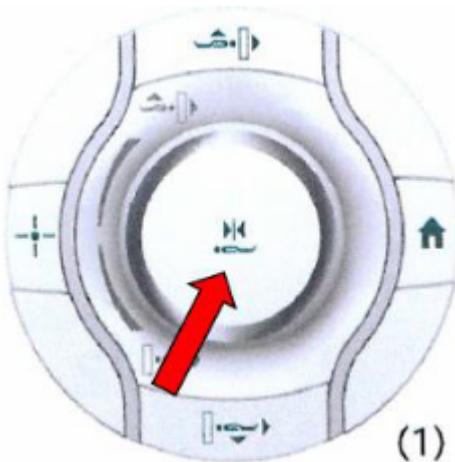
I have placed some paddings for your elbows, is there anything else you would need to feel comfortable?

Throughout the examination, remember not to create closed loops by crossing your legs or holding hands together.

- Gently move the participant with the manual regulation. Stop when the head is under the head-localizer. Ask the participant to close their eyes, press the laser alignment button and align the head-coil markers with the red light.



- Switch off the alignment light, now the participant can open their eyes. You can move the participant (always gently as before) inside the scanner manually, until the mm counter marks "Isometric" or you can press the rotary knob for two seconds. This will send the participant to the isocenter automatically.



- Once the participant is lying on the scanner bed, check that no arms/legs rest on the GA or the RB tubes and may block them.
- Before continuing with the setup, make sure all cables and tubes leave the scanner's bed *perpendicularly* and lie on the floor. Tape them to the floor so that they don't move accidentally.

Final preparatory steps of the ET

Please note that some of the images used in this section are sourced from the [Eye Tracker Instruction Manual](#).

To ensure accurate performance and prevent minor drifts in the pupil and corneal reflection (CR) thresholds, perform the ET Setup 10-15 minutes after powering the ET on.

- Open the QCT experiment in *Psychopy* (`task-qct_bold.psyexp` file).
 - Run the experiment by pressing the green play button.
 - Press enter to begin the *camera setup mode*.
 - The camera setup mode contains a view of one eye, and you can switch that view between two modes: one is the field-of-view of the ET, the second is an automatic zoom on the eye itself (or a random part if the eye is not visible).
 - To ease the setup of the ET, switch to the field-of-view mode in the camera setup mode by pressing the or arrow. This will allow you to adjust the ET position as the infrared camera provides feedback inside the scanning room on the projection screen.

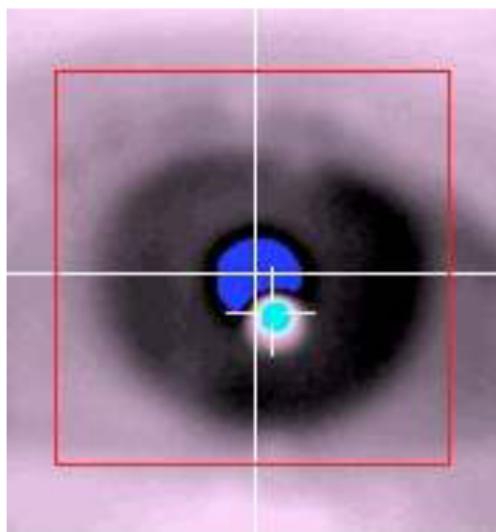
- Enter the scanning room and adjust the ET arm position and focus of the lens until the eye is fully visible. The right eye should be visible at the center of the coil's square window for the eye.

Adjusting the camera's field-of-view and focus

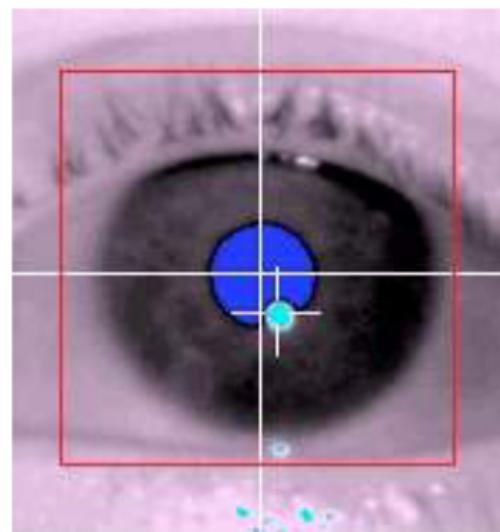
- To adjust the camera position, slightly unscrew the fixation locks of the camera arm, move the arm in search of the correct position, and tighten the locks again on the desired position.



- If the eye coverage is still inappropriate, realign the mirror frame position by sliding it along the rails attached to the coil. You may ask the participant to do it while inside the bore.
- If the eye coverage is still inappropriate, re-adjust the participant's head positioning inside the coil. You'll need to extract the bed outside of the bore for this by pressing the Home () button.
- If the eye coverage is still inappropriate, revise the vertical position of the infrared mirror with respect to the standard mirror (this will require new gloves and replacing the tape to stick the infrared mirror). Even a tiny adjustment can impact calibration and eye positioning.
- Repeat the previous steps until the eye is properly aimed and focused.
- If the image appears blurry, fine-tune the focus using the lens barrel. Refer to the example image below.

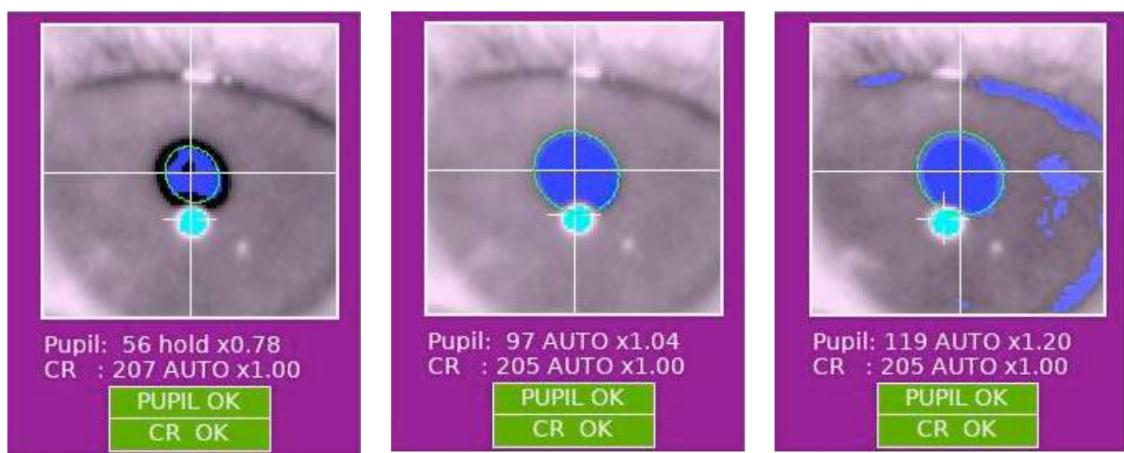


Poor Focus



Good Focus

- Press the A key to set the pupil and CR detection thresholds automatically.
- Fine-tune the pupil detection threshold using the and arrow keys if necessary. While checking the pupil/CR image and thresholding, ask the participant to look at the screen corners to verify correct detection even in extreme positions.



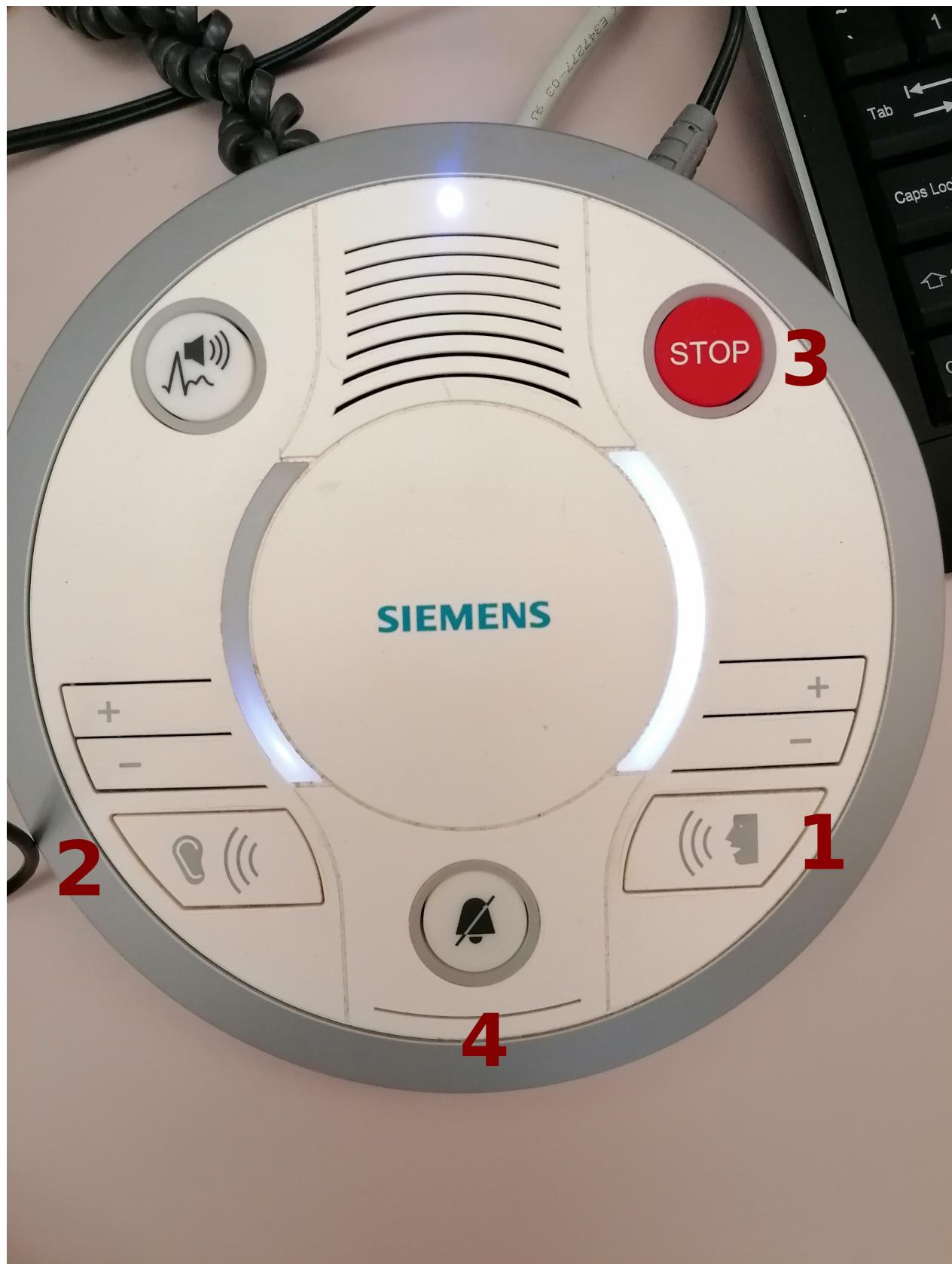
Threshold bias too low

Properly thresholded

Threshold bias too high

- As a last resort, you can also adjust the strength of the infrared light (emitter). This is the black box on the opposite side of the lens on the ET arm. Under the emitter there are two little screws. Unscrew, move the emitter front/back, check the contrast of the face image, re-screw.
- Switch the ET to *Eye camera* mode (zoomed in) and check the eye is still well covered by the view and the pupil is segmented.
- Check that two crosses appear on the eye.
- If the pupil is correctly seen, as well as the eye (indicated by the crosses following their movement), inform the participant that you are leaving the room, and that you are going to first check with them whether the speaker works well, immediately.
- Exit the camera mode by pressing Enter.

Check the communication with the participant



Emergency buttons

The  button (3) immediately stops the currently running sequence. The crossed-out bell button (4) stops the alarm if the participant actioned it.

- Make sure the speaker is audible (and not annoying) and confirm the participant's feedback. First, keep the speak mode button (1) pressed while you talk to the participant:

Hey [NAME], can you hear me well? Is the audio too loud or too low?

- Enable the feedback channel from the Scanning Room by pressing the listen mode button (2) once. Release the speak mode button (1) before you are ready to listen to participant responses.
- Set the volume control of your microphone and the participant's speaker by pressing the corresponding buttons.
- If this volume increase is not enough for the participant to hear you well, proceed as follow:
 - In the Siemens program, click on Configuration represented by a gear wheel () at the top right of the screen.
 - Click on *Configuration panel*
 - Under the section *Scan application*, locate the icon of the speaker and tune the volume to the maximum.
 - Click *Apply*

Running the scanning session

Familiarize with emergency procedures

You MUST know the security procedures in case of problem and keep yourself updated with changes. Some of the emergency procedures are found [here](#).

In addition to the brief guidelines given in these SOPs, further safety information is found in [REDACTED].

Before initiating the session

Double check the protocol with the correct phase-encoding direction was selected

For convenience, this is the session schedule (**today is 2023-10-25 17:05**):

session day	PE
1	2023-10-20 LR
2	2023-10-20 LR
3	2023-10-21 LR
4	2023-10-21 RL
5	2023-10-22 PA
6	2023-10-22 PA
7	2023-10-23 LR
8	2023-10-23 RL
9	2023-10-24 AP
10	2023-10-24 RL
11	2023-10-25 AP
12	2023-10-25 PA
13	2023-10-26 PA
14	2023-10-26 LR
15	2023-10-27 AP
16	2023-10-27 RL
17	2023-10-28 PA
18	2023-10-28 LR
19	2023-10-29 PA
20	2023-10-29 RL
21	2023-10-30 RL
22	2023-10-30 AP

session	day	PE
23	2023-10-31	AP
24	2023-10-31	AP
25	2023-11-01	RL
26	2023-11-01	PA
27	2023-11-02	AP
28	2023-11-02	RL
29	2023-11-03	PA
30	2023-11-03	AP
31	2023-11-04	PA
32	2023-11-04	AP
33	2023-11-05	LR
34	2023-11-05	LR
35	2023-11-06	LR
36	2023-11-06	RL

Report all observations in the session notes

It is easy to forget details about particular sessions, especially when so many sessions are acquired. They can however be very informative for quality control of your data or understand idiosyncrasies, so it is important to keep track of them. As such, please note any observation in the issue dedicated to collecting session notes that you should have opened in [the preparation of the session](#).

During the session

- Check in with the participant frequently, not necessarily only at the scripted points.
- Watch for motion and arousal state using the ET's camera. If you detect motion or the participant falls asleep at inadequate points, use the speaker to inform them.

Check experimental setup

DO NOT FORGET to check the readiness of the experimental setup at this point

Check the syncbox

- the box is on,
- Synchronization mode* is on,
- session has been started,
- volume count is reset to 0 out of 9999,
- USB* cable to [] is connected.
- Check the corresponding box in the issue collecting notes about the session.

Check the BIOPAC

- All cables are connected and not loose or hanging.
- The BIOPAC is turned on (switch it on if necessary).
- Check the corresponding box in the issue collecting notes about the session.

Check the GA

- the exhaust cap IS REMOVED
- the tubing coming from the scanning room is properly connected,
- the CO₂ BNC output is plugged through the filter to the BIOPAC AMI200, on input channel 3,
- the GA is on (switch it on if necessary),
- ensure the PUMP IS ON, and
- turn the pump's power knob to MAXIMUM position.
- Check the corresponding box in the issue collecting notes about the session.

Check the eye-tracker

- The ET computer is turned on (switch it on if necessary),
- The pupil is correctly detected (as described [here](#))
- Check the corresponding box in the issue collecting notes about the session.

Check [REDACTED]:

- has enough battery, and plug the power cord if necessary;
- USB cable to the MMBT-S Trigger Interface Box is connected;
- serial cable from the MMBT-S Trigger Interface Box is connected to the back of the SPT100D digital interface (gray block) of the BIOPAC;
- computer is ready, with psychopy open, and with the appropriate version of experiments; and
- leave the computer with a pleasant screen projecting (e.g., a gray background).
- Check the corresponding box in the issue collecting notes about the session.

Make sure to load the correct environment

- Deactivate conda (if active):

```
conda deactivate
```

- Load the new virtual environment: ``` shell source \$HOME/psychopyenv/bin/activate

Check █:

- has enough battery, and plug the power cord if necessary;
- computer is ready, with the *AcqKnowledge* software open and collecting data;
- check the ECG and RB signals, and fix unanticipated problems (e.g., the respiration belt needs to be fastened tighter);
- the *Amphetamine* app is running and keeping the computer unlocked while *AcqKnowledge* is working.
- Check the corresponding box in the issue collecting notes about the session.

When running multiple sessions back-to-back

- [] Restart a new session of the syncbox (within one session we usually see 9,000
 - [] Press the central button :fontawesome-solid-circle:{ .bluecolor } to stop
 - [] use the up :fontawesome-solid-caret-up:{ .bluecolor } and down :fontaweso
 - [] Press the central button :fontawesome-solid-circle:{ .bluecolor } again t
- [] In **AcqKnowledge**, make sure you stopped the previous recording and started a
- [] Start a *New examination* on the MR console:
 - [] Make sure all acquisitions are done,
 - [] close any open patient window,
 - [] find the patient in the system (or write new information for a new partic
 - [] right click on the patient and press `start new examination`.

Ensuring the quality of physiological signals

It is critical to check that physiological signals are looking good:

- Before starting the session, and
- from time to time within the session.

Thanks to César Caballero-Gaudés, Stefano Moia, Kristina Zvolanek, Elenor Morgenroth for the slide above¹ (<https://www.humanbrainmapping.org/i4a/pages/index.cfm?pageid=4055>)

Checking the RB

To ensure the best RB signal

Calibrate the RB with the tube unplugged while the participant is in the scanner (you may have to help the participant). Then, ask (and/or help) the participant to plug it back.

- The RB signal SHOULD NOT plateau (neither saturate at a peak value nor floor at the troughs). This means the RB is maxing out and it requires loosening.
- The envelope of your signal SHOULD remain approximately constant. If peaks drop or troughs rise, it might be a sign that the RB is too loose. Go back into the scanning room and tighten the RB.
- Check the corresponding box in the issue collecting notes about the session.

Checking the CO₂ signal

- The period of the CO₂ signal should remain constant. If it varies, the vacuum MAY be too low:
 - Check that the nasal cannula is correctly placed in the participant's nostrils.
 - Check that all the extension connections of the tube are air-tight
 - Check that the tube is not hanging at any point.
- The envelope of your signal SHOULD remain approximately constant. If the peaks diminish, it might be a sign that the participant is breathing through their mouth. In such a case, remind the participant to breathe through their nose.

Remind the participant they MUST breathe through their nose at all times

Hey [NAME],

Is everything okay?

I needed to ask you whether you are breathing through your nose because we are not recording sensible levels of CO₂.

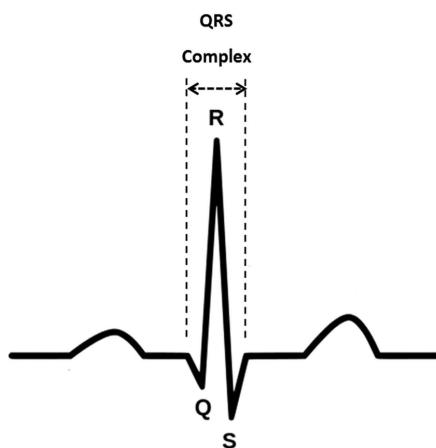
[WAIT FOR THEIR RESPONSE]

Thank you.

- Check the corresponding box in the issue collecting notes about the session.

Checking the ECG signal

- The period and the envelope of the signal should remain constant.
- We are placing the ECG electrodes in lead-1 mode, which should give an ECG signal that looks vaguely like the familiar QRS shape (see below). Typically, the signal does not look as neat as on the schema because the magnetic fields of the MR interfere with the electrodes (even if they are MR-compatible electrodes).



- Check the corresponding box in the issue collecting notes about the session.

Acquire a localizer (AAhead_scout)

- Indicate the participant that the scanning will soon start:

Tell the participant that we are starting

Hey [NAME], we are about to start our first scan run.

This is going to be a long session, so please make sure you are feeling as comfortable as you possibly can in there. Remember not to cross your legs or hold your hands together and check your back is also comfortable. I'm going to ask you to take a deep breath now, so I can check the respiration belt is properly set up. If it is too tight, please let me know.

[Allow a few moments for the participant to breathe while you check the recordings]

Okay, we seem to be able to track your respiration. Is the respiration belt too restraining? This is also a good moment to swallow, and to check your neck and head are in a comfortable position.

For this first part, all you have to do is stay still; you can relax and close your eyes if it helps.

Are you ready?

- Wait for the participant confirmation and set the speaker off afterward.
- Launch the AAhead_scout_64ch-head-coil protocol by pressing *Continue*.

Once the localizer is concluded:

- Drag and drop the image stack icon (something like , with an object on the top stack) onto the image viewer. That will open the localizer on the viewer.



- In the issue collecting notes about the session, check the box confirming that the localizer has been acquired.
 - If the quality looks good, check the box stating Localizer looked ok. If not, follow the paragraph below.

If the localizer presents very low quality

The localizer may present very low quality if the head-coil has not been properly initiated by the scanner

- In the issue collecting notes about the session, specifically under *anat* issues select the problem and describe it in detail in the anatomical scan notes section.
- Enter the scanning room, extract the participant from the scanner by pressing the home () button.
- Tell the participant that you need to reset the head coil
- Unplug and replug the head coil
- Check that the coil has been properly detected in the scanner's monitor
- Re-insert the participant in the scanner
- Re-run the AAhead_scout_{32,64}ch-head-coil protocol.

Acquire a high-resolution, anatomical image

- Launch the anat-T1w_mpimage protocol by pressing *Continue*.

While you are still running the MPRAGE sequence

- Open the parameters of the sequence named `fmap-phasediff_gre` and ensure that under *Contrast ↳ Reconstruction* the option *Magnitude et phase* is selected. This is crucial so that both the magnitude and the phase difference field map images are saved.
- Repeat the configuration of *Magnitude et phase* for all sequences name `fmap-epi_acq-bold_dir-{RL,LR,PA,AP}_*`.
- Repeat the configuration of *Magnitude et phase* for all sequences name `func-bold_task-{bht,qct,rest}_dir-{RL,LR,PA,AP}_cmrr_me4_sms4`.
- Open the `dwi-dwi_dir-{RL,LR,PA,AP}_279dir_monopolar` sequence and under the section *Diff.*, uncheck all the derivatives except for *Diff. Weighted Image*.
- Open the `fmap-epi_acq-b0_dir-{RL,LR,PA,AP}_*` sequences and under the section *Diff.*, uncheck all the derivatives except for *Diff. Weighted Image*.

- In the issue collecting notes about the session, check the box confirming that the `T1w` image has been acquired.
 - If the quality looks good, check the box stating `T1w looked okay`. If not, please follow [the instructions to repeat the scan](#) and report the problem in the session notes.

Acquire the dMRI EPI fieldmaps

- [Adjust the FoV](#) of the `fmap-epi_acq-b0_dir-{RL,LR,PA,AP}_6dir_monopolar*` sequences.
- Verify again the `fmap-epi_acq-b0_dir-{RL,LR,PA,AP}_6dir_monopolar` parameters under section *Diff.* All the derivatives MUST be unchecked except for *Diff. Weighted Image*.
- Inform the participant that the diffusion scan will follow.

Only for the participant of Cohort I

Hey Oscar, we are ready to proceed with the diffusion scan. The BIOPAC is functional and *AcqKnowledge* is properly registering the respiration belt and *ECG*. The gas analyzer is ON, but it is still warming up. The psychopy computer is ready. Are you ready?

Participant of Cohort II

Hey [NAME], the next block is a bit long. First, we will run four short sequences of less than one minute and then a long block of around 30 minutes.

You can close your eyes and even sleep if you wish.

I'm going to give you a short time (ten seconds or so) to swallow, and perhaps accommodate your back or your arms. However, please try not to move your head.

It is critical that you don't move, especially at all at the very beginning and the next 20 seconds after you hear the first blipping sounds.

Try to minimize swallowing and eye movements (for example, blinking) and maintain comfortable and shallow breathing. Remember to breathe through your nose, not through your mouth, so the expired CO₂ can be measured with the cannula.

Are you ready?

- Launch the DWI-EPI sequence `fmap-epi_acq-b0_dir-{RL,LR,PA,AP}_6dir_monopolar` for B_0 field mapping by pressing *Continue*.

While the fieldmaps are running:

- adjust the FoV** of the `dwi-dwi_dir-{RL,LR,PA,AP}_279dir_monopolar` sequence, and
- prepare the execution of the fixation program on the stimuli laptop (████), which will be played during the DWI by typing the following on a terminal:

Make sure to have the correct environment loaded before invoking the task

- Deactivate conda (if active):

```
conda deactivate
```

- Load the new virtual environment:

```
source $HOME/psychopyenv/bin/activate
```

```
cd ~/workspace/HCPH-fMRI-tasks  
python task-fixation_dwi.py
```

A modal dialog will ask you for the number of trial (automatically calculated, DO NOT modify) and the session number.

The following two steps MUST be executed in this order

- [] Drag and drop the modal dialog into the scanner's projector screen.
- [] Update the session number with the corresponding number.

At this point, the GA should have finished the warm-up so you can verify it is working

- Ask the participant to take three deep breathes, to then go back to a comfortable, normal respiration pace.
- Check on the *AcqKnowledge* window that the three breathes are distinctly registered (taking into account that there may be 10-25 seconds of delay because of the tubing).

Acquire the diffusion MRI run

- Verify again the dwi-dwi_dir-{RL,LR,PA,AP}_279dir_monopolar parameters under section *Diff*. All the derivatives MUST be unchecked except for *Diff. Weighted Image*.
- Inform the participant that before the long dMRI block, the ET must be calibrated.

Starting the dMRI block after calibrating the eye tracker

Hey [NAME], is everything alright thus far?

[Allow some time for response]

Before we start the long dMRI block, we need to calibrate the eye-tracker device, which follows your right eye during experiments.

You are going to see a round fixation point, and the point is going to move randomly over the screen space. Please follow it with your gaze, trying to look at it as stable as possible and without moving your head.

Are you ready?

- On the stimuli laptop (████), check the correct session number is set and hit *OK*.

The OK button MUST be clicked with this modal dialog on the projector's screen

Otherwise, the wrong screen will be selected by *Psychopy*

- Proceed with [the ET calibration](#). The ET control menu will appear after hitting *OK* on the modal dialog.
- Launch the diffusion dwi-dwi_dir-{RL,LR,PA,AP}_279dir_monopolar sequence by pressing *Continue*.

While the dMRI is running:

- [Adjust the FoV](#) for the following sequence (GRE fieldmap).

When the dMRI concludes:

- Wait for the current task program to finish on ████████.

If you must interrupt the task program, check first that the EDF files have been copied.

Acquire the GRE fieldmap

- In the corresponding issue for the collection of notes about the session, check the box confirming that the diffusion sequence has been acquired. Don't forget to report any observations there.

- Launch the GRE (*phase difference*) sequence `fmap-phasediff_gre` for B_0 field mapping by pressing *Continue*.

While the GRE fieldmap is running:

- Adjust the FoV** for the positive-control-task (`func-bold_task-qct_dir-{RL,LR,PA,AP}_cmrr_me4_sms4`) fMRI sequence,
- verify that in the next sequence parameters under *Contrast>Reconstruction* the option *Magnitude et phase* is selected,
- verify the *Number of measurements* with respect to the **task's timing** (2min 38s),
- verify that the EDF file with the ET recordings corresponding to the dMRI have been stored, and
- prepare the execution of the QCT by executing the following on a terminal:

Make sure to have the correct environment loaded before invoking the task

- Deactivate conda (if active):

```
conda deactivate
```

- Load the new virtual environment:

```
source $HOME/psychopyenv/bin/activate
```

```
cd ~/workspace/HCPH-fMRI-tasks
python task-qct_bold.py
```

A modal dialog will ask you for the number of trial (automatically calculated, DO NOT modify) and the session number.

The following two steps MUST be executed in this order

- [] Drag and drop the modal dialog into the scanner's projector screen.
- [] Update the session number with the corresponding number.

- In the issue collecting notes about the session, check the boxes confirming that each fieldmap has been acquired and that you check that the physiological signal are still recording. Don't forget to report any observations there.

Acquire the functional MRI block

- Inform the participant about the fMRI block

Starting the fMRI block

Hey [NAME], we are now to move into measuring the activity of your brain.

Is everything alright thus far?

[Allow some time for response]

Before we start, we are going to check if the eye-tracker is still accurate.

You are going to see a fixed, round fixation point. Please focus your gaze on it, trying to look at it as stable as possible and without moving your head.

If the eye-tracker is very off, we will re-calibrate it.

Are you ready?

- Wait for confirmation, respond to follow-up comments.
- On the stimuli laptop (████), check the correct session number is set and hit *OK*.

The OK button MUST be clicked with this modal dialog on the projector's screen

Otherwise, the wrong screen will be selected by *Psychopy*

- Initiate the ET drift correction procedure.** The ET control menu will appear after hitting *OK* on the modal dialog.

Quality-control task (QCT)

- Verify that the task's program is awaiting the scanner's trigger to start.
- Inform the participant that we will proceed with the quality-control task (QCT). Repeat task instructions.

Starting the positive control task

Hey [NAME], thanks for your collaboration with the eye tracking calibration.

The following block will collect some behavioral data and requires your collaboration. You will be exposed to several activities.

Whenever you see a red circle, please fix your gaze on it, wherever it is shown on the screen. If the red circle moves, we ask you to follow it with your eyes.

Some other times, you'll see either "RIGHT" or "LEFT" written on the screen. During those times, please tap your thumb and the other fingers of your right or left hand as indicated on the screen.

Before we start, please leave the alarm button on your tummy to free your hand for finger tapping. Please do not hesitate to grab it in case you need to squeeze it.

- Launch the `func-bold_task-qct_dir-{RL,LR,PA,AP}__cmrr_me4_sms4` protocol by pressing *Continue* .

- Confirm that the task program starts on █ after the calibration scans.

While the QCT is running:

- Adjust the FoV** for the following sequence,
- verify the *Number of measurements* with respect to the **task's timing** (20min 6s), and
- double check that it has the setting *Magnitude et phase* selected in the drop-down menu under *Contrast>Reconstruction*.

Once the QCT has concluded:

- Wait for the current task program to finish on █.

If you must interrupt the task program, check first that the **EDE** files have been copied.

- In the corresponding issue for the collection of notes about the session, check the box confirming that the quality control task **fMRI** has been acquired and that you check that the physiological signals are still being recorded. Don't forget to report any observations there.

BOLD fieldmaps

- Launch the **BOLD-EPI** sequence **fmap-epi_acq-bold_dir-{RL,LR,PA,AP}_cmrr_me4_sms4** for B_0 field mapping by pressing *Continue*.

While the BOLD fieldmaps are running:

- Adjust the FoV** for the following sequence,
- verify the *Number of measurements* with respect to the **task's timing** (20min 6s), and
- double check that it has the setting *Magnitude et phase* selected in the drop-down menu under *Contrast>Reconstruction*.

Do not attempt to initiate the next task program before fieldmaps conclude

The BOLD fieldmaps will be sending trigger pulses that will make the process almost impossible.

Once the BOLD fieldmaps are concluded:

- Prepare the execution of the **RSfMRI** by executing the following on a terminal:

Make sure to have the correct environment loaded before invoking the task

- Deactivate conda (if active):

```
conda deactivate
```

- Load the new virtual environment:

```
source $HOME/psychopyenv/bin/activate
```

```
cd ~/workspace/HCPH-fMRI-tasks  
python task-rest_bold.py
```

A modal dialog will ask you for the number of trial (automatically calculated, DO NOT modify) and the session number.

The following steps MUST be executed in this order

- [] Drag and drop the modal dialog into the scanner's projector screen.
- [] Update the session number with the corresponding number.

- On the stimuli laptop (█████), check the correct session number is set and hit *OK*.

The OK button MUST be clicked with this modal dialog on the projector's screen

Otherwise, the wrong screen will be selected by *Psychopy*

Resting state fMRI

- Inform the participant:

Drift-check ET before continuing

Thanks [NAME], that was a short behavioral task.

Before moving on, we will run another check of the eye tracker, please focus your sight on the fixation point.

Is everything alright?

- Wait for confirmation, respond to follow-up comments
- Initiate the ET drift correction procedure.** The ET control menu must have appeared after hitting *OK* on the modal dialog.
 - Once the ET is calibrated, verify that the task is left and awaiting for the sequence's trigger to start.
- Inform the participant that the next sequence is resting-state fMRI (RSfMRI).

Starting the resting-state block

Hey [NAME], we are about to start resting-state fMRI.

For this scan, all you have to do is stay still, and look at the movie. Please do not close your eyes, and it is particularly critical that you don't move at all in the initial moments of the acquisition block.

Are you ready?

- Launch the RSfMRI sequence `func-bold_task-rest_dir-{RL,LR,PA,AP}_cmrr_me4_sms4` by pressing *Continue*.
- Confirm that the task program starts on after the calibration scans.

While the RSfMRI is running:

- [Adjust the FoV](#) for the following sequence,
- verify the *Number of measurements* with respect to the [task's timing](#) (5min 41s), and
- double check that it has the setting *Magnitude et phase* selected in the drop-down menu under *Contrast>Reconstruction*.

Once the RSfMRI is concluded:

- Wait for the current task program to finish on .

If you must interrupt the task program, check first that the EDF files have been copied.

- In the corresponding issue for the collection of notes about the session, check the box confirming that the quality control task fMRI has been acquired and that you check that the physiological signals are still being recorded. Don't forget to report any observations there.
- Prepare the execution of the BHT by executing the following on a terminal:

Make sure to have the correct environment loaded before invoking the task

- Deactivate conda (if active):

```
conda deactivate
```

- Load the new virtual environment:

```
source $HOME/psychopyenv/bin/activate
```

```
cd ~/workspace/HCPH-fMRI-tasks  
python task-bht_bold.py
```

A modal dialog will ask you for the number of trial (automatically calculated, DO NOT modify) and the session number.

The following steps MUST be executed in this order

- [] Drag and drop the modal dialog into the scanner's projector screen.
- [] Update the session number with the corresponding number.

- On the stimuli laptop (█████), check the correct session number is set and hit *OK*.

The OK button MUST be clicked with this modal dialog on the projector's screen

Otherwise, the wrong screen will be selected by *Psychopy*

Breath-holding task (BHT)

- Inform the participant:

Drift-check ET before continuing

Thanks [NAME], that was a long behavioral task.

Before moving on, we will run another check of the eye tracker, please focus your sight on the fixation point.

Is everything alright?

- Wait for confirmation, respond to follow-up comments
- Initiate the ET drift correction procedure.** The ET control menu must have appeared after hitting *OK* on the modal dialog.
 - Once the ET is *drift-checked* and no calibration is needed, verify that the ET menu is removed and the task program awaits for the sequence's trigger to start.
- Inform the participant that the next sequence is breath-holding task fMRI. Repeat the instructions for the task.

Starting the breath-holding task

Hey [NAME], we will proceed now with a breath-holding task.

I remind you that you have to breathe following the cues of the colored rectangle.

Green means "BREATHE IN", orange means "BREATHE OUT" and red means "HOLD YOUR BREATH".

Remember to not follow the breathing instructions during the first block and to exhale the small amount of air you have remaining at the end of the hold.

Are you ready?

- Launch the `func-bold_task-bht_dir-{RL,LR,PA,AP}_cmrr_me4_sms4` sequence by pressing *Continue*.
- Confirm that the task program starts on [] after the calibration scans.

While the BHT is running:

- Determine whether there is enough time to run the anatomical T2-weighted run. If so,
 - [adjust the FoV](#) for the following sequence; or alternatively
 - wait for the sequence to complete.

Once the BHT is concluded:

- Wait for the current task program to finish on [].

If you must interrupt the task program, check first that the **EDF** files have been copied.

- Check the box confirming that it has been acquired in the issue collecting notes about the session. Don't forget to report any observations there.

Acquire a T2w image (if time permits)

- Launch the `anat-T2w_flair` protocol by pressing *Continue*, or
- skip the T₂-weighted collection.

Stop physiology collection

The following step MAY be done while the T2w is running.

- Stop the *AcqKnowledge* recording on the [] computer.

The following steps MAY be done while the T2w is running IF (and only if) there's no back-to-back session upon conclusion of the current

- Switch the BIOPAC MP160 module off.
- Turn off the pump of the GA.
- Switch the GA off.
- Put the exhaust and inlet caps back.

Concluding the session

- Inform the participant:

Session is finished

Thanks [NAME], the session has concluded and we will shortly let you out of the scanner.

Session completed

The exam is over, you can proceed with the [tear-down protocol](#).

Session tear-down

Showing the participant out

- Enter the scanner room, and announce yourself to the participant:

Hi [NAME], thanks a lot for your collaboration. We will get you out in a second.

- Extract the participant [following the standard procedure](#).
- Unplug the head coil from the bed connector, lift the lever that releases the upper part of the coil and put it aside (e.g., inside the bore or on a chair next to the scanner).
- Remove the tape band across the coil and touching the participants forehead.
- Lift the nasal cannula and put it away so the participant does not get tangled.
- Assist the participant to remove the padding elements around their head.
- Help the participant sit down.
- Instruct the participant to remove the earplugs and dispose of them.
- Ask them about the experience:

Get feedback about the session from the participant

[NAME], how was your experience? Have you been able to feel comfortable throughout the session? What advice, indication do you feel we could've provided you for a better experience?

- Disconnect the tube from the RB and then lift the velcro attachment to remove the RB.
- Prepare the belt on the bed to be removed from the room when you show the participant out.
- Help the participant carefully remove the ECG leads.
- Disconnect the three ECG terminals from the cable and put them in their pouch.
- Disconnect the last section of the cannula and dispose of it in the trash can.
- Help the participant step down and accompany them out to the control room.
- Help the participant recover their personal belongings and change clothes if necessary.
- Solicit more feedback on participant's comfort for future sessions.
- Ask the participant to fill out the After scan part of the covariates collection on the issue you opened [earlier](#).
- Solicit tickets and receipts for transportation.
- Give the participant the corresponding compensation for the participation and transportation.
- Ask the participant to sign the receipt of the amount of the financial compensation.

Clearing up the Scanning Room

ET arm, ET cables, infrared mirror and stimuli screen

- Unplug the two cables (signal and power) connected to the ET arm. Put their extremities aside far from the scanner.
- Agree with another experimenter, who will exit the room, sit on the other side of the access tubes in the Control Room, and pull cables (fiber and power of the ET) and tubes (RB and GA) out of the room. At the same time, you carefully feed them so they do not suffer abrasion from touching the edges of the tube.

Extracting the cables and tubes requires two experimenters

- The experimenter currently outside in the Control Room will re-enter the Scanner Room with the plastic bag of the mirror and a fresh pair of gloves and will leave them prepared on the bed.
- Remove the mirror frame from its rails mounted on the head coil and lay it on the bed.
- Put the gloves on and detach the infrared mirror from the standard mirror.

The infrared mirror MUST be manipulated with clean gloves at all times.

- Immediately insert the infrared mirror back into its plastic pouch.
- Take the pouch containing the infrared mirror outside to the Control Room and place it back in its designated box, with extreme care.
- Clean the standard mirror removing all residues of glue from the scotch tape.
- Re-attach the mirror to the coil's frame.
- Take the projector's screen off and store it in its designated shelf.
- Disconnect the ECG cable from the filter of the access panel, roll the cable.

Readyng the scanner for the next session

Every setting altered for the experiment MUST be put back to its original status at the end of the experiment (e.g., position of the bed, coil, emergency button, padding elements, etc.)

- Put the used bed-sheet and the blanket inside the soiled linen bag.

Put them away in the trash if they are disposable

- Dispose all single-use sanitary protections.
- Put the pillows back in their designated storage places.

- Remove the head coil and put it in the scanner's bore.
- Remove the back padding elements and put them back in their designated storage.
- Reinstall the spine coil.
- Wipe the bed and the head coil (bottom and upper parts).

Cleaning wipes are available on shelf in the Scanning Room.

- Lock the head coil back with its bottom part without plugging the connectors.
- Put the head coil away with the other head-coils on the shelf next to the scanner.

If the next user is already there or you know the current coil will be also used in the next session, plug it back into the bed socket.

- Return the bed to its *Home* position by pressing the button ([more info](#)).
- Take the ET arm outside to the Control Room and place it in a stable place.
- Take the ECG electrodes, ECG cable, the RB, and the plexiglass panel outside to the control room.
- Exit and close the external door.

Clearing up the Control Room

Finalize the *boxing* of the ET elements

- Put the lens cover.

- Unscrew the ET lens, while ALWAYS keeping one hand under the lens while screwing/unscrewing it and put it back into its pouch.



- Store the ET arm in its designated box.

REMEMBER | the infrared mirror is inside that box already: DO NOT crush the mirror.

Finalize the *boxing* of other physiological recording instruments

- Store the ECG cable and the pouch with the ECG leads in its designated box / storage.
- Carefully roll the fiber and power cable of the ET, and place them in the rolling table of the ET PC.
- Carefully roll the GA tube and put it in its designated bag.
- Carefully roll the RB tube and put it in its designated bag.
- Disconnect the MMBT-S Interface, and the two corresponding cables (pink USB, 25-pin parallel), and insert them in their designated bags.
- Remove the cable connecting the GA to the AMI100D module of the BIOPAC, roll it and put it in its designated bag.
- Put the GA and the corresponding cables in the designated box.
- Disconnect and bag the remaining cables connected to the BIOPAC:
 - Ethernet to the [redacted] computer.

- Power cord.
- Retrieve and bag the *AcqKnowledge USB License Key* from the [REDACTED] computer.
- Store the *fMRI box*, BIOPAC and GA boxes back in room [REDACTED].

Finalizing with the ET's PC

- Exit the EyeLink 1000 Plus Host PC application by pressing Ctrl+Alt+Q on the ET PC and next click on the Shutdown button from the File Manager toolbar.
- Secure the rolled cable with the scotch tape on the ET PC Tower.
- Take the ET PC Tower and the plexiglass back into room [REDACTED].
- Switch the projector off before exiting room [REDACTED].

Finalizing the support laptops

- Unplug from [REDACTED] the USB cable coming from the SyncBox.
- Switch the SyncBox off, and make sure you leave it connected exactly as you found it.
- Unplug from [REDACTED] the HDMI cable from the display switch.
- Check that you leave the display switch as you found it.
- Switch off the [REDACTED] computer.
- Exit the *Amphetamine* session and lock the screen of the [REDACTED] computer.

Turn off the MRI system if no more sessions are scheduled afterward

It is critical to follow the steps in order, ensuring each step is completed before proceeding further



- Turn off the satellite station ([REDACTED], the computer on the left side of the control desk)

- Turn off the control station ([] , the computer on the right side of the control desk)
- Push the blue button displaying an overdotted circle and the SYSTEM OFF label above, which is found right above the key
- Turn the key into the *closed lock* position ()

Emergency procedures

Reminder: Phone number of internal emergency services can be found in the agenda of all the phones of the hospital.

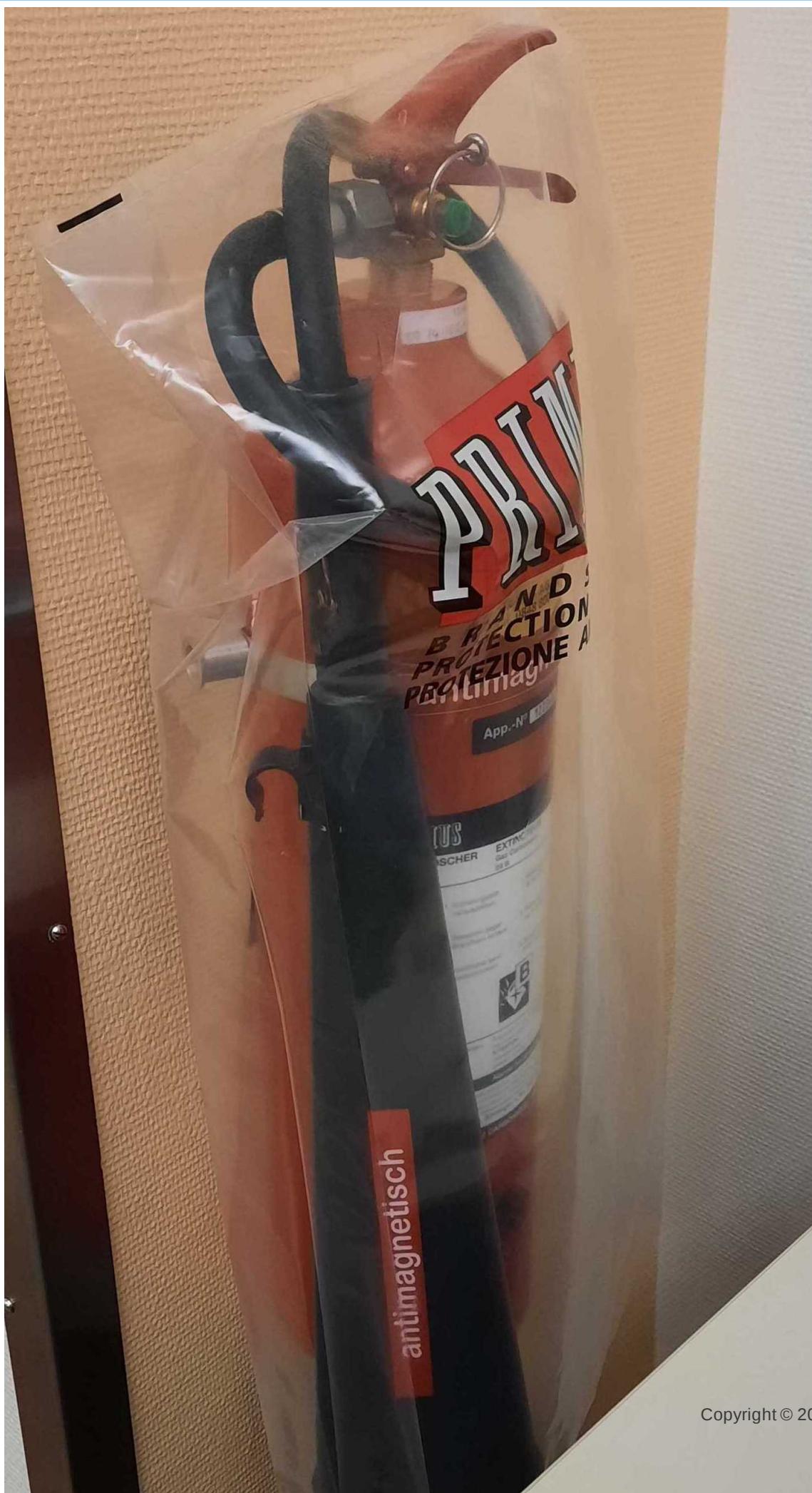
Fire in the scanning room

- Immediately call the internal firefighter service at ##-##.
 - Enter in the MRI room and cut the electricity in the MRI room by pressing the red button next to the entrance.

Cutting electricity will NOT turn off the magnetic field!

- Remove the subject from the scanner's room, applying the [manual extraction procedure described below](#).
 - Close the scanner's room.
 - Retrieve the [MR-compatible extinguisher](#) from its designated corner of the control room (see picture below) and put it in front of the scanning room.

Conventional extinguishers MUST NOT be entered in the scanning room because the magnetic field is still active



Emergency quench

The quench button is to be used only in the case of an emergency in which a person is injured and the only safe way to avoid further injury is to decrease the magnetic field strength of the magnet.

- Lift the security cover to free the *red, mushroom-shaped button* with the STOP word written on it, and push it.



Fire in the scanner's room does not justify quenching unless the high field poses a direct threat to a person's health

Participant set the alarm

If at any point the participant rings the alarm, you **MUST** check on the participant IMMEDIATELY with the scanner's speaker system.

- Press the speaker button (1 in the picture below) and ask if everything is alright. It is possible that the participant triggered the alarm by mistake.



Pressing the speaker button (1) or the crossed-bell button (4) will turn the alarm off and open the speaker line to talk to the participant.

- Assess the participant and the situation by asking them what is wrong and checking the camera inside the room and the scanner's console.

If you can anticipate that the participant will need to be retrieved

Initiate the extraction of the bed from the scanner console using the *Room in* menu (lower left corner of the screen), and then click on the *home* () button.

Alarm event requires further safety procedures

- Enter the scanning room if you do not get a response or the answer is unclear.

If there is an impending risk to the participant's health and it is safe for you and other operators to intervene, take actions to avert the dangerous situation.

For example, if the participant is choking because of the accidental occlusion of their respiratory ways after the displacement of some experimental instrument or sensor, immediately extract them from the scanner's bore with the fastest procedure available to you and remove the occluding instruments.

Similarly, suppose the participant suffers an acute panic attack and starts violently and uncontrollably shaking on the table. In that case, you will first lift the security side rails of the bed and securely restrain the participant further within the scanning table if necessary. This is critical to preempt their body from falling off the table while the head coil is still attached. Only when you can safely do so, extract them from the bore and remove the head coil.

Participant possibly needs to be retrieved but there isn't impending risk to their health

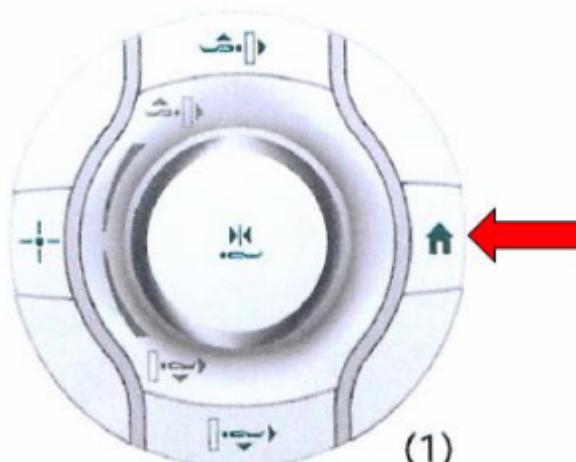
- If the alarm is still blaring, press the large, circular button at either side of the scanner's bore.



- Make the participant aware that you entered the room and ask them what is wrong.

If the participant is unresponsive, extract them from the scanner's bore using the standard procedure (the *Home* button). In case you previously cut the electricity or failure of the standard procedure, follow the manual procedure described in the first steps of [manual extraction protocol](#).

- Determine whether the participant can continue the session after some comforting or information or if it must be stopped at that point (e.g., the participant is feeling claustrophobic and cannot continue).
- If the session must be stopped, or you determine it is necessary to extract the participant before making that decision, hit the "Home" button to bring the participant outside the



scanner's bore quickly.

In case you feel unsafe

If you feel unsafe for any reason (for example, because a patient behaves aggressively or threatens you), CALL SECURITY at ##-##-##.

Technical difficulties

If you are facing technical difficulties:

- Seek help from anyone on the BH7 floor.
- If you still have problems or didn't find anyone (e.g., scanning on a weekend), call the ER's [MRI](#) staff at ##-##-##.

A person requires medical attention

At any moment, you may determine that the participant will require medical attention:

- The participant's health has been threatened or is actively at risk (e.g., elevated heart frequency, lack of pulse, respiratory issues, unconsciousness, dizziness, unsteadiness, etc.)

- The participant is unresponsive
- The participant reports feeling unwell and needs attention
- You think they may need medical attention but you are unsure.

If you determine that someone needs medical attention, call the resuscitation unit ##-###

The resuscitation unit ##-### is the number to call in any case, even if the participant is not in life-threatening condition.

The phone number of the emergency services can be found on all the phones at [CHUV](#).

After you called the resuscitation unit:

- Press on the heart button —(1) in the picture below— on the wall, after lifting the security lid.

The heart button (1) initiates a bea

In case you pressed the heart button by mistake, turn it off by pressing the adjacent green button (2).

- If the participant remains in the scanning room, re-enter the room and proceed with the [manual extraction protocol](#).

Danger

If the resuscitation team needs to shock the participant for cardiac resuscitation, it must never be done on the MR table.

Manual extraction procedure

- If the bed is inside the bore:
 - Unlock the manual retrieval of the scanner's bed
 - Pull the bed all the way out of the bore
 - Lock the manual retrieval back
- Lift the table's breaks locking the wheels
- Lift the manual lock of the table's attachment to the bore.
- Pull the bed out of the scanning room
- Reassess the participant's health in the control room and determine a course of action.

Resetting the scanner's table after it's been manually detached

- Dock the table onto the scanner's bore by insert the arrow-shaped prong into the docking bay.
- Wait for the MRI screen to indicate it is ready for docking, push down the right attachment pedal with your foot for locking.
- Simultaneously press the up and down buttons to activate the automatic recalibration of the table.

Immediately report incidents

MRI coordinators must be informed

Once the situation is resolved, and before anything else, send an email to [REDACTED] and [REDACTED]. Make sure to report any potential risk you can anticipate to clinical activity the following day.

Data management

Before data acquisition (storage preparation)

DataLad must be version 0.19 or later

This project maintains data under version control thanks to *DataLad*¹ (<https://doi.org/10.5281/zenodo.808846>). For instructions on how to setup *DataLad* on your PC, please refer to the [official documentation](https://handbook.datalad.org/en/latest/intro/installation.html) (<https://handbook.datalad.org/en/latest/intro/installation.html>) . When employing high-performance computing (HPC), we provide some specific guidelines.

Please read the [DataLad Handbook](https://handbook.datalad.org/en/latest/index.html) (<https://handbook.datalad.org/en/latest/index.html>), especially if you are new to this tool

Creating a *DataLad* dataset

- Designate a host and folder where data will be centralized. In the context of this study, the primary copy of data will be downloaded into <hostname>, under the path /data/datasets/hcph-pilot-sourcedata for the piloting acquisitions and /data/datasets/hcph-sourcedata for the experimental data collection.
- Install the bids *DataLad procedure* provided from this repository to facilitate the correct intake of data and metadata:

```
PYTHON_SITE_PACKAGES=$( python -c 'import sysconfig; print(sysconfig.get_python_lib())' )\nln -s <path>/code/datalad/cfg_bids.py ${PYTHON_SITE_PACKAGES}/cfg_bids.py
```

DataLad's documentation does not recommend this approach

For safety, you can prefer to use *DataLad*'s recommendations and place the cfg_bids.py file in some of the suggested paths.

- Check the new *procedure* is available as bids:

```
$ datalad run-procedure --discover\n  cfg_bids (/home/oesteban/.miniconda/lib/python3.9/site-packages)\n  cfg_yoda (/home/oesteban/.miniconda/lib/python3.9/site-packages)\n  cfg_metadatatypes (/home/oesteban/.miniconda/lib/python3.9/site-packages)\n  cfg_text2git (/home/oesteban/.miniconda/lib/python3.9/site-packages)\n  cfg_no annex (/home/oesteban/.miniconda/lib/python3.9/site-packages)
```

Learn more about the [YODA principles \(DataLad Handbook\)](#) (<https://handbook.datalad.org/en/latest/basics/101-127-yoda.html>)

- Create a *DataLad* dataset for the original dataset:

```
cd /data/datasets/  
datalad create -c bids hcph
```

- Configure a [RIA store](#) (https://handbook.datalad.org/en/latest/beyond_basics/101-147-riastores.html), where large files will be pushed (and pulled from when installing the dataset in other computers)

Creating a RIA sibling to store large files

```
cd hcph  
datalad create-sibling-ria -s ria-storage --alias hcph \  
    --new-store-ok --storage-sibling=only \  
    "ria+ssh://<username>@<hostname>:<path>/dataset/"
```

- Configure a [GitHub sibling](#) (<https://handbook.datalad.org/en/0.15/basics/101-139-hostingservices.html>), to host the Git history and the annex metadata:

Creating a GitHub sibling to store DataLad's infrastructure and dataset's metadata

```
datalad siblings add --dataset . --name github \  
    --pushurl git@github.com:<organization>/<repo_name>.git \  
    --url https://github.com/<organization>/<repo_name>.git \  
    --publish-depends ria-storage
```

Client side operations (when consuming the data)

Installing the *DataLad* dataset

Wherever you want to process the data, you'll need to `datalad install` it before you can pull down (`datalad get`) the data. To access the metadata (e.g., sidecar JSON files of the BIDS structure), you'll need to have access to the git repository that corresponds to the data (https://github.com/<organization>/<repo_name>.git) To fetch the dataset from the RIA store, you will need your SSH key be added to the authorized keys.

Getting access to the RIA store

These steps must be done just once before you can access the dataset's data:

- Create a secure SSH key (<https://docs.github.com/en/authentication/connecting-to-github-with-ssh/generating-a-new-ssh-key-and-adding-it-to-the-ssh-agent>) on the system(s) on which you want to install the dataset.
- Send the SSH public key you just generated (e.g., `~/.ssh/id_ed25519.pub`) over email to Oscar at `*@***.`
- Install and get the dataset normally:

Installing the dataset without fetching data from annex
Installing the dataset and fetch all data from annex, with 8 parallel threads

```
datalad install https://github.com/<organization>/<repo_name>.c
```

```
datalad install -g -J 8 https://github.com/<organization>/<repo_nam
```

Synchronizing your *DataLad* dataset

Once the dataset is installed, new sessions will be added as data collection goes on. When a new session is added, your *DataLad* dataset will remain at the same point in history (meaning, it will become out-of-date).

- Pull new changes in the git history. *DataLad* will first fetch Git remotes and merge for you.

```
cd hcph-dataset/ # ---- cd into the dataset's path
datalad update -r --how merge
```

- If you need the data, now you can get the data as usual:

```
find sub-001/ses-pilot019 -name "*.nii.gz" | xargs datalad get
```

Adding data or metadata

- Use `datalad save` indicating the paths you want to add, and include `--to-git` if the file contains only metadata (e.g., JSON files).

Adding data files (e.g., NIfTI and compressed TSV files)
Adding metadata files

```
find sub-001/ses-pilot019 -name "*.nii" -or -name "*.nii.gz" -o
xargs datalad save -m '"add(pilot019): new session data (N)
```

```
find sub-001/ses-pilot019 -name "*.json" -or -name "*.tsv" -or
xargs datalad save -m '"add(pilot019): new session metadata (M)
```

HPC users - instructions to install *DataLad*

When HPC is planned for processing, *DataLad* will be required on that system(s).

- Start an interactive session on the HPC cluster

Do not run the installation of *Conda* and *DataLad* in the login node

HPC systems typically recommend using their login nodes only for tasks related to job submission, data management, and preparing jobscripts. Therefore, the execution of resource-intensive tasks such as *fMRIprep* or building containers on login nodes can negatively impact the overall performance and responsiveness of the system for all users. Interactive sessions are a great alternative when available and should be used when creating the *DataLad* dataset. For example, in the case of systems operating *SLURM*, the following command would open a new interactive session:

```
srun --nodes=1 --ntasks-per-node=1 --time=01:00:00 --pty bash -i
```

- Install *DataLad*. Generally, the most convenient and user-sandboxed installation (i.e., without requiring elevated permissions) can be achieved by using *Conda*, but other alternatives (such as *lmod*) can be equally valid:

Install *DataLad* with *Conda*Install *DataLad* in HPC with *lmod* enabled

- Get and install *Conda* if it is not already deployed in the system:

```
wget https://repo.anaconda.com/miniconda/Miniconda3-latest
bash Miniconda3-latest-Linux-x86_64.sh
```

- Install *DataLad*:

```
conda install -c conda-forge -y "datalad>=0.19" datalad-co
```

- Check the availability and dependencies for a specific Python version (here we check 3.8.2):

```
module spider Python/3.8.2
```

- Load Python (please note `ml` below is a shorthand for `module load`)

```
ml GCCcore/9.3.0 Python/3.8.2
```

- Update `pip`:

```
python -m pip --user -U pip
```

- Install `DataLad`:

```
python -m pip install --user "datalad>=0.19" datalad-container
```

- Check `datalad` is properly installed, for instance:

```
$ datalad --version
datalad 0.19.2
```

DataLad crashes (Conda installations)

`DataLad` may fail with the following error:

```
ImportError: cannot import name 'getargspec' from 'inspect' (/home/users/cpro...
```

In such a scenario, create a `Conda` environment with a lower version of Python, and re-install `datalad`

```
conda create -n "datalad" python=3.10
conda activate datalad
conda install -c conda-forge datalad datalad-container
```

- Configure your Git identity settings.

```
cd ~
git config --global --add user.name "Jane Doe"
git config --global --add user.email doe@example.com
```

Post-session retrieval and BIDS

Within 48h after the FIRST session

Anatomical images must be screened for incidental findings within 48h after the first session

- Send the T1-weighted and T2-weighted scan to [REDACTED] for screening and incidental findings.
- Indicate on [our recruits spreadsheet \(/redacted.html\)](#) that the participant's first session has been submitted for screening.
- Wait for response from [REDACTED] and note down the result of the screening in our [our recruits spreadsheet \(/redacted.html\)](#).

To do so, you'll need to first [download the data from PACS](#) and then [convert the data into BIDS](#).

What to do when there are incidental findings

- Discuss with [REDACTED] how to proceed with the participant.
- Exclude the participant from the study if [REDACTED] evaluates they don't meet the participation (inclusion and exclusion) criteria.

Within one week after the completed session

Download the data from the [PACS](#) with *PACSMAN* (only authorized users)

- Log-in into the *PACSMAN* computer (**)
- Mount a remote filesystem through sshfs:

```
sshfs <hostname>:/data/datasets/hcpp-hcph-pilot-sourcedata \
      $HOME/data/hcpp-hcph-pilot \
      <args>
```

- Edit the query file `vim $HOME/queries/last-session.csv` (most likely, just update with the session's date)

```
mydata-onesession.csv
```

```
PatientID,StudyDate
2022_11_07*,20230503
```

- Prepare and run *PACSMAN*, pointing the output to the mounted directory.

```
pacsmen --save -q $HOME/queries/last-session.csv \
--out_directory $HOME/data/hcph-pilot/ \
--config /opt/PACSMAN/files/config.json
```

- Remove write permissions on the newly downloaded data:

```
chmod -R a-w $HOME/data/hcph-pilot/sub-01/ses-*
```

- Unmount the remote filesystem:

```
sudo umount $HOME/data/hcph-pilot
```

Retrieve physiological recordings (from [])

Copy original DICOM datasets into the archive of Stockage hOrus

- Setup a cron job to execute automatically the synchronization:

```
crontab -e
[ within your file editor add the following line ]
0 2 * * * rsync -avurP /data/datasets/hcph-pilot-sourcedata* <|
```

Within two weeks after the completed session

Convert imaging data to BIDS with *HeuDiConv*

We use *HeuDiConv* to convert from the DICOM format generated by the scanner. In addition, starting from the piloting session five, we abide by *ReproIn conventions*. To support backward compatibility (and some extra, currently unsupported features by the original heuristic file), we have our own heuristic file.

Our custom heuristic file

Our heuristic file largely derives from *ReproIn's* at the time of writing (<https://github.com/nipy/heudiconv/blob/55524168b02519bbf0a3a1c94caf29a419728a0/heudiconv/heuristics/reproin.py>). The heuristic has a `protocols2fix: dict[str | re.Pattern[str], list[tuple[str, str]]]` (lines 113-148), where replacement patterns to permit backward compatibility are written.

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```
517 # emacs: -*- mode: python; py-indent-offset: 4; indent-tabs-
518 # vi: set ft=python sts=4 ts=4 sw=4 et:
519 #
520 # Copyright 2023 The Axon Lab <theaxonlab@gmail.com>
521 #
522 # Licensed under the Apache License, Version 2.0 (the "License");
523 # you may not use this file except in compliance with the License.
524 # You may obtain a copy of the License at
525 #
526 #     http://www.apache.org/licenses/LICENSE-2.0
527 #
528 # Unless required by applicable law or agreed to in writing,
529 # distributed under the License is distributed on an "AS IS"
530 # WITHOUT WARRANTIES OR CONDITIONS OF ANY KIND, either express
531 # or implied. See the License for the specific language governing
532 # permissions and limitations under the License.
533 #
534 # We support and encourage derived works from this project,
535 # about our expectations at
536 #
537 #     https://www.nipreps.org/community/licensing/
538 #
539 # STATEMENT OF CHANGES: This file is derived from sources listed
# and this file has been changed.
# The original file this work derives from is found at:
# https://github.com/nipy/heudiconv/blob/55524168b02519bbf0a...
#
# ORIGINAL WORK'S ATTRIBUTION NOTICE:
#
#     Copyright [2014-2019] [Heudiconv developers]
#
# Licensed under the Apache License, Version 2.0 (the "License");
# you may not use this file except in compliance with the License.
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#
#     http://www.apache.org/licenses/LICENSE-2.0
#
# Unless required by applicable law or agreed to in writing,
# distributed under the License is distributed on an "AS IS"
# WITHOUT WARRANTIES OR CONDITIONS OF ANY KIND, either express
# or implied. See the License for the specific language governing
# permissions and limitations under the License.
"""
Reproin heuristic."""

from __future__ import annotations
```

```
from warnings import warn
from collections import Counter
import logging
import re

import pydicom as dcm

from heudiconv.utils import SeqInfo
from heudiconv.heuristics.reproin import (
    _apply_substitutions,
    get_study_hash,
    get_study_description,
)

lgr = logging.getLogger("heudiconv")

DWI_RES = {
    "1.6mm-iso": "highres",
    "2mm-iso": "lowres",
}

IGNORE_PROTOCOLS = (
    "DEV",
    "LABEL",
    "REPORT",
    "ADC",
    "TRACEW",
    "FA",
    "ColFA",
    "B0",
    "TENSOR",
    "10meas", # dismiss a trial of fmap acquisition
    "testJB", # dismiss a test trial of the cmrr sequence
)

bids_regex = re.compile(r"_(?=(dir|acq|task|run)-([A-Za-z0-9]+))"

# Terminology to harmonise and use to name variables etc
# experiment
# subject
# [session]
# exam (AKA scanning session) - currently seqinfo, unless brou
#     series (AKA protocol?)
#         - series_spec - deduced from fields the spec (literal val
```

```

# - series_info - the dictionary with fields parsed from ser

# Which fields in seqinfo (in this order) to check for the Repro]
series_spec_fields = ("protocol_name", "series_description")

# dictionary from accession-number to runs that need to be marked
# NOTE: even if filename has number that is 0-padded, internally
# is done
fix_accession2run: dict[str, list[str]] = {
    # e.g.:
    # 'A000035': ['^8-', '^9-'],
}

# A dictionary containing fixes/remapping for sequence names per
# Keys are md5sum of study_description from DICOMs, in the form c
# You can use `heudiconv -f reproin --command ls --files PATH
# to list the "study hash".
# Values are list of tuples in the form (regex_pattern, substitut
# If the key is an empty string `''`, it would apply to any stu
protocols2fix: dict[str | re.Pattern[str], list[tuple[str, str]]]
    """:
        (
            ("t1_mprage_pre_Morpho", "anat-T1w_acq-morphobox__mprage"
            (
                "micro_struct_137dir_BIPOLAR_b3000_1.6mm-iso",
                "dwi-dwi_acq-highres_dir-unknown__137dir_bipolar",
            ),
            (
                "micro_struct_137dir_BIPOLAR_b3000_1.6mm-iso",
                "dwi-dwi_acq-highres_dir-unknown__137dir_bipolar",
            ),
            (
                "micro_struct_137dir_BIPOLAR_b3000_2mm-iso",
                "dwi-dwi_acq-lowres_dir-unknown__137dir_bipolar",
            ),
            ("gre_field_mapping_1.6mmiso", "fmap-phasediff__gre"),
            (
                "cmrr_mbep2d_bold_me4_sms4_fa75_750meas",
                "func-bold_task-rest__750meas",
            ),
            (
                "cmrr_mbep2d_bold_me4_sms4_fa80",
                "func-bold_task-rest_acq-fa80_cmrr",
            ),
            (
                "cmrr_mbep2d_bold_me4_testJB",
                "func-bold_task-rest_acq-testJB_cmrr",
            ),
        ),

```

```

(
    "cmrr_mbep2d_bold_fmap_fa80",
    "fmap-epi_acq-bold_dir-unknown_cmrr_mbepd2d_fa80",
),
("cmrr_mbep2d_bold_me4_sms4", "func-bold_task-qct_cmrr")
(_task-qc_, _task-qct_),
("anat-T2w_flair", "anat-FLAIR_spcir"),
("AAHead_Scout_*", "anat-scout"),
]

# e.g., QA:
# '43b67d9139e8c7274578b7451ab21123':
# [
#     ('BOLD_p2_s4_3\.5mm', 'func_task-rest_acq-p2-s4-3.5mm')
#     ('BOLD_', 'func_task-rest'),
#     ('_p2_s4', '_acq-p2-s4'),
#     ('_p2', '_acq-p2'),
# ],
# ''': # for any study example with regexes used
# [
#     ('AAHead_Scout_*', 'anat-scout'),
#     ('^dti_*', 'dwi'),
#     ('^.*_distortion_corr.*_([ap]+)_([12])', r'fmap-epi'
#     ('^(.+)_ap.*_r(0[0-9])', r'func_task-\1_run-\2'),
#     ('^t1w_*', 'anat-T1w'),
#     # problematic case -- multiple identically named p€
#     # I guess we will just sacrifice ability to detect
#     # And we cannot just use _run+ since it would incre
#     # for ap and then for pa. We will rely on having a
#     # Added _acq-mb8 so they match the one in funcs
#     ('func_task-discorr_acq-ap', r'fmap-epi_dir-ap_acq-
#     ('func_task-discorr_acq-pa', r'fmap-epi_dir-pa_acq-
# ]
}

# list containing StudyInstanceUID to skip -- hopefully doesn't h
dicoms2skip: list[str] = [
    # e.g.
    # '1.3.12.2.1107.5.2.43.66112.30000016110117002435700000001',
]

DEFAULT_FIELDS = {
    # Let it just be in each json file extracted
    "Acknowledgements": "See README.md.",
}

POPULATE_INTENDED_FOR_OPTS = {
    "matching_parameters": ["ImagingVolume", "Shims"],
}

```

```

    "criterion": "Closest",
}

def filter_dicom(dcldata: dcm.dataset.Dataset) -> bool:
    """Return True if a DICOM dataset should be filtered out, else False.
    return True if dcldata.StudyInstanceUID in dicoms2skip else False

def filter_files(_fn: str) -> bool:
    """Return True if a file should be kept, else False.

    ATM reproin does not do any filtering. Override if you need to.
    """
    return not _fn.endswith((".csv", ".dvs"))

def fix_canceled_runs(seqinfo: list[SeqInfo]) -> list[SeqInfo]:
    """Function that adds cancelme_ to known bad runs which were
    if not fix_accession2run:
        return seqinfo # nothing to do
    for i, s in enumerate(seqinfo):
        accession_number = s.accession_number
        if accession_number and accession_number in fix_accession2run:
            lgr.info(
                "Considering some runs possibly marked to be "
                "canceled for accession %s",
                accession_number,
            )
            # This code is reminiscent of prior logic when operating
            # on a single accession, but left as is for now
            badruns = fix_accession2run[accession_number]
            badruns_pattern = "|".join(badrus)
            if re.match(badrus_pattern, s.series_id):
                lgr.info("Fixing bad run {}".format(s.series_id))
                fixedkwargs = dict()
                for key in series_spec_fields:
                    fixedkwargs[key] = "cancelme_" + getattr(s, key)
                seqinfo[i] = s._replace(**fixedkwargs)
    return seqinfo

def fix_dbic_protocol(seqinfo: list[SeqInfo]) -> list[SeqInfo]:
    """Ad-hoc fixup for existing protocols.
    """

```

It will operate in 3 stages on `protocols2fix` records.

1. consider a record which has md5sum of study_description

```

2. apply all substitutions, where key is a regular expression
   successfully searches (not necessarily matches, so anchor
   study_description
3. apply "catch all" substitutions in the key containing an epsilon
   character
3. is somewhat redundant since `re.compile('.*')` could match
   anything, but kept for simplicity of its specification.

"""

study_hash = get_study_hash(seqinfo)
study_description = get_study_description(seqinfo)

# We will consider first study specific (based on hash)
if study_hash in protocols2fix:
    _apply_substitutions(
        seqinfo, protocols2fix[study_hash], "study (%s) specific"
    )
# Then go through all regexps returning regex "search" result
# on study_description
for sub, substitutions in protocols2fix.items():
    if isinstance(sub, re.Pattern) and sub.search(study_description):
        _apply_substitutions(
            seqinfo, substitutions, "%r regex matching" % sub
        )
# and at the end - global
if "" in protocols2fix:
    _apply_substitutions(seqinfo, protocols2fix[""], "global")

return seqinfo

def fix_seqinfo(seqinfo: list[SeqInfo]) -> list[SeqInfo]:
    """Just a helper on top of both fixers"""
    # add cancelme to known bad runs
    seqinfo = fix_canceled_runs(seqinfo)
    seqinfo = fix_dbic_protocol(seqinfo)
    return seqinfo

def create_key(template, outtype=("nii.gz",), annotation_classes=()):
    if template is None or not template:
        raise ValueError("Template must be a valid format string")
    return template, outtype, annotation_classes

def infotodict(seqinfo):
    """Heuristic evaluator for determining which runs belong where
       based on sequence info
   """

```

```
allowed template fields - follow python string module:

item: index within category
subject: participant id
seqitem: run number during scanning
subindex: sub index within group
"""

seqinfo = fix_seqinfo(seqinfo)
lgr.info("Processing %d seqinfo entries", len(seqinfo))

t1w = create_key(
    "sub-{subject}/{session}/anat/sub-{subject}_{session}_acc")
t2w = create_key(
    "sub-{subject}/{session}/anat/sub-{subject}_{session}_acc")
t2_flair = create_key(
    "sub-{subject}/{session}/anat/sub-{subject}_{session}{rur}")
dwi = create_key(
    "sub-{subject}/{session}/dwi/sub-{subject}_{session}_acq")
mag = create_key(
    "sub-{subject}/{session}/fmap/sub-{subject}_{session}{rur}")
phdiff = create_key(
    "sub-{subject}/{session}/fmap/sub-{subject}_{session}{rur}")
epi = create_key(
    "sub-{subject}/{session}/fmap/sub-{subject}_{session}" +
    "_acq-{acquisition}_dir-{dir}{run_entity}{part_entity}_er")
func = create_key(
    "sub-{subject}/{session}/func/sub-{subject}_{session}" +
    "_task-{task}{acq_entity}{dir_entity}{run_entity}{part_entity}_er")
sbref = create_key(
    "sub-{subject}/{session}/func/sub-{subject}_{session}_tas")

info = {
    t1w: [],
    t2w: [],
    t2_flair: [],
    dwi: [],
    mag: [],
```

```
phdiff: [],
epi: [],
func: [],
sbref: [],
}
epi_mags = []
bold_mags = []

for s in seqinfo:
    """
    The namedtuple `s` contains the following fields:

    * total_files_till_now
    * example_dcm_file
    * series_id
    * dcm_dir_name
    * unspecified2
    * unspecified3
    * dim1
    * dim2
    * dim3
    * dim4
    * TR
    * TE
    * protocol_name
    * is_motion_corrected
    * is_derived
    * patient_id
    * study_description
    * referring_physician_name
    * series_description
    * image_type
    """

# Ignore derived data and reports
if (
    s.is_derived == "True"
    or s.is_derived is True
    or s.dcm_dir_name.split("_")[-1] in IGNORE_PROTOCOLS
):
    continue

thisitem = {
    "item": s.series_id,
}
thiskey = None
thisitem.update({k: v for k, v in bids_regex.findall(s.pr
```

```

thisitem["run_entity"] = f"{thisitem.pop('run', '')}"]

if s.protocol_name.lower().startswith("anat-t1w"):
    thiskey = t1w
    acquisition_present = thisitem.pop("acq", None)
    thisitem["acquisition"] = (
        ("original" if s.dcm_dir_name.endswith("_ND") else "unspecified"
         if not acquisition_present
         else acquisition_present
    )
elif s.protocol_name.lower().startswith("anat-t2w"):
    thiskey = t2w
    acquisition_present = thisitem.pop("acq", None)
    thisitem["acquisition"] = (
        ("original" if s.dcm_dir_name.endswith("_ND") else "unspecified"
         if not acquisition_present
         else "unspecified"
    )
elif s.protocol_name.lower().startswith("anat-flair"):
    thiskey = t2_flair
elif s.protocol_name.startswith("dwi-dwi"):
    thiskey = dwi
elif s.protocol_name.startswith("fmap-phasediff"):
    thiskey = phdiff if "P" in s.image_type else mag
elif s.protocol_name.startswith("fmap-epi"):
    thiskey = epi
    thisitem["part_entity"] = ""
    thisitem["acquisition"] = (
        "b0" if s.sequence_name.endswith("ep_b0") else "b1"
    )

# Check whether phase was written out:
# 1. A magnitude needs to exist immediately before it
# 2. Magnitude and phase must have the same number of
series_id_idx, series_id_name = s.series_id.split("-")
prev_series_id = f"{int(series_id_idx) - 1}-{series_id_name}"
if prev_series_id in epi_mags:
    thisitem["part_entity"] = "_part-phase"
    info[thiskey][epi_mags.index(prev_series_id)]["phase"] = True

    epi_mags.append(f"{s.series_id}-{s.series_files}")

elif s.protocol_name.startswith("func-bold"):
    # Likely an error
    if s.series_files < 100:
        warn(
            f"Dropping exceedingly short BOLD file with {s.series_files} "
)

```

```

        )
        continue

    thiskey = func

    thisitem["part_entity"] = ""
    # Some functional runs may come with acq
    func_acq = thisitem.pop("acq", None)
    thisitem["acq_entity"] = "" if not func_acq else f"_e{func_acq}"

    # Some functional runs may come with dir
    func_dir = thisitem.pop("dir", None)
    thisitem["dir_entity"] = "" if not func_dir else f"_d{func_dir}"

    # Check whether phase was written out:
    # 1. A magnitude needs to exist immediately before it
    # 2. Magnitude and phase must have the same number of digits
    series_id_idx, series_id_name = s.series_id.split("-")
    prev_series_id = f"{int(series_id_idx) - 1}-{series_id_name}"
    if prev_series_id in bold_mags:
        thisitem["part_entity"] = "_part-phase"
        info[thiskey][bold_mags.index(prev_series_id)]["phase"] = "phase"

    bold_mags.append(f"{s.series_id}-{s.series_files}")

    if thiskey is not None:
        info[thiskey].append(thisitem)

for mod, items in info.items():
    if len(items) < 2:
        continue

    info[mod] = _assign_run_on_repeat(items)

return info

def _assign_run_on_repeat(modality_items):
    """
    Assign run IDs for repeated inputs for a given modality.
    """

    Examples
    -----
    >>> _assign_run_on_repeat([
        {"item": "discard1", "acq": "bold", "dir": "PA"},
        {"item": "discard2", "acq": "bold", "dir": "AP"},
        {"item": "discard3", "acq": "bold", "dir": "PA"},
```

```
... ]) # doctest: +NORMALIZE_WHITESPACE
[{'item': 'discard1', 'acq': 'bold', 'dir': 'PA', 'run_entity': 1},
 {'item': 'discard2', 'acq': 'bold', 'dir': 'AP', 'run_entity': 1},
 {'item': 'discard3', 'acq': 'bold', 'dir': 'PA', 'run_entity': 1}

>>> _assign_run_on_repeat([
...     {"item": "discard1", "acq": "bold", "dir": "PA"}, {"item": "discard2", "acq": "bold", "dir": "AP"}, {"item": "discard3", "acq": "bold", "dir": "PA"}, {"item": "discard4", "acq": "bold", "dir": "AP"}, ... ]) # doctest: +NORMALIZE_WHITESPACE
[{'item': 'discard1', 'acq': 'bold', 'dir': 'PA', 'run_entity': 1}, {'item': 'discard2', 'acq': 'bold', 'dir': 'AP', 'run_entity': 1}, {'item': 'discard3', 'acq': 'bold', 'dir': 'PA', 'run_entity': 1}, {'item': 'discard4', 'acq': 'bold', 'dir': 'AP', 'run_entity': 1}

>>> _assign_run_on_repeat([
...     {"item": "discard1", "acq": "bold", "dir": "PA", "rur": 1}, {"item": "discard2", "acq": "bold", "dir": "AP"}, {"item": "discard3", "acq": "bold", "dir": "PA", "rur": 2}, ... ]) # doctest: +NORMALIZE_WHITESPACE
[{'item': 'discard1', 'acq': 'bold', 'dir': 'PA', 'run': '1'}, {'item': 'discard2', 'acq': 'bold', 'dir': 'AP'}, {"item": "discard3", "acq": "bold", "dir": "PA", "run": "2"}]

>>> _assign_run_on_repeat([
...     {"item": "discard1", "acq": "bold", "dir": "PA", "rur": 1}, {"item": "discard2", "acq": "bold", "dir": "AP"}, {"item": "discard3", "acq": "bold", "dir": "PA", "rur": 2}, ... ]) # doctest: +NORMALIZE_WHITESPACE
[{'item': 'discard1', 'acq': 'bold', 'dir': 'PA', 'run_entity': 1}, {"item": "discard2", "acq": "bold", "dir": "AP"}, {"item": "discard3", "acq": "bold", "dir": "PA", 'run_entity': 2}

>>> _assign_run_on_repeat([
...     {"item": "discard1", "acq": "bold", "dir": "PA", "part_entit": 1}, {"item": "discard2", "acq": "bold", "dir": "PA", "part_entit": 1}, {"item": "discard3", "acq": "bold", "dir": "AP", "part_entit": 1}, {"item": "discard4", "acq": "bold", "dir": "AP", "part_entit": 1}, ... ]) # doctest: +NORMALIZE_WHITESPACE
[{'item': 'discard1', 'acq': 'bold', 'dir': 'PA', 'part_entit': 1}, {"item": "discard2", "acq": "bold", "dir": "PA", 'part_entit': 1}, {"item": "discard3", "acq": "bold", "dir": "AP", 'part_entit': 1}, {"item": "discard4", "acq": "bold", "dir": "AP", 'part_entit': 1}

"""

modality_items = modality_items.copy()
```

```
str_patterns = [
    "_".join([f"{s[0]}-{s[1]}" for s in item.items() if s[0]
              for item in modality_items
    ])
strcount = Counter(str_patterns)

for string, count in strcount.items():
    if count < 2:
        continue

runid = 1

for index, item_string in enumerate(str_patterns):
    if string == item_string:
        modality_items[index].update(
            {
                "run_entity": f"_run-{runid}",
            }
        )
        runid += 1

return modality_items
```

During piloting, we changed a number of settings

For example, the first four sessions did not follow *Reproin* conventions and filenames varied substantially. Please note the `protocols2fix` variable in our heuristic file, where the compatibility is implemented.

- Run *HeuDiconv* with our heuristic file <path>/code/heudiconv/reproin.py:

Executing HeuDiconv

```
#!/bin/bash
heudiconv -s "001" -ss "pilot001" -b -l . -o /data/datasets/hcp
    -f <sops_clone_path>/code/heudiconv/reproin.py \
    --files /data/datasets/hcph-pilot-sourcedata/\
        sub-01\
        ses-18950702/
```

Session number MUST be updated manually**Example of the dataset organization**

Piloting sessions 15 and 16 look like this:

```
ses-pilot015
├── anat
│   ├── sub-001_ses-pilot015_acq-original_T1w.json
│   ├── sub-001_ses-pilot015_acq-original_T1w.nii.gz
│   ├── sub-001_ses-pilot015_acq-undistorted_T1w.json
│   ├── sub-001_ses-pilot015_acq-undistorted_T1w.nii.gz
│   ├── sub-001_ses-pilot015_T2w.json
│   └── sub-001_ses-pilot015_T2w.nii.gz
├── dwi
│   ├── sub-001_ses-pilot015_acq-highres_dir-LR_dwi.bval
│   ├── sub-001_ses-pilot015_acq-highres_dir-LR_dwi.bvec
│   ├── sub-001_ses-pilot015_acq-highres_dir-LR_dwi.json
│   └── sub-001_ses-pilot015_acq-highres_dir-LR_dwi.nii.gz
└── fmap
    ├── sub-001_ses-pilot015_acq-b0_dir-RL_epi.json
    ├── sub-001_ses-pilot015_acq-b0_dir-RL_epi.nii.gz
    ├── sub-001_ses-pilot015_acq-bold_dir-RL_part-mag_epi.json
    ├── sub-001_ses-pilot015_acq-bold_dir-RL_part-mag_epi.nii.gz
    ├── sub-001_ses-pilot015_acq-bold_dir-RL_part-phase_epi.json
    ├── sub-001_ses-pilot015_acq-bold_dir-RL_part-phase_epi.nii.gz
    ├── sub-001_ses-pilot015_magnitude1.json
    ├── sub-001_ses-pilot015_magnitude1.nii.gz
    ├── sub-001_ses-pilot015_magnitude2.json
    ├── sub-001_ses-pilot015_magnitude2.nii.gz
    ├── sub-001_ses-pilot015_phasediff.json
    └── sub-001_ses-pilot015_phasediff.nii.gz
└── func
    ├── sub-001_ses-pilot015_task-bht_echo-1_part-mag_bold.json
    ├── sub-001_ses-pilot015_task-bht_echo-1_part-mag_bold.nii.gz
    └── sub-001_ses-pilot015_task-bht_echo-1_part-phase_bold.json
```

```
    └── sub-001_ses-pilot015_task-bht_echo-1_part-phase_bold.nii.gz
    └── sub-001_ses-pilot015_task-bht_echo-2_part-mag_bold.json
    └── sub-001_ses-pilot015_task-bht_echo-2_part-mag_bold.nii.gz
    └── sub-001_ses-pilot015_task-bht_echo-2_part-phase_bold.json
    └── sub-001_ses-pilot015_task-bht_echo-3_part-mag_bold.json
    └── sub-001_ses-pilot015_task-bht_echo-3_part-mag_bold.nii.gz
    └── sub-001_ses-pilot015_task-bht_echo-3_part-phase_bold.json
    └── sub-001_ses-pilot015_task-bht_echo-3_part-phase_bold.nii.gz
    └── sub-001_ses-pilot015_task-bht_echo-4_part-mag_bold.json
    └── sub-001_ses-pilot015_task-bht_echo-4_part-mag_bold.nii.gz
    └── sub-001_ses-pilot015_task-bht_echo-4_part-phase_bold.json
    └── sub-001_ses-pilot015_task-bht_echo-4_part-phase_bold.nii.gz
    └── sub-001_ses-pilot015_task-bht_part-mag_events.tsv
    └── sub-001_ses-pilot015_task-bht_part-phase_events.tsv
    └── sub-001_ses-pilot015_task-qct_echo-1_part-mag_bold.json
    └── sub-001_ses-pilot015_task-qct_echo-1_part-mag_bold.nii.gz
    └── sub-001_ses-pilot015_task-qct_echo-1_part-phase_bold.json
    └── sub-001_ses-pilot015_task-qct_echo-1_part-phase_bold.nii.gz
    └── sub-001_ses-pilot015_task-qct_echo-2_part-mag_bold.json
    └── sub-001_ses-pilot015_task-qct_echo-2_part-mag_bold.nii.gz
    └── sub-001_ses-pilot015_task-qct_echo-2_part-phase_bold.json
    └── sub-001_ses-pilot015_task-qct_echo-2_part-phase_bold.nii.gz
    └── sub-001_ses-pilot015_task-qct_echo-3_part-mag_bold.json
    └── sub-001_ses-pilot015_task-qct_echo-3_part-mag_bold.nii.gz
    └── sub-001_ses-pilot015_task-qct_echo-3_part-phase_bold.json
    └── sub-001_ses-pilot015_task-qct_echo-3_part-phase_bold.nii.gz
    └── sub-001_ses-pilot015_task-qct_echo-4_part-mag_bold.json
    └── sub-001_ses-pilot015_task-qct_echo-4_part-mag_bold.nii.gz
    └── sub-001_ses-pilot015_task-qct_echo-4_part-phase_bold.json
    └── sub-001_ses-pilot015_task-qct_echo-4_part-phase_bold.nii.gz
    └── sub-001_ses-pilot015_task-qct_part-mag_events.tsv
    └── sub-001_ses-pilot015_task-qct_part-phase_events.tsv
    └── sub-001_ses-pilot015_task-rest_echo-1_part-mag_bold.json
    └── sub-001_ses-pilot015_task-rest_echo-1_part-mag_bold.nii.gz
    └── sub-001_ses-pilot015_task-rest_echo-1_part-phase_bold.json
    └── sub-001_ses-pilot015_task-rest_echo-1_part-phase_bold.nii.gz
    └── sub-001_ses-pilot015_task-rest_echo-2_part-mag_bold.json
    └── sub-001_ses-pilot015_task-rest_echo-2_part-mag_bold.nii.gz
    └── sub-001_ses-pilot015_task-rest_echo-2_part-phase_bold.json
    └── sub-001_ses-pilot015_task-rest_echo-2_part-phase_bold.nii.gz
    └── sub-001_ses-pilot015_task-rest_echo-3_part-mag_bold.json
    └── sub-001_ses-pilot015_task-rest_echo-3_part-mag_bold.nii.gz
    └── sub-001_ses-pilot015_task-rest_echo-3_part-phase_bold.json
    └── sub-001_ses-pilot015_task-rest_echo-3_part-phase_bold.nii.gz
    └── sub-001_ses-pilot015_task-rest_echo-4_part-mag_bold.json
    └── sub-001_ses-pilot015_task-rest_echo-4_part-mag_bold.nii.gz
    └── sub-001_ses-pilot015_task-rest_echo-4_part-phase_bold.json
    └── sub-001_ses-pilot015_task-rest_echo-4_part-phase_bold.nii.gz
    └── sub-001_ses-pilot015_task-rest_part-mag_events.tsv
    └── sub-001_ses-pilot015_task-rest_part-phase_events.tsv
└── sub-001_ses-pilot015_scans.tsv

ses-pilot016
└── anat
    ├── sub-001_ses-pilot016_acq-original_T1w.json
    ├── sub-001_ses-pilot016_acq-original_T1w.nii.gz
    ├── sub-001_ses-pilot016_acq-undistorted_T1w.json
    ├── sub-001_ses-pilot016_acq-undistorted_T1w.nii.gz
    └── sub-001_ses-pilot016_T2w.json
```

```
    └── sub-001_ses-pilot016_T2w.nii.gz
  └── dwi
      ├── sub-001_ses-pilot016_acq-highres_dir-RL_dwi.bval
      ├── sub-001_ses-pilot016_acq-highres_dir-RL_dwi.bvec
      ├── sub-001_ses-pilot016_acq-highres_dir-RL_dwi.json
      └── sub-001_ses-pilot016_acq-highres_dir-RL_dwi.nii.gz
  └── fmap
      ├── sub-001_ses-pilot016_acq-b0_dir-AP_epi.json
      ├── sub-001_ses-pilot016_acq-b0_dir-AP_epi.nii.gz
      ├── sub-001_ses-pilot016_acq-b0_dir-LR_epi.json
      ├── sub-001_ses-pilot016_acq-b0_dir-LR_epi.nii.gz
      ├── sub-001_ses-pilot016_acq-b0_dir-PA_epi.json
      ├── sub-001_ses-pilot016_acq-b0_dir-PA_epi.nii.gz
      ├── sub-001_ses-pilot016_acq-b0_dir-RL_epi.json
      ├── sub-001_ses-pilot016_acq-b0_dir-RL_epi.nii.gz
      ├── sub-001_ses-pilot016_acq-bold_dir-AP_part-mag_epi.json
      ├── sub-001_ses-pilot016_acq-bold_dir-AP_part-mag_epi.nii.gz
      ├── sub-001_ses-pilot016_acq-bold_dir-AP_part-phase_epi.json
      ├── sub-001_ses-pilot016_acq-bold_dir-AP_part-phase_epi.nii.gz
      ├── sub-001_ses-pilot016_acq-bold_dir-LR_part-mag_epi.json
      ├── sub-001_ses-pilot016_acq-bold_dir-LR_part-mag_epi.nii.gz
      ├── sub-001_ses-pilot016_acq-bold_dir-LR_part-phase_epi.json
      ├── sub-001_ses-pilot016_acq-bold_dir-LR_part-phase_epi.nii.gz
      ├── sub-001_ses-pilot016_acq-bold_dir-PA_part-mag_epi.json
      ├── sub-001_ses-pilot016_acq-bold_dir-PA_part-mag_epi.nii.gz
      ├── sub-001_ses-pilot016_acq-bold_dir-PA_part-phase_epi.json
      ├── sub-001_ses-pilot016_acq-bold_dir-PA_part-phase_epi.nii.gz
      ├── sub-001_ses-pilot016_acq-bold_dir-RL_part-mag_epi.json
      ├── sub-001_ses-pilot016_acq-bold_dir-RL_part-mag_epi.nii.gz
      ├── sub-001_ses-pilot016_acq-bold_dir-RL_part-phase_epi.json
      ├── sub-001_ses-pilot016_acq-bold_dir-RL_part-phase_epi.nii.gz
      ├── sub-001_ses-pilot016_magnitude1.json
      ├── sub-001_ses-pilot016_magnitude1.nii.gz
      ├── sub-001_ses-pilot016_magnitude2.json
      ├── sub-001_ses-pilot016_magnitude2.nii.gz
      ├── sub-001_ses-pilot016_phasediff.json
      └── sub-001_ses-pilot016_phasediff.nii.gz
  └── func
      ├── sub-001_ses-pilot016_task-bht_echo-1_part-mag_bold.json
      ├── sub-001_ses-pilot016_task-bht_echo-1_part-mag_bold.nii.gz
      ├── sub-001_ses-pilot016_task-bht_echo-1_part-phase_bold.json
      ├── sub-001_ses-pilot016_task-bht_echo-1_part-phase_bold.nii.gz
      ├── sub-001_ses-pilot016_task-bht_echo-2_part-mag_bold.json
      ├── sub-001_ses-pilot016_task-bht_echo-2_part-mag_bold.nii.gz
      ├── sub-001_ses-pilot016_task-bht_echo-2_part-phase_bold.json
      ├── sub-001_ses-pilot016_task-bht_echo-2_part-phase_bold.nii.gz
      ├── sub-001_ses-pilot016_task-bht_echo-3_part-mag_bold.json
      ├── sub-001_ses-pilot016_task-bht_echo-3_part-mag_bold.nii.gz
      ├── sub-001_ses-pilot016_task-bht_echo-3_part-phase_bold.json
      ├── sub-001_ses-pilot016_task-bht_echo-3_part-phase_bold.nii.gz
      ├── sub-001_ses-pilot016_task-bht_echo-4_part-mag_bold.json
      ├── sub-001_ses-pilot016_task-bht_echo-4_part-mag_bold.nii.gz
      ├── sub-001_ses-pilot016_task-bht_echo-4_part-phase_bold.json
      ├── sub-001_ses-pilot016_task-bht_echo-4_part-phase_bold.nii.gz
      ├── sub-001_ses-pilot016_task-bht_part-mag_events.tsv
      ├── sub-001_ses-pilot016_task-bht_part-phase_events.tsv
      ├── sub-001_ses-pilot016_task-qct_echo-1_part-mag_bold.json
      ├── sub-001_ses-pilot016_task-qct_echo-1_part-mag_bold.nii.gz
      └── sub-001_ses-pilot016_task-qct_echo-1_part-phase_bold.json
```

```

    └── sub-001_ses-pilot016_task-qct_echo-1_part-phase_bold.nii.gz
    └── sub-001_ses-pilot016_task-qct_echo-2_part-mag_bold.json
    └── sub-001_ses-pilot016_task-qct_echo-2_part-mag_bold.nii.gz
    └── sub-001_ses-pilot016_task-qct_echo-2_part-phase_bold.json
    └── sub-001_ses-pilot016_task-qct_echo-2_part-phase_bold.nii.gz
    └── sub-001_ses-pilot016_task-qct_echo-3_part-mag_bold.json
    └── sub-001_ses-pilot016_task-qct_echo-3_part-mag_bold.nii.gz
    └── sub-001_ses-pilot016_task-qct_echo-3_part-phase_bold.json
    └── sub-001_ses-pilot016_task-qct_echo-3_part-phase_bold.nii.gz
    └── sub-001_ses-pilot016_task-qct_echo-4_part-mag_bold.json
    └── sub-001_ses-pilot016_task-qct_echo-4_part-mag_bold.nii.gz
    └── sub-001_ses-pilot016_task-qct_echo-4_part-phase_bold.json
    └── sub-001_ses-pilot016_task-qct_echo-4_part-phase_bold.nii.gz
    └── sub-001_ses-pilot016_task-qct_part-mag_events.tsv
    └── sub-001_ses-pilot016_task-qct_part-phase_events.tsv
    └── sub-001_ses-pilot016_task-rest_echo-1_part-mag_bold.json
    └── sub-001_ses-pilot016_task-rest_echo-1_part-mag_bold.nii.gz
    └── sub-001_ses-pilot016_task-rest_echo-1_part-phase_bold.json
    └── sub-001_ses-pilot016_task-rest_echo-1_part-phase_bold.nii.gz
    └── sub-001_ses-pilot016_task-rest_echo-2_part-mag_bold.json
    └── sub-001_ses-pilot016_task-rest_echo-2_part-mag_bold.nii.gz
    └── sub-001_ses-pilot016_task-rest_echo-2_part-phase_bold.json
    └── sub-001_ses-pilot016_task-rest_echo-2_part-phase_bold.nii.gz
    └── sub-001_ses-pilot016_task-rest_echo-3_part-mag_bold.json
    └── sub-001_ses-pilot016_task-rest_echo-3_part-mag_bold.nii.gz
    └── sub-001_ses-pilot016_task-rest_echo-3_part-phase_bold.json
    └── sub-001_ses-pilot016_task-rest_echo-3_part-phase_bold.nii.gz
    └── sub-001_ses-pilot016_task-rest_echo-4_part-mag_bold.json
    └── sub-001_ses-pilot016_task-rest_echo-4_part-mag_bold.nii.gz
    └── sub-001_ses-pilot016_task-rest_echo-4_part-phase_bold.json
    └── sub-001_ses-pilot016_task-rest_echo-4_part-phase_bold.nii.gz
    └── sub-001_ses-pilot016_task-rest_part-mag_events.tsv
    └── sub-001_ses-pilot016_task-rest_part-phase_events.tsv
└── sub-001_ses-pilot016_scans.tsv

```

We started to generate phase and magnitude only after session 15

As a result, the piloting data up to session 14 will look more like:

```

    └── ses-pilot014
        └── anat
            └── sub-001_ses-pilot014_acq-original_T1w.json
            └── sub-001_ses-pilot014_acq-original_T1w.nii.gz
            └── sub-001_ses-pilot014_acq-undistorted_T1w.json
            └── sub-001_ses-pilot014_acq-undistorted_T1w.nii.gz
            └── sub-001_ses-pilot014_T2w.json
            └── sub-001_ses-pilot014_T2w.nii.gz
        └── dwi
            └── sub-001_ses-pilot014_acq-highres_dir-PA_dwi.bval
            └── sub-001_ses-pilot014_acq-highres_dir-PA_dwi.bvec
            └── sub-001_ses-pilot014_acq-highres_dir-PA_dwi.json
            └── sub-001_ses-pilot014_acq-highres_dir-PA_dwi.nii.gz
        └── fmap
            └── sub-001_ses-pilot014_acq-b0_dir-AP_epi.json
            └── sub-001_ses-pilot014_acq-b0_dir-AP_epi.nii.gz
            └── sub-001_ses-pilot014_acq-bold_dir-PA_run-1_epi.json

```

```
    └── sub-001_ses-pilot014_acq-bold_dir-PA_run-1_epi.nii.gz
    └── sub-001_ses-pilot014_acq-bold_dir-PA_run-2_epi.json
    └── sub-001_ses-pilot014_acq-bold_dir-PA_run-2_epi.nii.gz
    └── sub-001_ses-pilot014_magnitude1.json
    └── sub-001_ses-pilot014_magnitude1.nii.gz
    └── sub-001_ses-pilot014_magnitude2.json
    └── sub-001_ses-pilot014_magnitude2.nii.gz
    └── sub-001_ses-pilot014_phasediff.json
    └── sub-001_ses-pilot014_phasediff.nii.gz
    └── func
        ├── sub-001_ses-pilot014_task-bht_echo-1_bold.json
        ├── sub-001_ses-pilot014_task-bht_echo-1_bold.nii.gz
        ├── sub-001_ses-pilot014_task-bht_echo-2_bold.json
        ├── sub-001_ses-pilot014_task-bht_echo-2_bold.nii.gz
        ├── sub-001_ses-pilot014_task-bht_echo-3_bold.json
        ├── sub-001_ses-pilot014_task-bht_echo-3_bold.nii.gz
        ├── sub-001_ses-pilot014_task-bht_echo-4_bold.json
        ├── sub-001_ses-pilot014_task-bht_echo-4_bold.nii.gz
        ├── sub-001_ses-pilot014_task-bht_events.tsv
        ├── sub-001_ses-pilot014_task-bht_run-1_echo-1_bold.json
        ├── sub-001_ses-pilot014_task-bht_run-1_echo-1_bold.nii.gz
        ├── sub-001_ses-pilot014_task-bht_run-1_echo-2_bold.json
        ├── sub-001_ses-pilot014_task-bht_run-1_echo-2_bold.nii.gz
        ├── sub-001_ses-pilot014_task-bht_run-1_echo-3_bold.json
        ├── sub-001_ses-pilot014_task-bht_run-1_echo-3_bold.nii.gz
        ├── sub-001_ses-pilot014_task-bht_run-1_echo-4_bold.json
        ├── sub-001_ses-pilot014_task-bht_run-1_echo-4_bold.nii.gz
        ├── sub-001_ses-pilot014_task-bht_run-1_events.tsv
        ├── sub-001_ses-pilot014_task-bht_run-2_echo-1_bold.json
        ├── sub-001_ses-pilot014_task-bht_run-2_echo-1_bold.nii.gz
        ├── sub-001_ses-pilot014_task-bht_run-2_echo-2_bold.json
        ├── sub-001_ses-pilot014_task-bht_run-2_echo-2_bold.nii.gz
        ├── sub-001_ses-pilot014_task-bht_run-2_echo-3_bold.json
        ├── sub-001_ses-pilot014_task-bht_run-2_echo-3_bold.nii.gz
        ├── sub-001_ses-pilot014_task-bht_run-2_echo-4_bold.json
        ├── sub-001_ses-pilot014_task-bht_run-2_echo-4_bold.nii.gz
        ├── sub-001_ses-pilot014_task-bht_run-2_events.tsv
        ├── sub-001_ses-pilot014_task-qct_echo-1_bold.json
        ├── sub-001_ses-pilot014_task-qct_echo-1_bold.nii.gz
        ├── sub-001_ses-pilot014_task-qct_echo-2_bold.json
        ├── sub-001_ses-pilot014_task-qct_echo-2_bold.nii.gz
        ├── sub-001_ses-pilot014_task-qct_echo-3_bold.json
        ├── sub-001_ses-pilot014_task-qct_echo-3_bold.nii.gz
        ├── sub-001_ses-pilot014_task-qct_echo-4_bold.json
        ├── sub-001_ses-pilot014_task-qct_echo-4_bold.nii.gz
        ├── sub-001_ses-pilot014_task-qct_events.tsv
        ├── sub-001_ses-pilot014_task-rest_echo-1_bold.json
        ├── sub-001_ses-pilot014_task-rest_echo-1_bold.nii.gz
        ├── sub-001_ses-pilot014_task-rest_echo-2_bold.json
        ├── sub-001_ses-pilot014_task-rest_echo-2_bold.nii.gz
        ├── sub-001_ses-pilot014_task-rest_echo-3_bold.json
        ├── sub-001_ses-pilot014_task-rest_echo-3_bold.nii.gz
        ├── sub-001_ses-pilot014_task-rest_echo-4_bold.json
        ├── sub-001_ses-pilot014_task-rest_echo-4_bold.nii.gz
        └── sub-001_ses-pilot014_task-rest_events.tsv
    └── sub-001_ses-pilot014_scans.tsv
```

Convert physiological recordings into BIDS with *phys2bids*

We will use *phys2bids* (<https://phys2bids.readthedocs.io/en/latest/>) to convert physiological recordings from the proprietary format of BIOPAC's software AcqKnowledge. A quick link to the BIDS specifications on physiological recordings is [here](https://bids-specification.readthedocs.io/en/stable/04-modality-specific-files/06-physiological-and-other-continuous-recordings.html) (<https://bids-specification.readthedocs.io/en/stable/04-modality-specific-files/06-physiological-and-other-continuous-recordings.html>).

- Plot an overview of the data with the following command. This command generates a `PNG` plot of the data within the current directory without processing the data itself. The physiological data folder is specified via the `-in` command line argument.

```
phys2bids -in /data/datasets/hcp-h-pilot-sourcedata/physio/sess:
```

- Check that all the channels are present in the `PNG` plot.
- If this is the case, proceed to process the file using the subsequent command. Use the `-ntp` argument to specify the number of volumes for each task, and the `-tr` argument to indicate the task's repetition time. Define the output directory with `-outdir` and provide the path to the heuristic file using `-heur`. Adjust the subject and session numbers accordingly. Should scanner trigger transmission encounter issues and manual adjustments are made to the trigger data, it is possible to allocate one trigger per task. Set the repetition time duration as the task length, as demonstrated in the example below.

```
phys2bids -in modified-last-session_multiscan.txt -chtrig 4 -n1
```

- Execute the script `write_event_file.py` as shown below to generate task event files. This script creates `JSON` and `TSV` files containing event information and generates `PNG` plots for each task, displaying both physiological data and corresponding events. These plots are saved in the current directory. The script must be executed with the following command, where `outputdir` is the output directory of *phys2bids*:

```
python write_event_file.py --path ./outputdir/sub-001/ses-pilot
```

Once the script is executed, the `BIDS` folder (consisting solely of physiological data in this case) will have the following structure:

```
ses-pilot016
  └── func
      ├── sub-001_ses-pilot016_task-bht_events.json
      ├── sub-001_ses-pilot016_task-bht_events.tsv
      ├── sub-001_ses-pilot016_task-bht_physio.json
      ├── sub-001_ses-pilot016_task-bht_physio.tsv.gz
      └── sub-001_ses-pilot016_task-qct_events.json
```

```

    └── sub-001_ses-pilot016_task-qct_events.tsv
    └── sub-001_ses-pilot016_task-qct_physio.json
    └── sub-001_ses-pilot016_task-qct_physio.tsv.gz
    └── sub-001_ses-pilot016_task-rest_events.json
    └── sub-001_ses-pilot016_task-rest_events.tsv
    └── sub-001_ses-pilot016_task-rest_physio.json
    └── sub-001_ses-pilot016_task-rest_physio.tsv.gz

```

Convert eye-tracking into **BIDS** with *bidsphysio*

We will adapt *bidsphysio* (<https://github.com/cbinyu/bidsphysio>) to convert eye-tracking from the EDF proprietary format of EyeLink (SR Instruments).

Instead of the current specifications, we will use the following BEP (<https://bids-specification-1128.org.readthedocs.build/en/1128/modality-specific-files/eye-tracking.html>)

Once the script is executed, the **BIDS** folder (consisting solely of eye-tracking data in this case) will have the following structure:

```

ses-pilot016
  └── func
      ├── sub-001_ses-pilot016_task-bht_eyetrack.json
      ├── sub-001_ses-pilot016_task-bht_eyetrack.tsv.gz
      ├── sub-001_ses-pilot016_task-qct_eyetrack.json
      ├── sub-001_ses-pilot016_task-qct_eyetrack.tsv.gz
      ├── sub-001_ses-pilot016_task-rest_eyetrack.json
      └── sub-001_ses-pilot016_task-rest_eyetrack.tsv.gz

```

Add new data to the *DataLad* dataset

As new sessions are collected, the corresponding **BIDS** structures MUST be saved within the *DataLad* dataset and pushed to remote storage systems:

- Save the files in the dataset history using the command below. Replace <session_id> below with the number of the session (e.g., pilot017):

```
datalad save -r -m "add: session <session_id>" sub-001/ses-<se
```

Always double-check that data are annexed and the metadata committed to git

Although the [creation of a procedure](#) should ensure data and metadata are added to the appropriate version control (Git or Git-Annex), it is possible that some metadata or data formats are not anticipated, or do not follow the general rules.

A generally good strategy is to avoid recursion (i.e., do not use the `-r` flag), and leverage Bash's `find` and `xargs` tools. For example, the following command line selects metadata files that should be committed to Git within one session (`pilot020`) and saves them:

```
find sub-001/ses-pilot020 -name "*.tsv" -or -name "*.json" -or -name "*.bvec"
```

Correspondingly, we can store NIfTI data and physiological information:

```
find sub-001/ses-pilot020 -name "*.nii.gz" -or -name "_eyetrack.tsv.gz" -or -i
```

Please read [DataLad's save documentation](http://docs.datalad.org/en/stable/generated/man/datalad-save.html) (<http://docs.datalad.org/en/stable/generated/man/datalad-save.html>)

Saving batches of sessions

It is possible to save several sessions with the following *Bash* script by enumerating them in the array defined in the first line here:

```
SESSIONS=( 001 003 pilot21 ); \
for SESSION in ${SESSIONS[@]}; do \
    find sub-001/ses-$SESSION -name "*.tsv" -or -name "*.json" -or -name "*.bvec" -o \
    find sub-001/ses-$SESSION -name "*.nii.gz" -or -name "_eyetrack.tsv.gz" -o \
done
```

- Push the new data to the remote storage (if your git containing *DataLad* and the Git annex is different from `origin`, e.g., `github`, replace the name below):

```
datalad push --to ria-storage
datalad push --to origin
```

Always double-check that data in the annex are uploaded to the RIA store

QC of unprocessed data

Executing MRIQC

- Register the MRIQC container with DataLad containers-run
- Run MRIQC:

```
datalad containers-run \
    --container-name containers/mriqc \
    --input sourcedata \
    --output . \
    '{inputs}' '{outputs}' participant --session lastsession -v
```

- Screen the T1w, DWI and BOLD visual reports, assign a quality assessment using Q'Kay
- If either the dMRI or the RSfMRI quality is insufficient, schedule an extra session after the initially-planned scanning period to reacquire it.

Processing

Preprocessing

Executing *fMRIprep*

Because *fMRIprep* creates a single anatomical reference for all sessions, we generate such reference first by setting the `--anat-only` flag. If that *fMRIprep* execution finishes successfully, the anatomical processing outcomes will be stored in the output folder. We will then run one *fMRIprep* process for each dataset's session, which is the recommended way for datasets with a large number of sessions (e.g., more than six sessions). We avert that session-wise *fMRIprep*'s processes run into race conditions by pre-computing the anatomical reference.

- Submit the anatomical workflow:

Launch each session through *fMRIprep* in parallel

```
cd code/fmriprep  
bash ss-fmriprep.sh
```

The sbatch file to run *fMRIprep* with `--anat-only`

```
#!/bin/bash  
# Copyright 2023 The Axon Lab <theaxonlab@gmail.com>  
#  
# Licensed under the Apache License, Version 2.0 (the "License");  
# you may not use this file except in compliance with the License.  
# You may obtain a copy of the License at  
#  
#     http://www.apache.org/licenses/LICENSE-2.0  
#  
# Unless required by applicable law or agreed to in writing, software  
# distributed under the License is distributed on an "AS IS" BASIS,  
# WITHOUT WARRANTIES OR CONDITIONS OF ANY KIND, either express or implied.  
# See the License for the specific language governing permissions and  
# limitations under the License.  
#  
# We support and encourage derived works from this project, please read  
# about our expectations at  
#  
#     https://www.nipreps.org/community/licensing/  
#  
# STATEMENT OF CHANGES: This file is derived from work of the Nipreps  
# developers and has been adapted to run smoothly on our particular  
# dataset.  
#  
# ORIGINAL WORK'S ATTRIBUTION NOTICE:  
#  
#     Copyright 2021 The NiPreps Developers <nipreps@gmail.com>  
#
```

```
# Licensed under the Apache License, Version 2.0 (the "License");
# you may not use this file except in compliance with the License.
# You may obtain a copy of the License at
#
#     http://www.apache.org/licenses/LICENSE-2.0
#
# Unless required by applicable law or agreed to in writing, software
# distributed under the License is distributed on an "AS IS" BASIS,
# WITHOUT WARRANTIES OR CONDITIONS OF ANY KIND, either express or implied
# See the License for the specific language governing permissions and
# limitations under the License.

#SBATCH --partition=russpold
#SBATCH --mem=30GB
#SBATCH --cpus-per-task=16
#SBATCH --time=20:00:00
#SBATCH --job-name=fmriprep
#SBATCH --error="slurm-%A.err"

# Run only the anatomical workflow of fMRIPrep

DATADIR="/oak/stanford/groups/russpold/inprocess/cprovins/hcpph-pilot/"
SUB="sub-001"
STUDY=`basename $DATADIR`

echo "Processing the anatomical workflow on subject: $SUB"

IMG="/oak/stanford/groups/russpold/users/cprovins/singularity_images/fmriprep

WORKDIR="${L_SCRATCH}/fmriprep/${STUDY}/"
mkdir -p ${WORKDIR}
OUTDIR="${DATADIR}/derivatives"
mkdir -p $OUTDIR

PATCHES=""

BINDINGS="-B ${DATADIR}/inputs:/data:ro \
-B ${WORKDIR}:/work \
-B ${OUTDIR}:/out \
-B ${DATADIR}/code/license.txt:/opt/freesurfer/license.txt \
$PATCHES"

FMRIPREP_CMD="/data /out/fmriprep-23.1.4 participant \
-w /work \
--bids-filter-file /work/filter_file_undistorted.json \
--anat-only --skip_bids_validation \
--nprocs 4 --mem 25G --omp-nthreads 16 -vv"

#Create json file to filter undistorted anatomical scans
echo '{
  "t1w": {
    "datatype": "anat",
    "acquisition": "undistorted",
    "suffix": "T1w"
  }
}' > /work/filter_file_undistorted.json

SING_CMD="singularity run -e $BINDINGS $IMG $FMRIPREP_CMD"
echo $SING_CMD
$SING_CMD
echo "Completed with return code: $?"
```

- Submit a *job array* with one scanning session each with the `--bids-filter-file` argument selecting the corresponding sessions, and point the `--fs-subjects-dir` argument to the folder where *FreeSurfer* results were stored.

Launch each session through fMRIPrep in parallel

```
cd code/fmriprep  
bash ss-fmriprep.sh
```

The sbatch file to run *fMRIPrep* session-wise

```
#!/bin/bash  
# Copyright 2023 The Axon Lab <theaxonlab@gmail.com>  
#  
# Licensed under the Apache License, Version 2.0 (the "License");  
# you may not use this file except in compliance with the License.  
# You may obtain a copy of the License at  
#  
#     http://www.apache.org/licenses/LICENSE-2.0  
#  
# Unless required by applicable law or agreed to in writing, software  
# distributed under the License is distributed on an "AS IS" BASIS,  
# WITHOUT WARRANTIES OR CONDITIONS OF ANY KIND, either express or implied.  
# See the License for the specific language governing permissions and  
# limitations under the License.  
#  
# We support and encourage derived works from this project, please read  
# about our expectations at  
#  
#     https://www.nipreps.org/community/licensing/  
#  
# STATEMENT OF CHANGES: This file is derived from work of the Nipreps  
# developers and has been adapted to run smoothly on our particular  
# dataset.  
#  
# ORIGINAL WORK'S ATTRIBUTION NOTICE:  
#  
#     Copyright 2021 The NiPreps Developers <nipreps@gmail.com>  
#  
#     Licensed under the Apache License, Version 2.0 (the "License");  
#     you may not use this file except in compliance with the License.  
#     You may obtain a copy of the License at  
#  
#         http://www.apache.org/licenses/LICENSE-2.0  
#  
#     Unless required by applicable law or agreed to in writing, software  
#     distributed under the License is distributed on an "AS IS" BASIS,  
#     WITHOUT WARRANTIES OR CONDITIONS OF ANY KIND, either express or implied  
#     See the License for the specific language governing permissions and  
#     limitations under the License.  
  
#SBATCH --partition=russpold  
#SBATCH --mem=55GB  
#SBATCH --cpus-per-task=16  
#SBATCH --time=20:00:00
```

```
#SBATCH --job-name=fmriprep
#SBATCH --error="slurm-%A_%a.err"

# Submit a Single Session through fMRIPrep

ARGS=($@)
DATADIR=$1
STUDY=`basename $DATADIR` 

if [[ -n ${SLURM_ARRAY_TASK_ID} ]]; then
    SES=${ARGS[expr ${SLURM_ARRAY_TASK_ID} + 1]}
else
    SES=$2
fi

echo "Processing: $SES"

IMG="/oak/stanford/groups/russpold/users/cprovins/singularity_images/fmriprep

WORKDIR="${L_SCRATCH}/fmriprep/${STUDY}/${SES}"
mkdir -p ${WORKDIR}
OUTDIR="${DATADIR}/derivatives"
mkdir -p $OUTDIR

PATCHES=""

BINDINGS="-B ${DATADIR}/inputs:/data:ro \
-B ${WORKDIR}:/work \
-B ${OUTDIR}:/out \
-B ${DATADIR}/code/license.txt:/opt/freesurfer/license.txt \
-B ${HOME}/.cache/templateflow/tpl-MNI152NLin6Asym/:${HOME}/.cache/templatefl
$PATCHES"

FMRIPREP_CMD="/data/out/fmriprep-23.1.4 participant \
-w /work \
--bids-filter-file /work/filter_file_${SES}.json \
--skip_bids_validation \
--fs-subjects-dir /out/fmriprep-23.1.4/sourcedata/freesurfer \
--anat-derivatives /out/fmriprep-23.1.4 \
--nprocs 4 --mem 45G --omp-nthreads 8 -vv"

#Create json file to filter one session only
echo '{"bold": {"datatype": "func", "session": "'${SES}'"}, "suffix": "bold"}' > /tmp/filter.json

SING_CMD="singularity run -e $BINDINGS $IMG $FMRIPREP_CMD"
echo $SING_CMD
$SING_CMD
echo "Completed with return code: $?"
```

Extracting functional connectivity

Computing functional connectivity

First, make sure that the preprocessed fMRI data are available as derivatives in your dataset. An example of data structure should be as follows:

```
└── derivatives
    ├── fmriprep-23.1.4
    │   ├── dataset_description.json
    │   └── sub-pilot
    │       ├── anat
    │       ├── figures
    │       └── ses-15
```

Then, the functional connectivity matrices can be computed using the `compute_fc.py` script. The simplest call of the script only needs a derivative dataset (usually from *fMRIPrep*). Following the above data structure, it would be called as follows:

```
python compute_fc.py path_to_dataset/derivatives/fmriprep-23.1.4
```

Default call of the `compute_fc.py` script

^

When using the default options, the pipeline will (in this order and for all functional tasks):

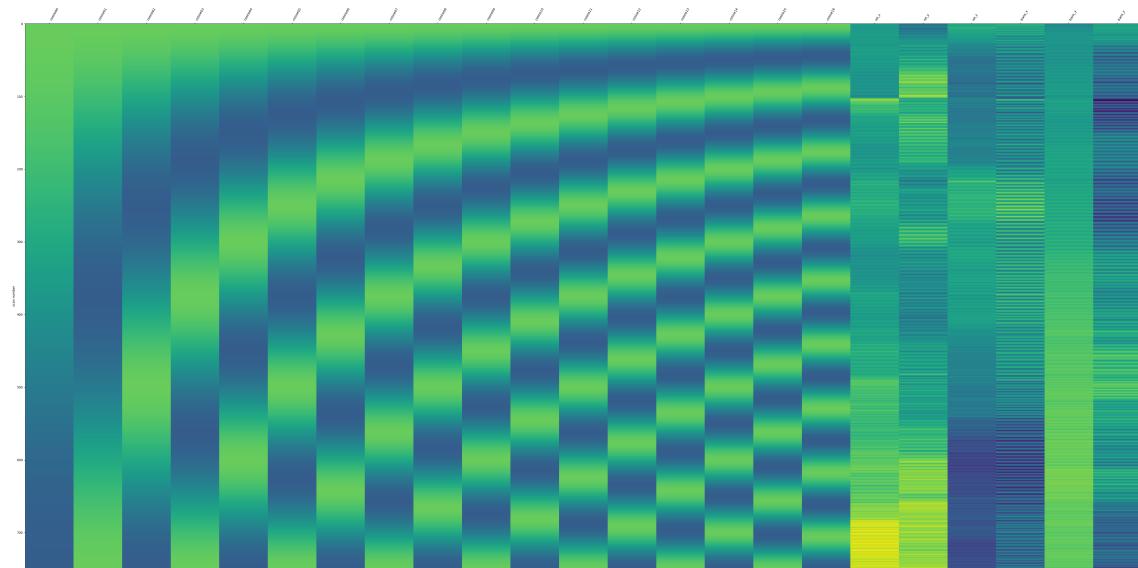
- Fetch the [DiFuMo](https://doi.org/10.1101/2020.11.12.26126) (<https://doi.org/10.1101/2020.11.12.26126>) atlas (64 dimensions)
- Extract the region-wise averaged timeseries
- Find high motion volumes that have framewise displacement higher than 0.4 mm or higher than 5 standardized DVAR. Then also flag as outlier the segments that are shorter than 5 timepoints.
- Interpolate high motion volumes with cubic spline interpolation
- Apply a low-pass butterworth filter (cutoff frequency of 0.15 Hz)
- Censor high motion volumes
- Remove confounds: motions (6 parameters) and discrete cosine transform basis (high-pass filtering)
- Standardize the timeseries
- Compute the functional connectivity matrices as the sparse inverse covariance (see this [example](https://nilearn.github.io/stable/auto_examples/03_connectivity/plot_inverse_covariance_connectome.html) (https://nilearn.github.io/stable/auto_examples/03_connectivity/plot_inverse_covariance_connectome.html), using [Graphical Lasso CV](https://scikit-learn.org/stable/modules/generated/sklearn.covariance.GraphicalLassoCV.html#sklearn.covariance.GraphicalLassoCV) (<https://scikit-learn.org/stable/modules/generated/sklearn.covariance.GraphicalLassoCV.html#sklearn.covariance.GraphicalLassoCV>) of scikit-learn)

Most parameters of the pipeline can be specified in the options (see `python compute_fc.py -h` for more details).

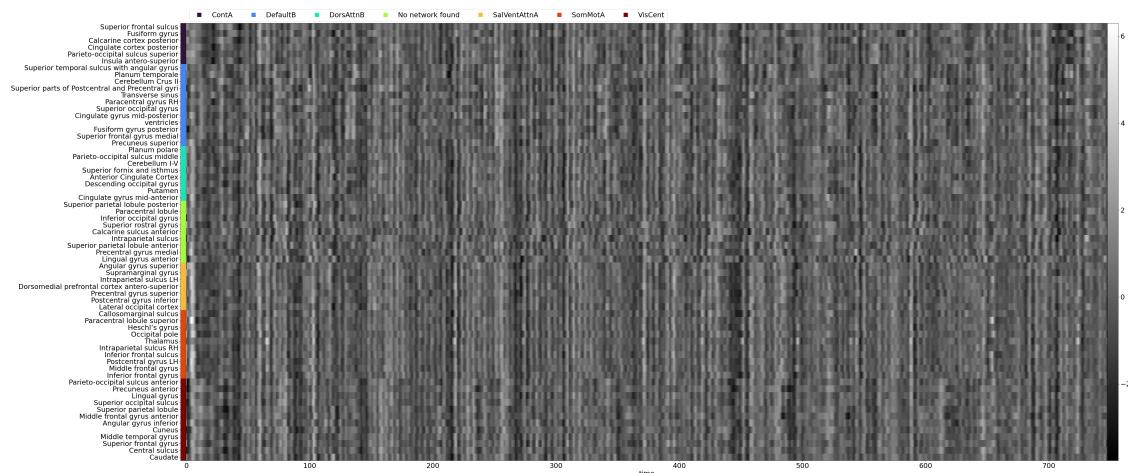
Finally, the pipeline will save the denoised timeseries and connectivity matrices as well as various visual reports (i.e., figures).

Example of visual report

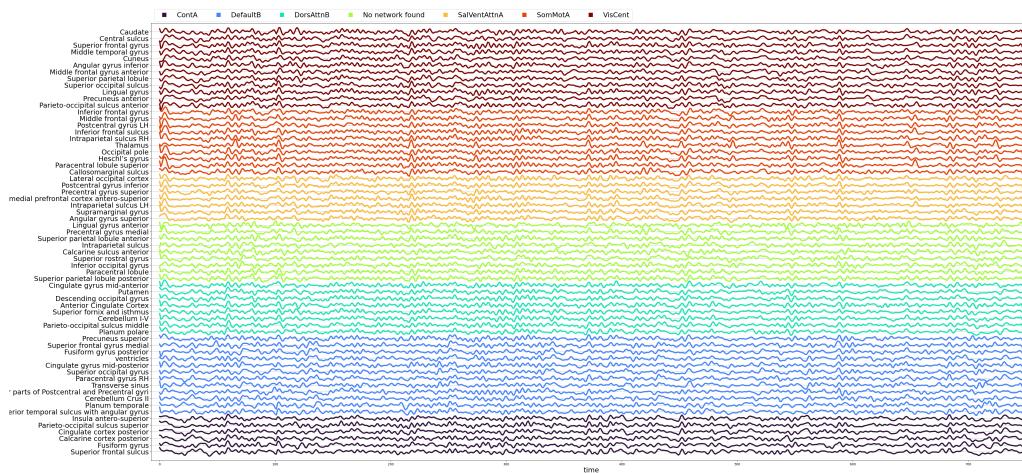
Denoising confounds as a *design matrix*:



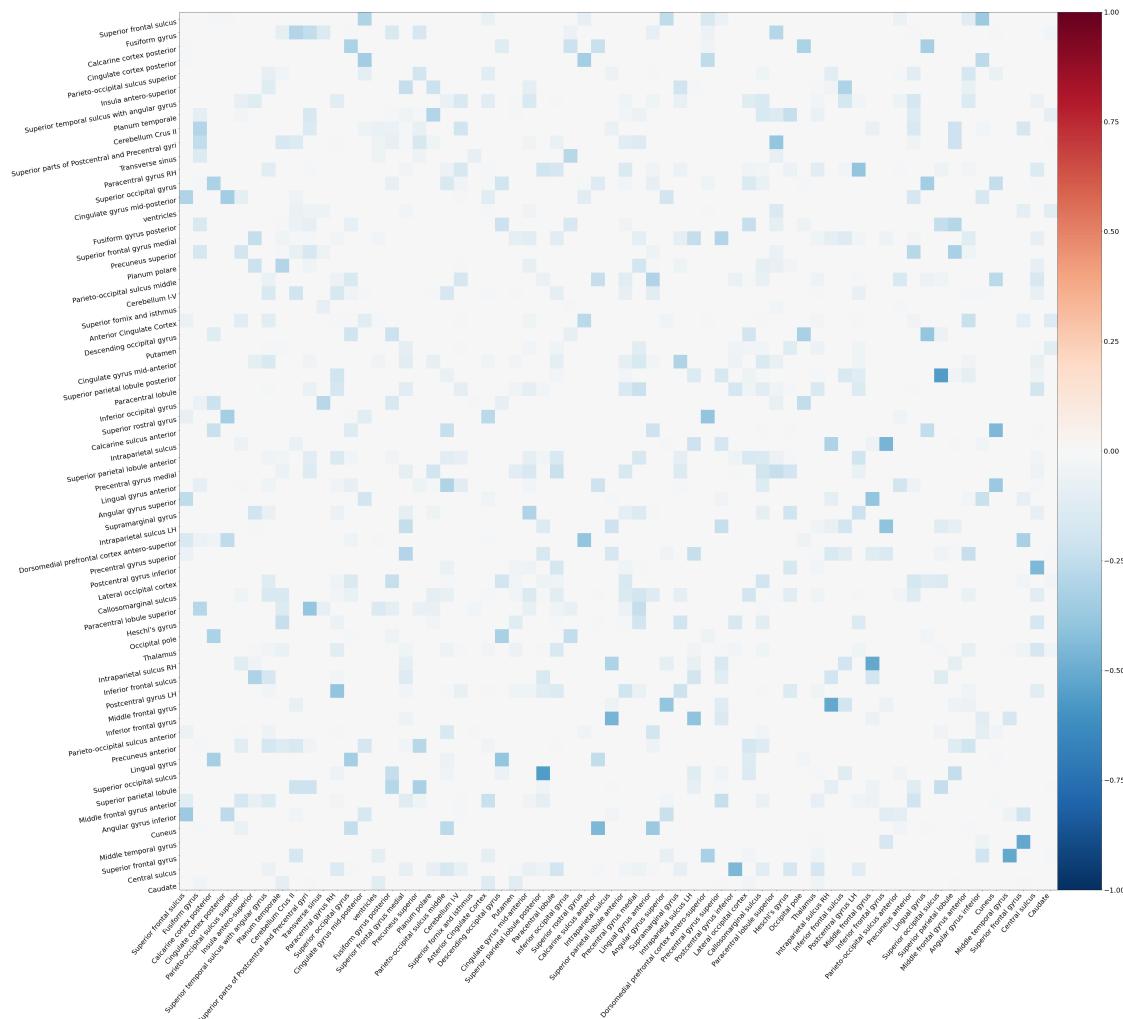
Denoised timeseries as a *carpet plot*:



Denoised timeseries as a *signal plot*:



Functional connectivity matrix as a *heatmap*:



The outputs will be stored in a **functional-connectivity** folder in the same parent directory as the preprocessed derivatives dataset. In the end, the data structure will look like this:

```
└── derivatives
    ├── fmriprep-23.1.4
    │   └── sub-pilot
    │       ├── anat
    │       ├── figures
    │       └── ses-15
    │           ├── anat
    │           └── func
    └── functional_connectivity
        └── DiFuMo64-LP
            └── sub-pilot
                ├── figures
                └── ses-15
                    └── func
```

Defacing

The first step before releasing the data is to deface the T1w and T2w images for all sessions. To perform defacing, we are using a software called PyDeface (Gulban et al. 2019). To proceed, run the following command in the command line:

```
bash ./code/defacing/run_pydeface.sh
```

References

- [1]: Gulban, Omer Faruk, Dylan Nielson, Russ Poldrack, John Lee, Chris Gorgolewski, Vanessa Sochat, and Satrajit Ghosh. 2019. “Poldracklab/Pydeface: V2.0.0.” Zenodo. doi: 10.5281/zenodo.3524401.

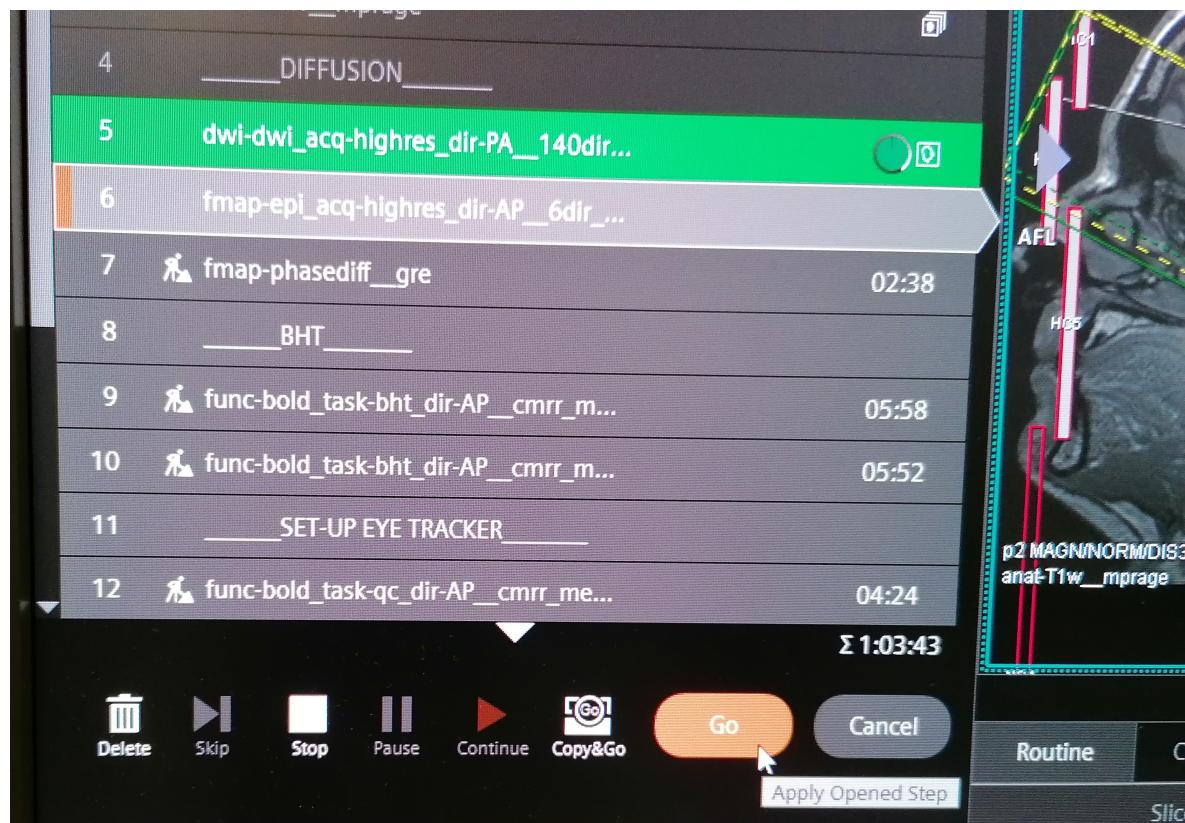
Appendices

Notes on the scanner's console and recording devices

Quick guide to the protocol settings and configuration

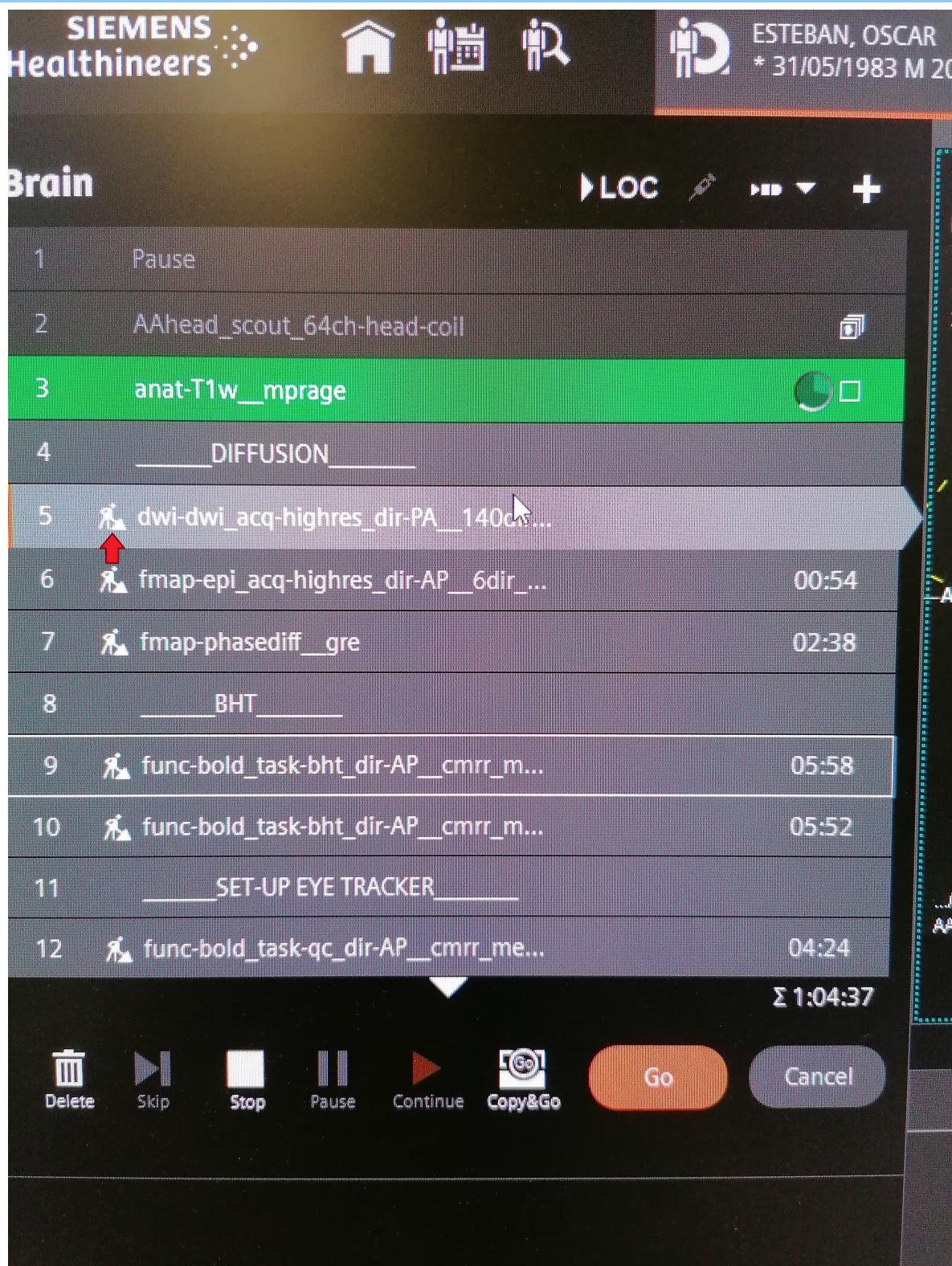
Editing a sequence

- Double click on the sequence name.
- After editing the sequence, you MUST store the changes if you want them to be kept by clicking on the Go button:

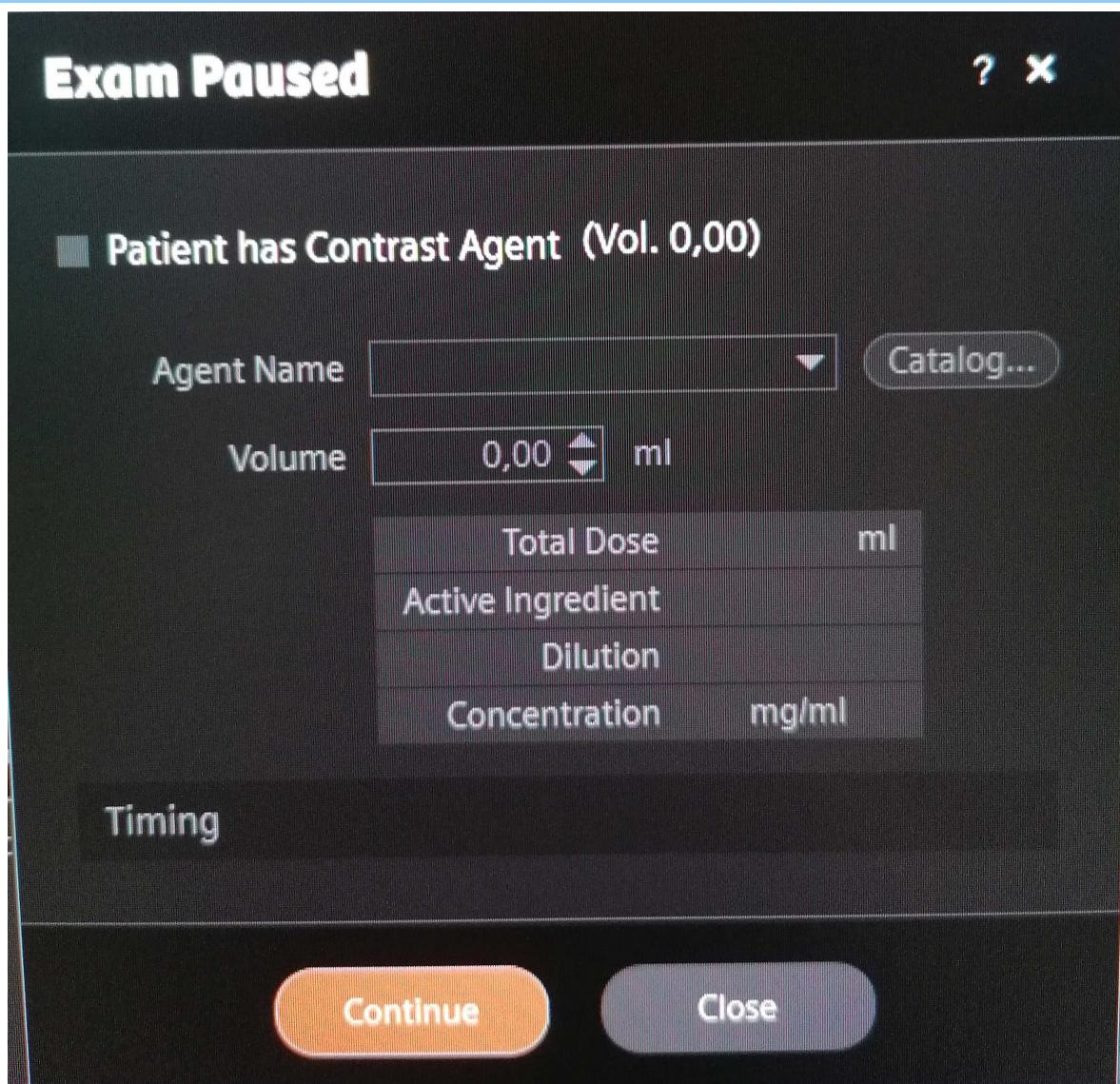


Setting sequences for automatic start

- You can set the worker icon on the left of the sequence by clicking on it if you want to pause before starting that sequence. If the worker is not present, the sequence will launch automatically.



- Blocks with a name between double underscores __ * __ introduce an *Exam Paused* break. Such breaks prompt a modal dialog with the *Exam Paused* title like this:



The *Patient has Contrast Agent* checkbox MUST always be unchecked, as this protocol does not involve a contrast agent"

- Click Continue when you are ready to proceed.

Setting the FoV

Using the anatomical image to adjust the field-of-view (FoV) is RECOMMENDED

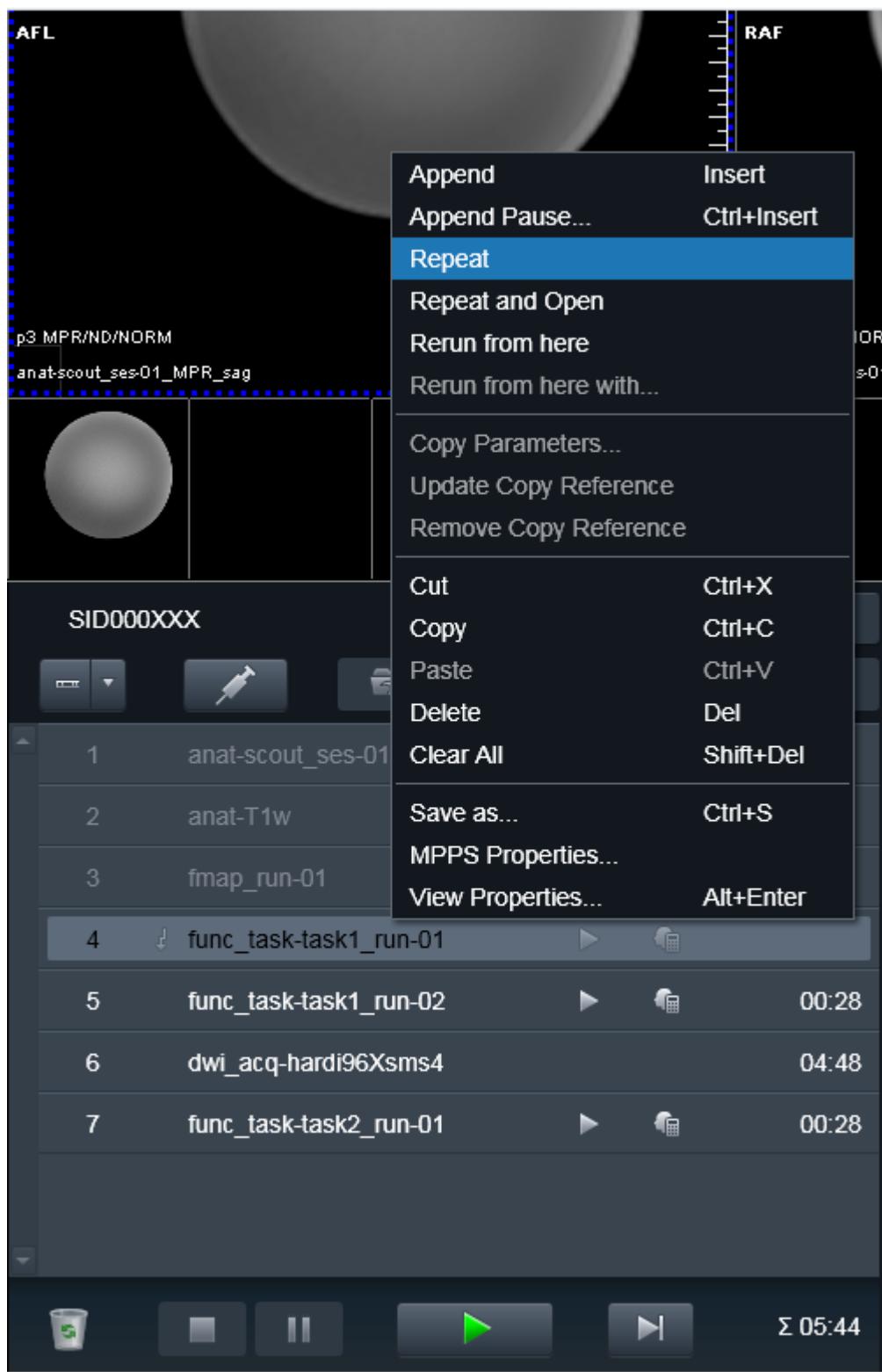
- Drag and drop the protocol's stack icon (MRI) corresponding to the anat-T1w_mprage sequence into the image viewer. The icon will appear AFTER the image has been acquired.
- Make sure that the FOV (yellow square) includes the whole brain by tilting or translating the FOV. If the full brain, including the cerebellum, do not fit in the FOV, favorise making sure that the cortex is fully enclosed in the yellow square. For reproducibility, it is better if the FOV across sequences have a similar center and a similar tilt. However, if it is not possible, the priority remains to include the whole brain in the FOV.

- If two sequences have the same resolution and the same number of slices, you can copy/paste the FOV
 - Open the sequence for which you want to adjust the FOV/geometry
 - Right click on the sequence for which the FOV has already been carefully positioned
 - Select Copy Parameters
 - Center of slice groups and saturation regions
- Once the FOV is well placed, store the new settings of the sequence by pressing Go.



Repeat scan

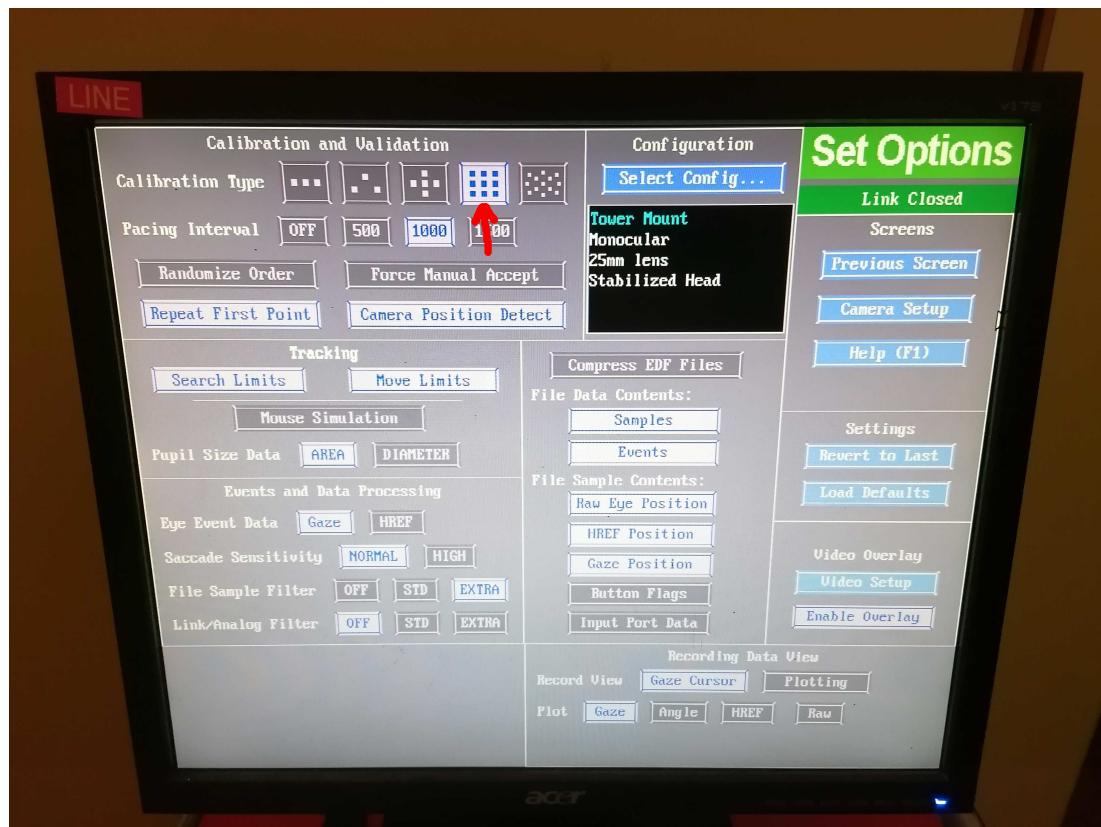
- If you have to interrupt a sequence because a problem occurred (e.g., the participant fell asleep, the stimuli were not adequately started, etc.), or you have to repeat a sequence because the image was of low quality, right click on the sequence that needs to be restarted and click on Repeat to restart the scan without changing anything in its name!



Eye-Tracker Calibration Process

- On the eye-tracking (ET) computer, ensure that the appropriate calibration type is selected (9-point for QCT and 5-point for resting state and breath-holding tasks):
 - Click on Set Options located on the right side of ET computer screen.

- Under Calibration type in the top left corner, choose the image containing either 9 or 5 points.

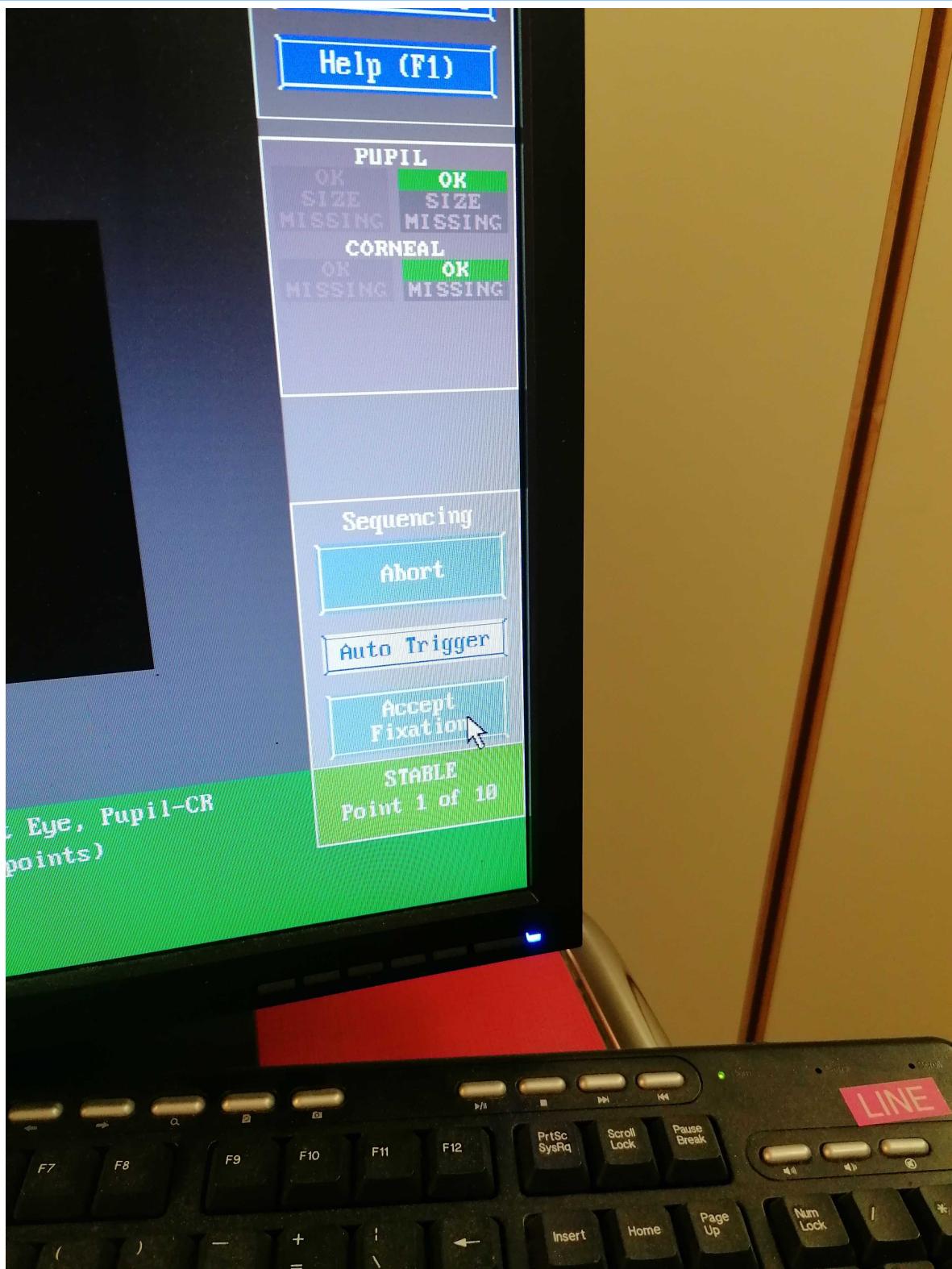


- Two crosses should appear on the ET computer screen: one at the center of the pupil and the other at the center of the corneal reflection.

If the two crosses do not appear, the coverage, focus and intensity of the ET are incorrect

- Repeat the steps for their setting up given in [the participant's preparation section](#)

- Initiate the ET calibration by pressing C on the laptop keyboard or by clicking on Calibration on the ET interface.
- Once the participant's gaze stabilizes on the first fixation point, the Accept Fixation button turns green. Click on it to confirm the initial position.

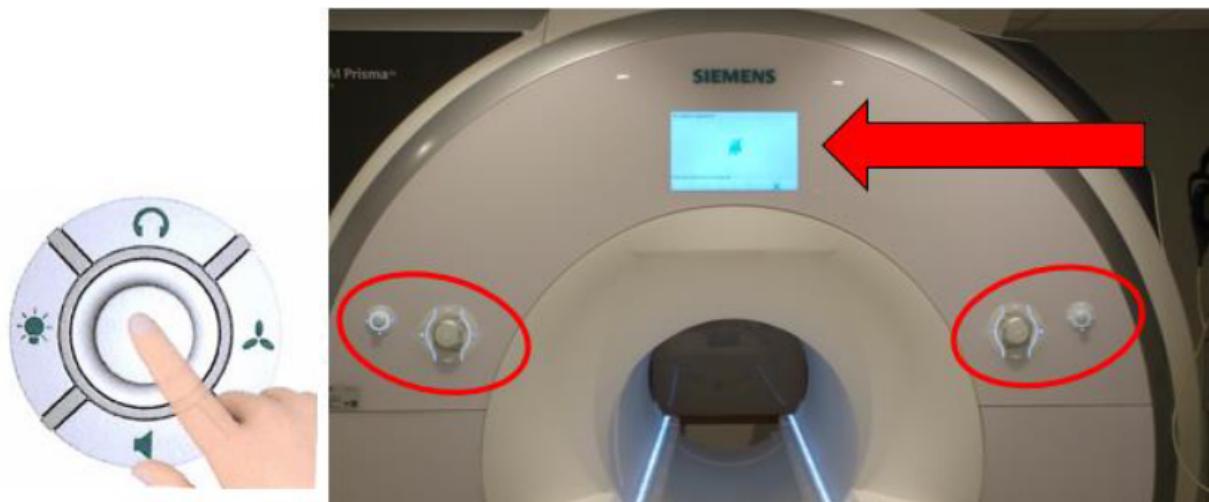


- Subsequent positions should be automatically validated when the gaze remains stable. If not, manually click the Accept Fixation button when it turns green.
- After the calibration, ensure that the fixation points' positions match the expected pattern corresponding to the 9- or 5-point calibration. If the pattern appears too distorted, restart the calibration.

- Upon successful calibration, initiate validation by clicking Validation on the ET interface or pressing the V key on the laptop keyboard. Follow the same instructions as in the calibration to validate positions.
- If validation fails, repeat previous steps and restart calibration. Otherwise, you can leave the calibration mode and proceed with the task program by pressing the Esc key on the laptop (████).

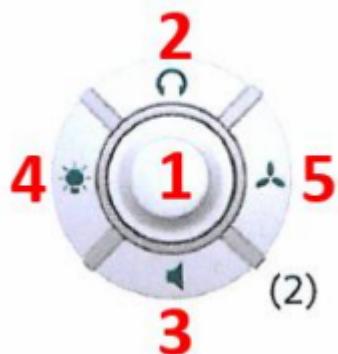
Scanner interface

The picture below shows you the scanner interface as you will see it when you operate the MR machine. The arrow points to the screen and the red circles indicate the control buttons.



Scanner's settings buttons

Adjust settings by pressing the respective button and then turning the central knob (1) to adjust the setting to the desired level:

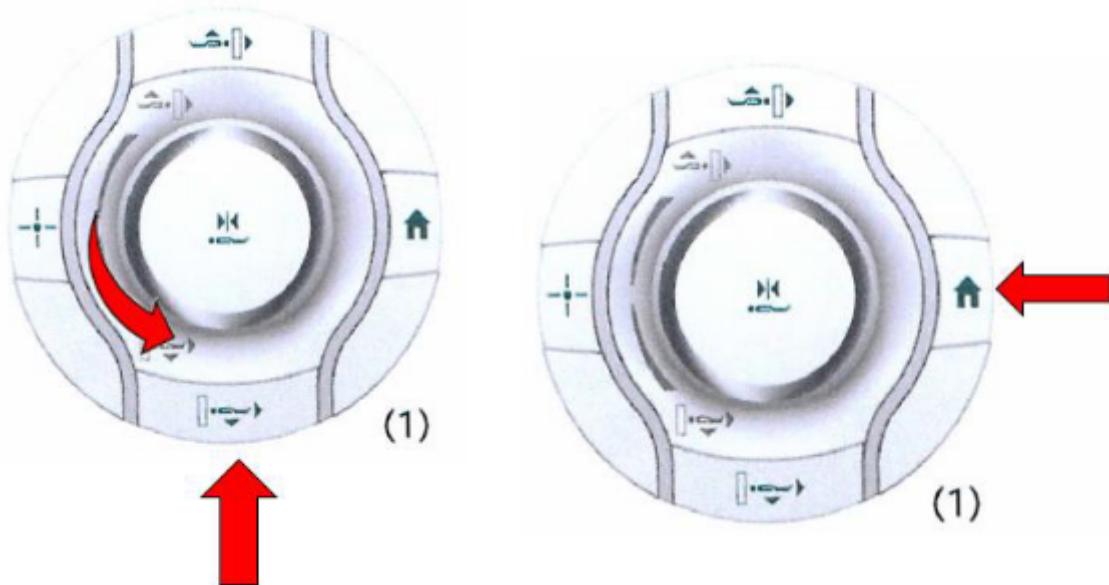


- Use the headphones button (2) to adjust the volume of the earphones.
- Use the speaker button (3) to adjust the volume of the air speaker in the scanning room.
- Use the light button (4) to adjust the intensity of the illumination inside the scanning room.
- Use the fan button (5) to adjust the ventilation in the scanning room.

The central knob (button 1) will turn off the alarm if pushed when the alarm is on

Standard extraction of the participant

There are two options to extract the participant, when the session has concluded or within the session if the participant needs to be extracted and there is no emergency (e.g., in case of technical error the scanner does not permit continuing the session and it needs to be aborted).



The participant can be extracted by pressing the extraction button (bottom arrow in the leftmost picture) and then gently rolling the central knob. Alternatively, you can just press the Home button (rightmost picture).

Notes on software installation and tips

Preparing Ubuntu for *Psychopy*

Psychopy is preferably installed in a pure *Python* environment

If an anaconda environment is activated, run the following command to deactivate it:

```
conda deactivate
```

- Ensure your Ubuntu system has all necessary dependencies:

```
sudo apt install python3-dev \
    libgtk-4-dev \
    libgstreamer1.0-dev \
    libgstreamer-plugins-base1.0-dev \
    freeglut3-dev \
    libwebkitgtk-6.0-dev \
    libjpeg8-dev \
    libpng-dev \
    libtiff-dev \
    libsdl1.2-dev \
    libnotify-dev \
    libsm-dev
```

Multiple screens

If you want to use multiple screens, install the corresponding libxcb extension:

```
sudo apt-get install libxcb-xinerama0
```

- Create a *Python* virtual environment:

```
python3 -m venv $HOME/psychopyenv
```

- Load the new virtual environment:

```
source $HOME/psychopyenv/bin/activate
```

- Update *Pypi* and *setuptools* to the latest version:

```
python -m pip install -U pip setuptools six wheel
```

- Update *Numpy* to the latest version:

```
python -m pip install -U numpy
```

- Download the *wxPython* sources:

```
python -m pip download wxPython
```

- Build *wxPython* (version of package may change on your settings, edit accordingly):

```
python -m pip wheel -v wxPython-4.2.1.tar.gz 2>&1 | tee build.log
```

- Install the wheel you just created:

```
python -m pip install wxPython-4.2.1-<python-version>-linux_x86_64.whl
```

- Test the installation (an empty window should we created without errors):

```
python -c "import wx; a=wx.App(); wx.Frame(None,title='hello world')"
```

- Install our *HCPH-signals* package (assumes these SOPs are checked out at <path>):

```
cd <path>/code/signals  
python -m pip install .
```

Psychopy installation

This block describes how to prepare an environment with a running *Psychopy* 3 installation.

Make sure to load the correct environment

- Deactivate conda (if active):

```
conda deactivate
```

- Load the new virtual environment:

```
source $HOME/psychopyenv/bin/activate
```

- Clone the *Psychopy* repository (<https://github.com/psychopy/psychopy>):

```
git clone https://github.com/psychopy/psychopy.git
```

- Navigate to the *Psychopy* directory and check-out tag 2023.2.3:

```
cd psychopy  
git checkout 2023.2.3
```

- Install *Psychopy* using the following command:

```
python -m pip install . [suggested]
```

- Install the *EyeLink* plugin for *Psychopy*:

```
python -m pip install git+https://github.com/oesteban/psychopy·
```

On MacOSX or if you don't have access to pip directly, *Psychopy*'s package manager

Open *Psychopy* as mentioned immediately below. Click *Tools* → *Plugin/Packages manager...*, then go to the *Packages* tab and hit the Open PIP terminal button (bottom left area). There, you can type:

```
pip install git+https://github.com/oesteban/psychopy-eyetracker-eyelink.git
```

- Install the *Pylink* module made by *SR Research*, it is distributed with the [installation of the eyelink-display-software](#) done previously:

```
python -m pip install /usr/share/EyeLink/SampleExperiments/Pytl
```

Find the appropriate version for your Python distribution

The example above is for *cPython* 3.10, alternative installations are:

```
/usr/share/EyeLink/SampleExperiments/Python/wheels/sr_research_pylink-2.1.762  
/usr/share/EyeLink/SampleExperiments/Python/wheels/sr_research_pylink-2.1.762  
/usr/share/EyeLink/SampleExperiments/Python/wheels/sr_research_pylink-2.1.762
```

```
/usr/share/EyeLink/SampleExperiments/Python/wheels/sr_research_pylink-2.1.762
/usr/share/EyeLink/SampleExperiments/Python/wheels/sr_research_pylink-2.1.762
/usr/share/EyeLink/SampleExperiments/Python/wheels/sr_research_pylink-2.1.762
/usr/share/EyeLink/SampleExperiments/Python/wheels/sr_research_pylink-2.1.762
```

- Try opening *Psychopy* by typing:

```
psychopy --no-splash -b
```

Check that the *EyeLink* eye tracker is available in the dropdown under the experiment's options

If the *EyeLink* is not available, most likely the appropriate *Pylink* is missing. See the last checkbox in the [installation of the eye tracker](#) to install it. Otherwise, make sure you installed the *EyeLink* plugin above.

The first time it runs, *Psychopy* will likely request some increased permissions

- Add a new psychopy group to your system.

```
sudo groupadd --force psychopy
```

- Add your current user to the new group:

```
sudo usermod -a -G psychopy $USER
```

- Raise security thresholds for *Psychopy*, by inserting the following into */etc/security/limits.d/99-psychopylimits.conf*:

```
@psychopy - nice -20
@psychopy - rtprio 50
@psychopy - memlock unlimited
```

Psychopy crashes when trying to run a experiment: `pyglet.gl.ContextException: Could not create GL context`

This is likely related to your computer having a GPU and a nonfunctional configuration:

```
$ glxinfo | grep OpenGL
X Error of failed request:  BadValue (integer parameter out of range for operation)
Major opcode of failed request:  151 (GLX)
Minor opcode of failed request:  24 (X_GLXCreateNewContext)
Value in failed request:  0x0
Serial number of failed request:  110
Current serial number in output stream:  111
```

A quick attempt to solve this would be adding our user to the video group.

However, that is unlikely to work out so you'll need to take more actions (see [this](https://github.com/mmatl/pyrender/issues/13) (<https://github.com/mmatl/pyrender/issues/13>), and [this](https://askubuntu.com/questions/1255841/how-do-i-fix-the-glxinfo-badvalue-error-on-ubuntu-18-04) (<https://askubuntu.com/questions/1255841/how-do-i-fix-the-glxinfo-badvalue-error-on-ubuntu-18-04>))

Psychopy crashes when trying to run a experiment: qt.qpa.plugin: Could not load the Qt platform plugin 'xcb'

If you installed `libxcb-xinerama0`, or you don't have multiple screens, first try:

```
python -m pip uninstall opencv-python
python -m pip install opencv-python-headless
```

If that doesn't work, try a brute force solution by installing `libxcb` fully:

```
sudo apt-get install libxcb-*
```

Psychopy does not recognize the SR Research eye tracker

If the eye tracker does not appear in the corresponding dropdown menu or your experiments fail [as described in this issue](#) (<https://github.com/psychopy/psychopy/issues/5947>), you almost certainly need to check the plugin is installed and available within *Psychopy*'s environment.

Setting up the synchronization service as a daemon in the background

It's fundamental to have a reliable means of communication with the BIOPAC digital inputs

The following guidelines set up a little service on a linux box that keeps listening for key presses (mainly, the s trigger from the trigger box), and RPC (remote procedure calls) from typically *Psychopy* or similar software.

The service is spun up automatically when you connect the MMBT-S modem interface that communicates with the BIOPAC (that is, the *N-shaped pink box*)

- To automatically start the program when the BIOPAC is connected, create a udev rule as follows:

```
sudo nano /etc/udev/rules.d/99-forward-trigger.rules
```

- Add the following rule to the file:

```
ACTION=="add", KERNEL=="ttyACM0", SUBSYSTEM=="tty", TAG+="systemd"
```

- Save the file and exit the editor.
- Run the following command to reload the udev rules:

```
sudo udevadm control --reload-rules
```

- Create a systemd service unit file:

```
sudo nano /etc/systemd/system/forward-trigger.service
```

- Add the following content to the file (Adapt the path to forward-trigger.py to the location on your computer):

```
[Unit]
Description=Forward Trigger Service
After=network.target

[Service]
ExecStart=/usr/bin/python3 /path/to/forward-trigger.py
WorkingDirectory=/path/to/forward-trigger/directory
StandardOutput=null

[Install]
WantedBy=multi-user.target
```

- Save the file and exit the text editor.
- Run the following command to enable the service to start at boot:

```
sudo systemctl enable forward-trigger
```

- Run the following command to reload the systemd daemon:

```
sudo systemctl daemon-reload
```