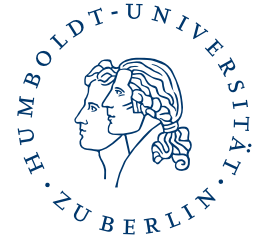

hu-neuro-pipeline

A Python-based and R-compatible pipeline for processing single trial EEG data

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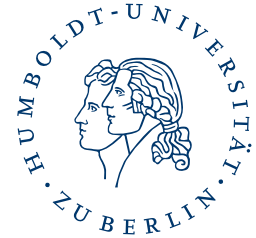
2023-01-11

The Frömer et al. (2018) pipeline



The Frömer et al. (2018) pipeline

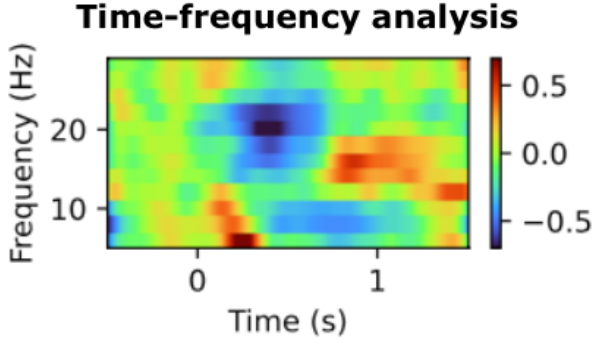
- Allows single trial analysis of ERP amplitudes
  - Random effects for items (Bürki et al., 2018)
  - Trial and item level covariates (Volpert-Esmond et al., 2021)
  - Continuous predictor variables
  - Unbalanced designs

Python implementation

+

MNE

+



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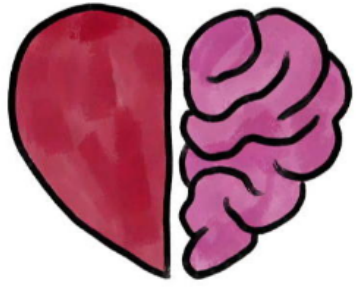


Python, I choose you!

Blog post: https://dominiquemakowski.github.io/post/2020-05-22-r_or_python
Online course: https://swcarpentry.github.io/python-novice-inflammation

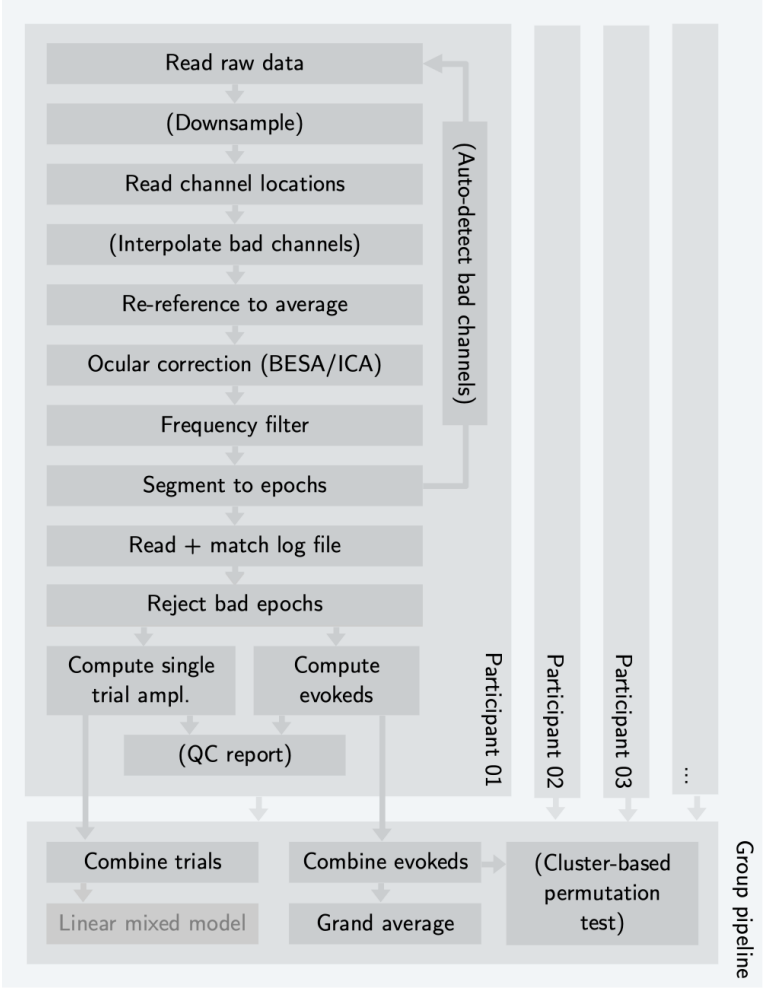
MNE-Python

- Versatile
  - EEG, MEG, ECoG, fNIRS
  - Preprocessing, statistics, time-frequency analysis, visualization, machine learning, connectivity, source localization, ...
- Open source
  - 329 contributors on GitHub (January 2023)
  - Funded by NIH, NSF, ERC, Google, Amazon, ...
  - Code review, automated tests, user forum, office hours, ...

Python implementation

- No MATLAB required
- No Python skills required – can be called from R
- New features:
  - Time-frequency analysis
  - Fully automatic ocular correction (ICA)
  - Automatic bad channel detection
  - Automatic missing trial detection
- Code standards + version control
  (https://github.com/alexenge/hu-neuro-pipeline/)

Python implementation



Installation

For Python users:

```
# Install via the command line from the Python Packaging Index (PyPI)
python3 -m pip install hu-neuro-pipeline
```

For R users:

```
# Install reticulate for interfacing with Python from R
install.packages("reticulate")

# Install Python (Miniconda distribution)
reticulate::install_miniconda()

# Install the actual package from PyPI
reticulate::py_install("hu-neuro-pipeline", pip = TRUE, python_version = "3.8")
```

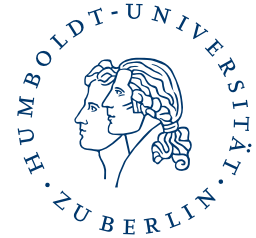
General usage


```r
# Import the Python package
pipeline <- reticulate::import("pipeline")

# Run the pipeline
res <- pipeline$group_pipeline(...)
```

Minimal example


```r
# Import the Python package
pipeline <- reticulate::import("pipeline")

# Run the pipeline
res <- pipeline$group_pipeline(
  # Input/output paths
  vhdr_files = "data/raw",
  log_files = "data/log",
  output_dir = "output",
  # Preprocessing options
  besa_files = "data/cali",
  # Epoching options
  triggers = c(201:208, 211:218),
  components = list(
    "name" = list("N2", "P3b"),
    "tmin" = list(0.25, 0.4),
    "tmax" = list(0.35, 0.55),
    "roi" = list(
      c("FC1", "FC2", "C1", "C2", "Cz"),
      c("CP3", "CP1", "CPz", "CP2", "CP4", "P3", "Pz", "P4", "PO3", "POz", "PO4")
    )
  ),
  # Averaging options
  average_by = c("n_b", "DeviantPosRL", "n_b/DeviantPosRL")
)
```

Minimal example



Pipeline inputs


```
# Input/output paths
vhdr_files = "data/raw",
log_files = "data/log",
output_dir = "output",
```

- Directory or list of raw EEG files (`.vhdr`)
- Directory or list of behavioral log files (`.txt`/`.tsv`/`.csv`)
- Output directory

Pipeline inputs

```
# Preprocessing options
besa_files = "data/cali",
```

- Directory path or list of BESA files (`.matrix`)
- Default bandpass filter (0.1–40 Hz)

Pipeline inputs

```
# Epoching options
triggers = c(201:208, 211:218),
components = list(
  "name" = list("N2", "P3b"),
  "tmin" = list(0.25, 0.4),
  "tmax" = list(0.35, 0.55),
  "roi" = list(
    c("FC1", "FC2", "C1", "C2", "Cz"),
    c("CP3", "CP1", "CPz", "CP2", "CP4", "P3", "Pz", "P4", "PO3", "POz", "PO4")
  )
),
```

- List of numerical EEG triggers
- List of ERP component definitions:
  - `name`: Column names for each component
  - `tmin` + `tmax`: Onset and offset times (in s)
  - `roi`: List of channel names for each component

Pipeline inputs


```
# Averaging options
average_by = c("n_b", "DeviantPosRL", "n_b/DeviantPosRL")
```

- List of column names (for main effects) and combinations of column names (for interaction effects, separated by "/")

More pipeline inputs

- Downsampling (`downsample_sfreq`)
- Interpolate bad channels (`bad_channels`)
- Frequency filter (`highpass_freq`, `lowpass_freq`)
- Epoch duration (`epochs_tmin`, `epochs_tmax`)
- Baseline duration (`baseline`)
- Skip log file rows (`skip_log_rows`, `skip_log_conditions`)
- Threshold for artifact rejection (`reject_peak_to_peak`)
- ...

See https://github.com/alexenge/hu-neuro-pipeline/blob/main/docs/inputs.md

Pipeline outputs

Extract directly from the pipeline run:

```
trials <- res[[1]]   # Single trial data frame
evokeds <- res[[2]]  # Evokeds data frame
config <- res[[3]]   # List of pipeline options
```

Or read from the output directory:

```
library(tidyverse)
trials <- read_csv("output/trials.csv")
evokeds <- read_csv("output/ave.csv")
config <- jsonlite::read_json("output/config.json")
```

See https://github.com/alexenge/hu-neuro-pipeline/blob/main/docs/outputs.md

Pipeline outputs

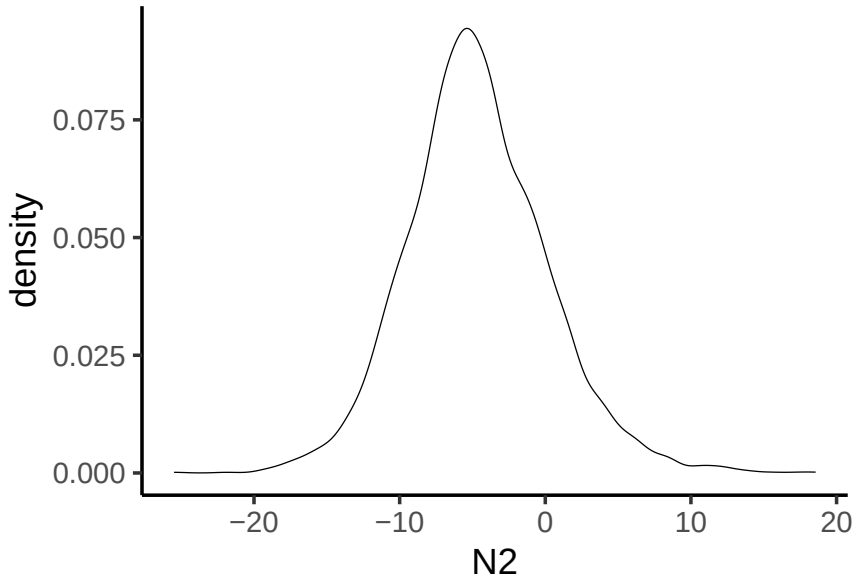
```
# Single trial data frame
print(trials)
```

```
## # A tibble: 3,840 x 32
##    participa~1 VPNum~2 version   wdh lfdNr n_b   Stand~3 Deviant Objek~4 BedCo~5
##    <chr>         <dbl>   <dbl> <dbl> <dbl> <chr> <chr>   <chr>     <dbl> <chr>
##  1 05                5       1     1     1 norm~ objekt~ objekt~       8 gngf
##  2 05                5       1     1     2 blurr objekt~ objekt~      10 un
##  3 05                5       1     1     3 blurr objekt~ objekt~      10 un
##  4 05                5       1     1     4 norm~ objekt~ objekt~       3 un
##  5 05                5       1     1     5 norm~ objekt~ objekt~      15 unuf
##  6 05                5       1     1     6 norm~ objekt~ objekt~       7 unuf
##  7 05                5       1     1     7 blurr objekt~ objekt~       2 un
##  8 05                5       1     1     8 norm~ objekt~ objekt~      16 gngf
##  9 05                5       1     1     9 norm~ objekt~ objekt~       9 gn
## 10 05                5       1     1    10 norm~ objekt~ objekt~      11 un
## # ... with 3,830 more rows, 22 more variables: BedCode_neu <chr>, bot <dbl>,
## #   DeviantPosRL <chr>, DeviantPosNR <dbl>, BedCodeRL <chr>, key <dbl>,
## #   ErrorCode <dbl>, RT <dbl>, Pos1 <chr>, Pos2 <chr>, Pos3 <chr>, Pos4 <chr>,
## #   Pos5 <chr>, Pos6 <chr>, Pos7 <chr>, Pos8 <chr>, Pos9 <chr>, Pos10 <chr>,
## #   Pos11 <chr>, Pos12 <chr>, N2 <dbl>, P3b <dbl>, and abbreviated variable
## #   names 1: participant_id, 2: VPNummer, 3: Standard, 4: Objektpaar,
## #   5: BedCode_alt
```

Pipeline outputs

```
# Single trial N2 mean amplitudes
ggplot(trials, aes(x = N2)) +
  geom_density() +
  theme_classic(base_size = 30)
```

```
## Warning: Removed 7 rows containing non-finite values (‘stat_density()‘).
```



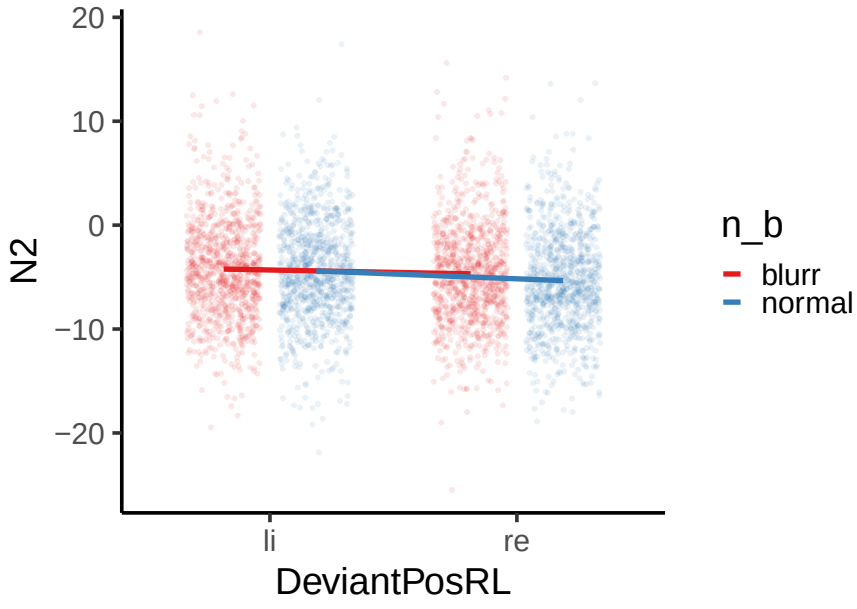
Pipeline outputs

```r
# Linear mixed-effects model
form <- N2 ~ n_b * DeviantPosRL + (1 | participant_id)
mod <- lme4::lmer(form, trials)
summary(mod)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: N2 ~ n_b * DeviantPosRL + (1 | participant_id)
##    Data: trials
##
## REML criterion at convergence: 22696.1
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -4.6856 -0.6130 -0.0002  0.6148  5.1121
##
## Random effects:
##  Groups         Name        Variance Std.Dev.
##  participant_id (Intercept)  2.287   1.512
##  Residual                   21.780   4.667
## Number of obs: 3833, groups:  participant_id, 2
##
## Fixed effects:
##                            Estimate Std. Error t value
## (Intercept)                 -4.2285     1.0800  -3.915
## n_bnormal                   -0.1796     0.2132  -0.842
## DeviantPosRLre              -0.4587     0.2132  -2.151
## n_bnormal:DeviantPosRLre    -0.4732     0.3015  -1.569
##
```

Pipeline outputs

```
# Single trial N2 mean amplitudes by condition
ggplot(trials, aes(x = DeviantPosRL, y = N2, color = n_b, group = n_b)) +
  geom_point(position = position_jitterdodge(0.3), alpha = 0.1) +
  stat_summary(
    geom = "line",
    size = 2.,
    position = position_dodge(0.75)
  ) +
  theme_classic(base_size = 30)
```



Pipeline outputs

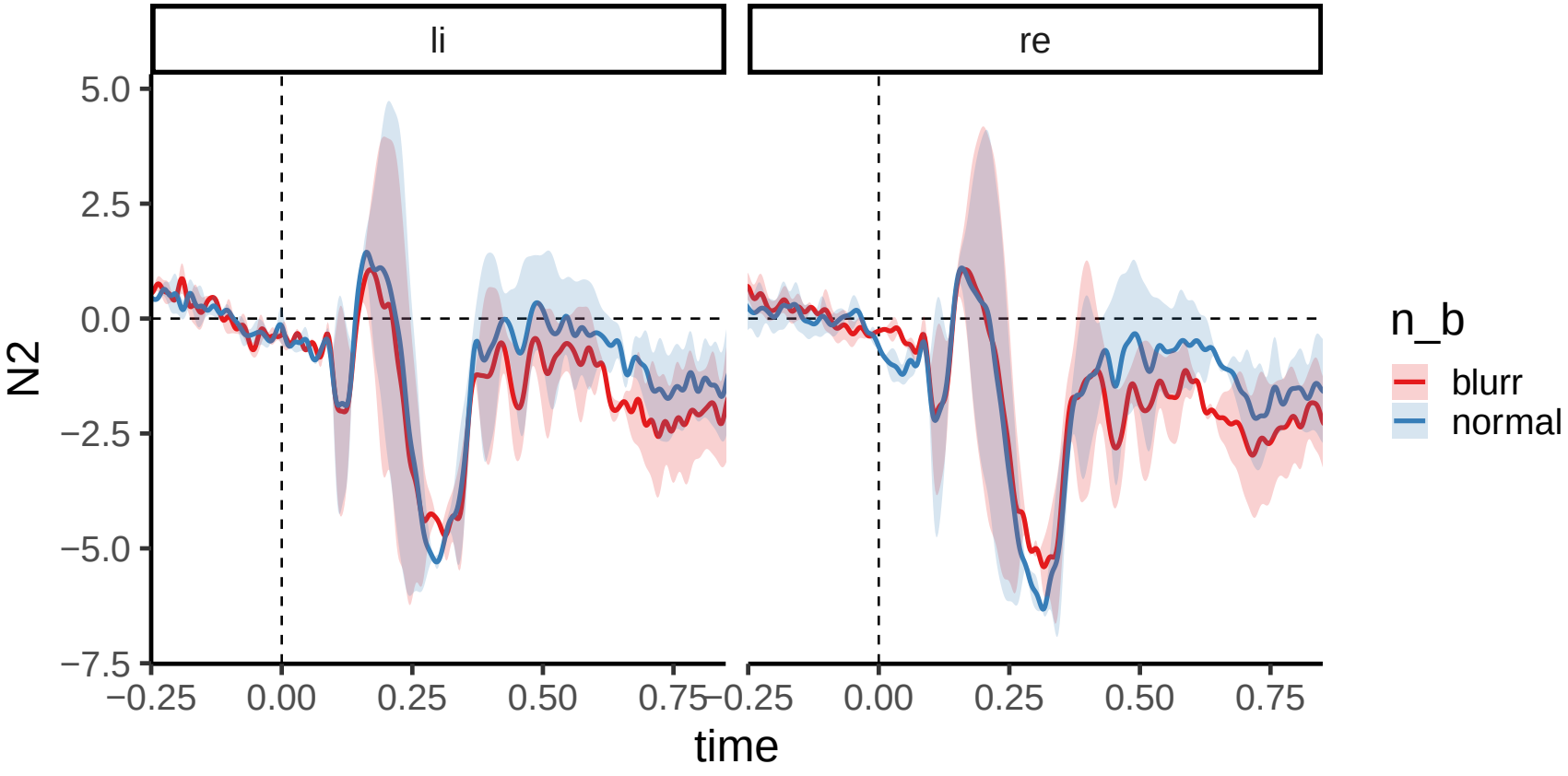
```
# Evokeds by participant and condition
print(evokeds)
```

```
## # A tibble: 16,000 x 70
##    particip~1 avera~2 n_b   Devia~3   time    Fp1   Fpz   Fp2    AF7   AF3   AFz
##    <chr>      <chr>   <chr> <chr>    <dbl>  <dbl> <dbl> <dbl>  <dbl> <dbl> <dbl>
##  1 05         n_b     norm~ <NA>    -0.5   -0.751 -1.49 -1.35 -1.14  -1.94 -1.86
##  2 05         n_b     norm~ <NA>    -0.498 -0.779 -1.46 -1.30 -1.16  -2.04 -1.93
##  3 05         n_b     norm~ <NA>    -0.496 -0.809 -1.43 -1.25 -1.15  -2.11 -2.00
##  4 05         n_b     norm~ <NA>    -0.494 -0.836 -1.40 -1.21 -1.13  -2.14 -2.06
##  5 05         n_b     norm~ <NA>    -0.492 -0.859 -1.39 -1.17 -1.10  -2.14 -2.10
##  6 05         n_b     norm~ <NA>    -0.49  -0.876 -1.39 -1.15 -1.05  -2.10 -2.12
##  7 05         n_b     norm~ <NA>    -0.488 -0.886 -1.42 -1.14 -1.01  -2.06 -2.12
##  8 05         n_b     norm~ <NA>    -0.486 -0.893 -1.46 -1.15 -0.976 -2.00 -2.10
##  9 05         n_b     norm~ <NA>    -0.484 -0.896 -1.51 -1.17 -0.952 -1.95 -2.09
## 10 05         n_b     norm~ <NA>    -0.482 -0.898 -1.56 -1.19 -0.942 -1.90 -2.07
## # ... with 15,990 more rows, 59 more variables: AF4 <dbl>, AF8 <dbl>, F9 <dbl>,
## #   F7 <dbl>, F5 <dbl>, F3 <dbl>, Fz <dbl>, F4 <dbl>, F6 <dbl>, F8 <dbl>,
## #   F10 <dbl>, FT7 <dbl>, FC5 <dbl>, FC3 <dbl>, FC1 <dbl>, FC2 <dbl>,
## #   FC4 <dbl>, FC6 <dbl>, FT8 <dbl>, T7 <dbl>, C5 <dbl>, C3 <dbl>, C1 <dbl>,
## #   Cz <dbl>, C2 <dbl>, C4 <dbl>, C6 <dbl>, T8 <dbl>, TP9 <dbl>, TP7 <dbl>,
## #   CP5 <dbl>, CP3 <dbl>, CP1 <dbl>, CPz <dbl>, CP2 <dbl>, CP4 <dbl>,
## #   CP6 <dbl>, TP8 <dbl>, TP10 <dbl>, P7 <dbl>, P5 <dbl>, P3 <dbl>, ...
```

Pipeline outputs

```
# Evokeds by participant/condition
evokeds %>%
  filter(average_by == "n_b/DeviantPosRL") %>%
  Rmisc::summarySEwithin(
    measurevar = "N2",
    withinvars = c("time", "n_b", "DeviantPosRL"),
    idvar = "participant_id"
  ) %>%
  mutate(time = as.numeric(levels(time))[time]) %>%
  ggplot(aes(
    x = time,
    y = N2,
    ymin = N2 - se,
    ymax = N2 + se,
    color = n_b,
    fill = n_b
  )) +
  facet_wrap(~DeviantPosRL) +
  geom_hline(yintercept = 0, linetype = "dashed") +
  geom_vline(xintercept = 0, linetype = "dashed") +
  geom_line(size = 1) +
  geom_ribbon(color = NA, alpha = 0.2) +
  coord_cartesian(xlim = c(-0.2, 0.8)) +
  theme_classic(base_size = 20)
```

Pipeline outputs



Pipeline outputs


```
# List of pipeline options
names(config)
```

```
##  [1] "vhdr_files"           "log_files"            "output_dir"
##  [4] "clean_dir"            "epochs_dir"           "report_dir"
##  [7] "to_df"                "downsample_sfreq"     "veog_channels"
## [10] "heog_channels"        "montage"              "bad_channels"
## [13] "besa_files"           "ica_method"           "ica_n_components"
## [16] "highpass_freq"        "lowpass_freq"         "triggers"
## [19] "triggers_column"      "epochs_tmin"          "epochs_tmax"
## [22] "baseline"             "skip_log_rows"        "skip_log_conditions"
## [25] "reject_peak_to_peak"  "components"           "average_by"
## [28] "perform_tfr"          "tfr_subtract_evoked"  "tfr_freqs"
## [31] "tfr_cycles"           "tfr_mode"             "tfr_baseline"
## [34] "tfr_components"       "perm_contrasts"       "perm_tmin"
## [37] "perm_tmax"            "perm_channels"        "perm_fmin"
## [40] "perm_fmax"            "n_jobs"               "auto_rejected_epochs"
```

```
# Number of rejected epochs per participant
lengths(config$auto_rejected_epochs)
```

```
## 05 07
##  7  0
```

More pipeline outputs

- Cleaned continuous data (`clean_dir`)
- Epoched data (`epochs_dir`)
- Automated QC reports (`reports_dir`)

Cluster-based permutation tests


```r
# Permutation test input
perm_contrasts = list(
  c("blurr", "normal"),
  c("blurr/re", "blurr/li"),
  c("normal/re", "normal/li")
)
```

```r
# Permutation test outputs
clusters <- read_csv("output/clusters.csv") # or clusters <- res[[4]]
print(na.omit(clusters))
```

```
## # A tibble: 5,748 x 6
##    contrast        time channel  t_obs cluster p_val
##    <chr>          <dbl> <chr>    <dbl> <chr>   <dbl>
##  1 blurr - normal 0     AF3      -18.1 neg_282     1
##  2 blurr - normal 0     FT7       52.8 pos_1       1
##  3 blurr - normal 0     C6       -30.0 neg_281     1
##  4 blurr - normal 0     POz       15.3 pos_96      1
##  5 blurr - normal 0.002 F10      -24.5 neg_280     1
##  6 blurr - normal 0.002 FT7       20.1 pos_1       1
##  7 blurr - normal 0.002 FC3       17.5 pos_95      1
##  8 blurr - normal 0.002 FC1       22.1 pos_95      1
##  9 blurr - normal 0.002 C6      -154.  neg_281     1
## 10 blurr - normal 0.002 CPz       16.6 pos_94      1
## # ... with 5,738 more rows
```

Artifact correction

- **Multiple source eye correction (MSEC)**
  - Requires `.matrix` files from BESA

Artifact correction

- **Independent component analysis (ICA)**
  - Different algorithms available (e.g., `ica_method = "fastica"`)
  - Can specify initial number of principal components with `ica_n_components`
  - Automatic detection + exclusion of eye movement components based on correlation with HEOG and VEOG (see https://mne.tools/stable/generated/mne.preprocessing.ICA.html#mne.preprocessing.ICA.find_bads_eog)
  - Verify in QC reports
  - Other selection methods (manual selection, ICLabel) not yet implemented

Artifact rejection

- Per-channel peak-to-peak amplitude threshold via `reject_peak_to_peak` (default: `200.0`)
- In addition to or instead of BESA or ICA

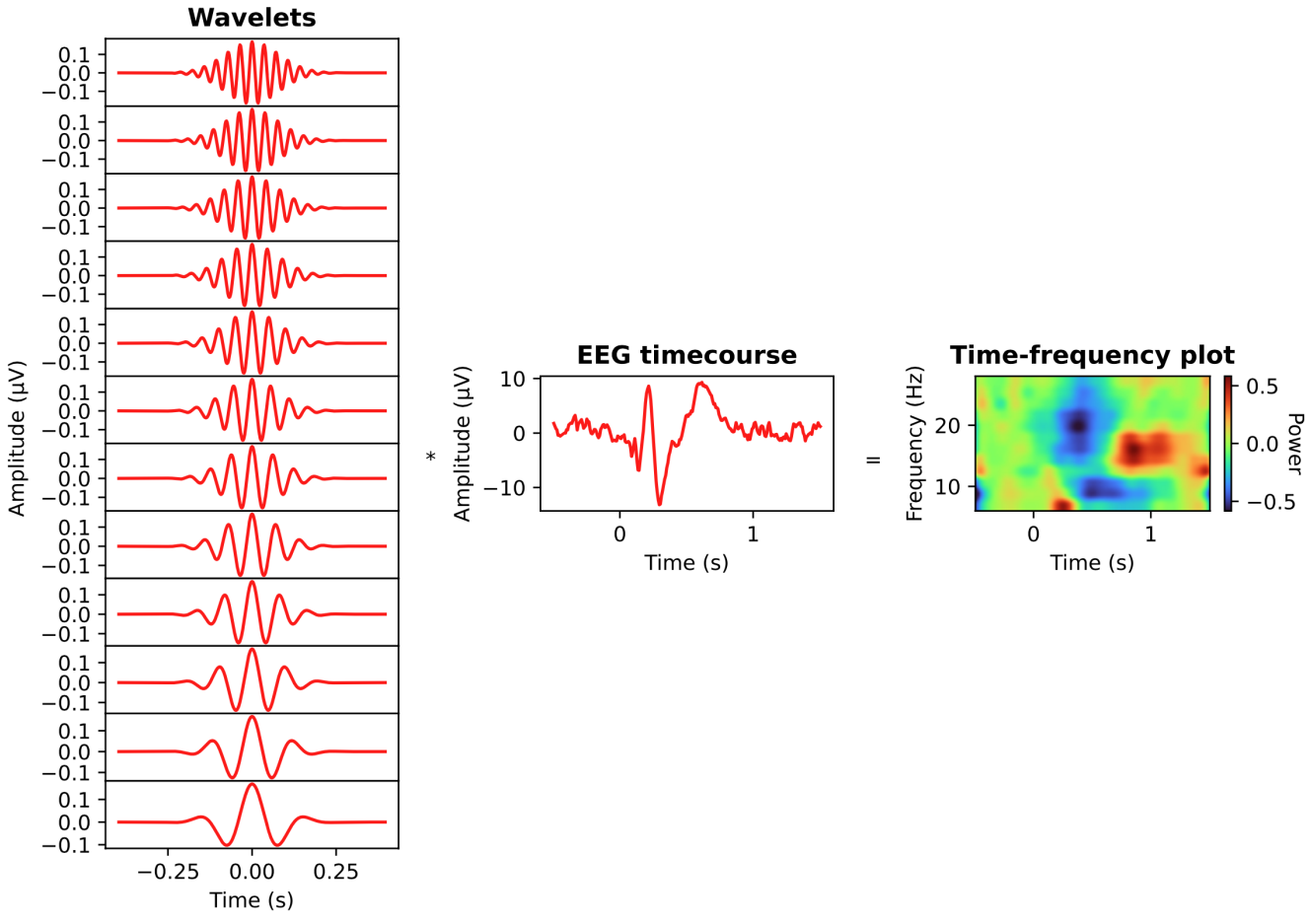
Repairing bad channels

- Pass participant-specific vectors of bad channel labels
  - E.g., `bad_channels = list("05" = c("C3", "P7"), ...)`
- Uses spherical spline interpolation
- Experimental: Automatic bad channel detection (`bad_channels = "auto"`)
  - Based on channel *SD*s across epochs

Detect missing epochs

- Requires log file column with the EEG trigger for every trial
- Specify name of this column as `triggers_column = ...`
- Pipeline magically detects and deletes log file trials with missing EEG

Time-frequency analysis



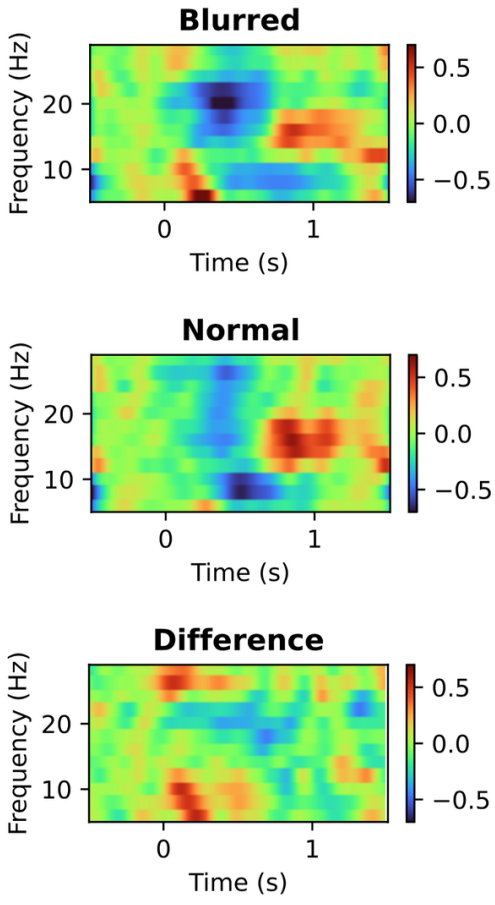
See https://github.com/alexenge/tfr-workshop

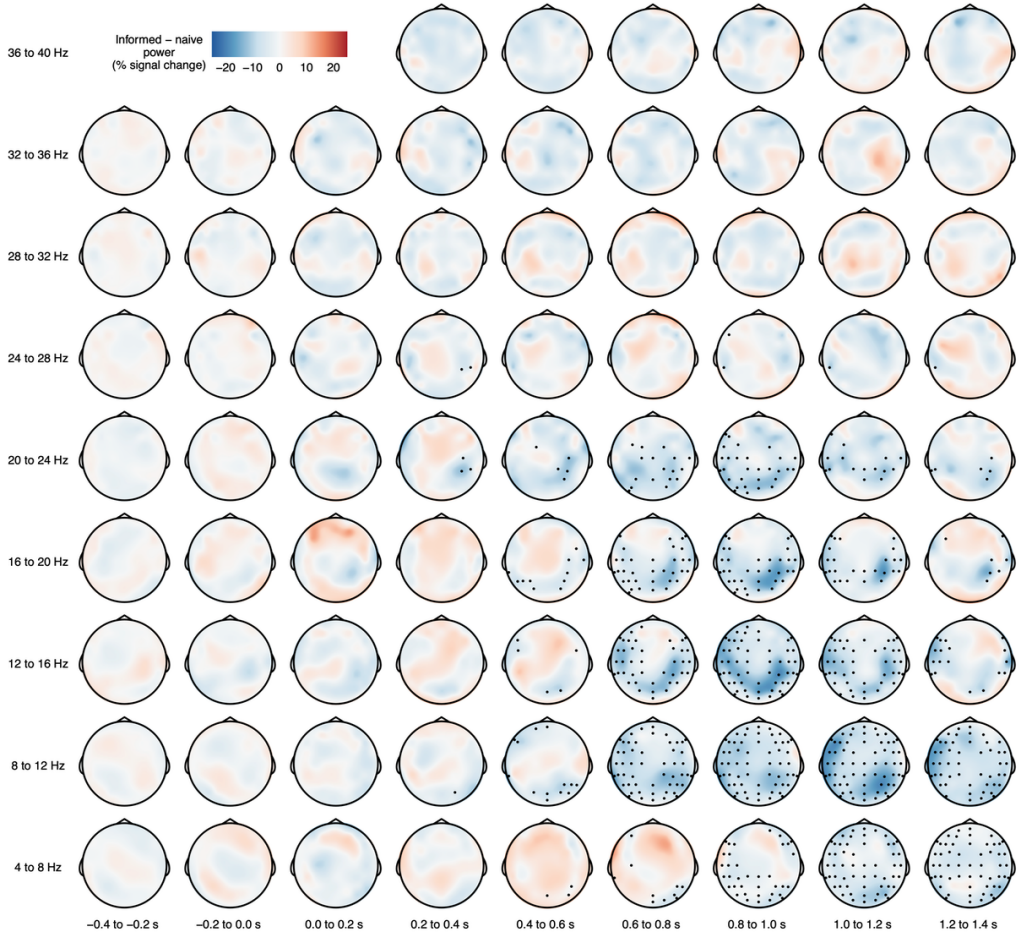
Time-frequency analysis

```
# Time-frequency analysis options
perform_tfr = TRUE,
tfr_components = list(
  "name" = list("alpha"),
  "tmin" = list(0.0), "tmax" = list(0.2),
  "fmin" = list(8.0), "fmax" = list(14.0),
  "roi" = list(c("PO9", "PO7", "PO3", "POz", "PO4", "PO8", "PO10", "O1", "Oz", "O2"))
)
```

- `tfr_components` extracts single trial power values
- Can additionally specify:
  - Morlet frequencies (`tfr_freqs`, default 4, 5, 6, . . . , 40 Hz)
  - Numbers of cycles (`tfr_cycles`, default 2, 2.5, 3, . . . , 20)
  - Baseline window (`tfr_baseline`, default -450 ms to -50 ms)
  - Baseline method (`tfr_method`, default percent signal change)

Time-frequency analysis

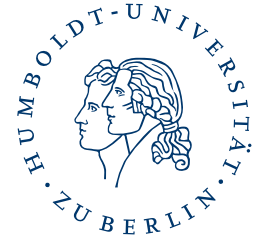




Plans

- Improve documentation
- Unit tests
- RIDE correction for speech artifacts
- Mixed models with `pymer4` (?)
- Better permutation tests (Frossard & Renaud, 2021, 2022)
- BIDS interface
- Your ideas + contributions?

Thanks



References

Bürki, A., Frossard, J., & Renaud, O. (2018). Accounting for stimulus and participant effects in event-related potential analyses to increase the replicability of studies. *Journal of Neuroscience Methods*, *309*, 218–227. https://doi.org/10.1016/j.jneumeth.2018.09.016

Frömer, R., Maier, M., & Abdel Rahman, R. (2018). Group-level EEG-processing pipeline for flexible single trial-based analyses including linear mixed models. *Frontiers in Neuroscience*, *12*, 48. https://doi.org/10.3389/fnins.2018.00048

Frossard, J., & Renaud, O. (2021). Permutation tests for regression, ANOVA, and comparison of signals: The permuco package. *Journal of Statistical Software*, *99*, 1–32. https://doi.org/10.18637/jss.v099.i15

Frossard, J., & Renaud, O. (2022). The cluster depth tests: Toward point-wise strong control of the family-wise error rate in massively univariate tests with application to M/EEG. *NeuroImage*, *247*, 118824. https://doi.org/10.1016/j.neuroimage.2021.118824

Volpert-Esmond, H. I., Page-Gould, E., & Bartholow, B. D. (2021). Using multilevel models for the analysis of event-related potentials. *International Journal of Psychophysiology*, *162*, 145–156. https://doi.org/10.1016/j.ijpsycho.2021.02.006