

Package: PhysioNeurophys (via r-universe)

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Title TMS and Peripheral Motor Neurophysiology Analysis

Version 0.4.1

Description Provides transcranial magnetic stimulation (TMS) and peripheral motor-neurophysiology analysis for PhysioExperiment objects. Includes motor-evoked-potential amplitude and latency, Boltzmann recruitment curves, H-reflex recruitment and Hmax/Mmax metrics, F-wave persistence and latency, paired-pulse inhibition and facilitation, cortical silent-period timing, TMS-EEG pulse removal, source-informed SSP-SIR and SOUND cleaning, TMS-evoked-potential summaries, the PREP2 upper-limb stroke-prognosis algorithm, and a governed TMS pulse and intensity metadata schema.

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corticalSilentPeriod	<i>Measure the cortical silent period</i>
----------------------	---

Description

Detects sustained suppression and recovery of rectified tonic EMG after a TMS pulse using a baseline-relative threshold.

Usage

```
corticalSilentPeriod(  
  x,  
  search_window_ms = c(50, 400),  
  epoch_start_ms = 0,  
  baseline_window_ms = NULL,  
  threshold_fraction = 0.25,
```

```

    min_silence_ms = 10,
    min_return_ms = 5,
    channel = 1,
    assay_name = NULL
  )

```

Arguments

x	An epoched tonic-EMG PhysioExperiment.
search_window_ms	Post-stimulus CSP search window.
epoch_start_ms	Time of the first epoch sample relative to the pulse.
baseline_window_ms	Optional quiet-reference interval. The default uses all pre-stimulus samples.
threshold_fraction	Fraction of median rectified baseline below which EMG is considered silent.
min_silence_ms	Required duration of suppression.
min_return_ms	Required duration of recovered activity.
channel	One channel label or 1-based index.
assay_name	Optional assay name.

Value

A data frame with onset, offset, and duration for each trial.

References

Rossini PM, Burke D, Chen R, et al. (2015). Non-invasive electrical and magnetic stimulation of the brain, spinal cord, roots and peripheral nerves: basic principles and procedures for routine clinical and research application. *Clinical Neurophysiology*, 126:1071-1107. doi:[10.1016/j.clinph.2015.02.001](https://doi.org/10.1016/j.clinph.2015.02.001)

Examples

```

data <- array(rep(c(-1, 1), 250), c(500, 1, 1))
data[181:330, 1, 1] <- 0
pe <- PhysioExperiment(
  assays = list(raw = data),
  samplingRate = 1000
)
corticalSilentPeriod(pe, epoch_start_ms = -100)

```

fWaveDetect

*Detect and summarize F-waves***Description**

Measures late F-wave peak-to-peak amplitude and onset latency after peripheral stimulation, then reports persistence, latency dispersion, and the mean F/M amplitude ratio.

Usage

```
fWaveDetect(
  x,
  f_window_ms = c(20, 60),
  m_window_ms = c(2, 12),
  epoch_start_ms = 0,
  amplitude_threshold = 0.04,
  baseline_window_ms = NULL,
  threshold_sd = 3,
  min_consecutive_ms = 0.5,
  channel = 1,
  assay_name = NULL
)
```

Arguments

x	A <code>PhysioExperiment</code> with time x channels x trials data.
f_window_ms	F-wave search window relative to the stimulus, in milliseconds.
m_window_ms	Direct M-wave window relative to the stimulus, in milliseconds.
epoch_start_ms	Time of the first epoch sample relative to the stimulus.
amplitude_threshold	Minimum F-wave peak-to-peak amplitude in the assay's native unit.
baseline_window_ms	Optional latency baseline interval. The default uses all pre-stimulus samples.
threshold_sd	Baseline standard-deviation multiplier for onset.
min_consecutive_ms	Required onset-threshold duration.
channel	One channel label or 1-based index.
assay_name	Optional assay name.

Value

An `f_wave_result` list containing per-trial waves, a one-row summary, and analysis settings.

References

Fisher MA (2007). F-waves: physiology and clinical uses. *TheScientificWorldJournal*, 7:144-160.
[doi:10.1100/tsw.2007.49](https://doi.org/10.1100/tsw.2007.49)

Examples

```
pe <- make_mep(n_trials = 5, mep_latency_ms = 25, seed = 3)
fWaveDetect(
  pe, m_window_ms = c(10, 18), f_window_ms = c(20, 60),
  epoch_start_ms = -20
)
```

getTMSpulses	<i>Retrieve TMS pulse metadata</i>
--------------	------------------------------------

Description

Retrieve TMS pulse metadata

Usage

```
getTMSpulses(x)
```

Arguments

x A `PhysioExperiment`.

Value

A six-column data frame with one row per stored pulse, or a typed zero-row table when TMS metadata are absent.

Examples

```
getTMSpulses(make_mep(n_trials = 3))
```

hMaxMMax	<i>Calculate the Hmax/Mmax ratio</i>
----------	--------------------------------------

Description

Calculate the Hmax/Mmax ratio

Usage

```
hMaxMMax(recruitment)
```

Arguments

`recruitment` An H-reflex recruitment table returned by [hReflexRecruitment\(\)](#), or a data frame containing `intensity`, `h_p2p`, and `m_p2p`.

Value

A one-row data frame containing observed maxima, their lowest tied intensities, and the dimensionless Hmax/Mmax ratio.

Examples

```
recruitment <- data.frame(
  intensity = c(10, 20, 30),
  h_p2p = c(0.2, 1, 0.8),
  m_p2p = c(0.5, 1.5, 2)
)
hMaxMMax(recruitment)
```

hReflexLatency	<i>Estimate H-reflex onset latency</i>
----------------	--

Description

Uses the baseline-standard-deviation threshold and persistent-run detector from [mepLatency\(\)](#) within an H-reflex-specific search window.

Usage

```
hReflexLatency(
  x,
  h_window_ms = c(20, 45),
  epoch_start_ms = 0,
  baseline_window_ms = NULL,
  threshold_sd = 3,
```

```

    min_consecutive_ms = 1,
    channel = 1,
    assay_name = NULL
  )

```

Arguments

x	A PhysioExperiment with time x channels x trials data.
h_window_ms	H-reflex window relative to the stimulus, in milliseconds.
epoch_start_ms	Time of the first epoch sample relative to the stimulus.
baseline_window_ms	Optional baseline interval. The default uses all pre-stimulus samples.
threshold_sd	Baseline standard-deviation multiplier.
min_consecutive_ms	Required duration of a threshold crossing.
channel	One channel label or 1-based index.
assay_name	Optional assay name.

Value

A data frame containing onset sample and stimulus-relative H-reflex latency for each trial.

Examples

```

pe <- make_mep(n_trials = 3, mep_latency_ms = 25, seed = 2)
hReflexLatency(pe, epoch_start_ms = -20)

```

hReflexRecruitment	<i>Measure an H-reflex recruitment series</i>
--------------------	---

Description

Measures peak-to-peak direct motor (M) and Hoffmann-reflex (H) responses in separate post-stimulus windows for each trial.

Usage

```

hReflexRecruitment(
  x,
  intensity,
  m_window_ms = c(2, 12),
  h_window_ms = c(20, 45),
  epoch_start_ms = 0,
  channel = 1,
  assay_name = NULL
)

```

Arguments

x	A <code>PhysioExperiment</code> with time x channels x trials data.
intensity	Finite stimulation intensity, one value per trial. Values remain in the caller's native stimulator unit.
m_window_ms	Direct M-wave window relative to the stimulus, in milliseconds.
h_window_ms	H-reflex window relative to the stimulus, in milliseconds.
epoch_start_ms	Time of the first epoch sample relative to the stimulus.
channel	One channel label or 1-based index.
assay_name	Optional assay name.

Value

A data frame with one row per trial and M/H peak-to-peak amplitudes and fiducial samples.

References

Palmieri RM, Ingersoll CD, Hoffman MA (2004). The Hoffmann reflex: methodologic considerations and applications for use in sports medicine and athletic training research. *Journal of Athletic Training*, 39:268-277.

Examples

```
pe <- make_mep(n_trials = 3, intensities = c(30, 40, 50), seed = 1)
hReflexRecruitment(
  pe, c(10, 20, 30),
  m_window_ms = c(10, 18), h_window_ms = c(20, 60),
  epoch_start_ms = -20
)
```

hReflexThreshold	<i>Estimate the H-reflex recruitment threshold</i>
------------------	--

Description

Finds the lowest stimulation intensity whose mean H amplitude reaches an absolute cutoff or a fraction of the observed Mmax.

Usage

```
hReflexThreshold(recruitment, criterion = 0.05, scale = c("mmax", "absolute"))
```

Arguments

recruitment	An H-reflex recruitment table returned by <code>hReflexRecruitment()</code> , or a data frame containing intensity, h_p2p, and m_p2p.
criterion	Non-negative absolute amplitude, or a fraction in $[0, 1]$ when scale = "mmax".
scale	Whether criterion is relative to Mmax or in native amplitude units.

Value

A one-row data frame containing the first qualifying intensity, applied cutoff, and scale.

Examples

```
recruitment <- data.frame(
  intensity = c(10, 20, 30),
  h_p2p = c(0.1, 0.5, 1),
  m_p2p = c(0.2, 0.8, 2.5)
)
hReflexThreshold(recruitment, criterion = 0.2)
```

make_mep

*Simulate epoched TMS motor-evoked potentials***Description**

Generates biphasic MEP waveforms with known latency and a Boltzmann amplitude-intensity relationship.

Usage

```
make_mep(
  n_time = 600,
  n_channels = 1,
  n_trials = 12,
  sr = 5000,
  epoch_start_ms = -20,
  intensities = NULL,
  plateau = 2,
  s50 = 50,
  k = 5,
  mep_latency_ms = 20,
  mep_dur_ms = 10,
  baseline_sd = 0.02,
  seed = NULL
)
```

Arguments

n_time	Number of samples per epoch.
n_channels	Number of MEP channels.
n_trials	Number of TMS trials.
sr	Sampling rate in Hz.
epoch_start_ms	Time of the first sample relative to the TMS pulse.
intensities	Per-trial stimulation intensity in %MSO.

plateau, s50, k Boltzmann recruitment parameters.
 mep_latency_ms Planted MEP onset latency.
 mep_dur_ms Duration of the one-cycle biphasic waveform.
 baseline_sd Gaussian baseline-noise standard deviation.
 seed Optional random seed.

Value

An epoched PhysioExperiment with TMS pulse metadata.

Examples

```
pe <- make_mep(n_trials = 5, seed = 1)
dim(SummarizedExperiment::assay(pe))
getTMSpulses(pe)
```

mepAmplitude	<i>Measure motor-evoked-potential amplitude</i>
--------------	---

Description

Calculates peak-to-peak MEP amplitude within a response window for every selected channel and trial.

Usage

```
mepAmplitude(
  x,
  response_window_ms = c(10, 60),
  epoch_start_ms = 0,
  channels = NULL,
  assay_name = NULL
)
```

Arguments

x A PhysioExperiment with time x channels x trials MEP data.
 response_window_ms Two response-window limits relative to the TMS pulse, in milliseconds.
 epoch_start_ms Time of the first epoch sample relative to the pulse.
 channels Optional channel labels or 1-based indices.
 assay_name Optional assay name.

Value

A data frame with one row per selected channel and trial.

References

Rossini PM, Burke D, Chen R, et al. (2015). Non-invasive electrical and magnetic stimulation of the brain, spinal cord, roots and peripheral nerves: basic principles and procedures for routine clinical and research application. *Clinical Neurophysiology*, 126:1071-1107. doi:10.1016/j.clinph.2015.02.001

Examples

```
pe <- make_mep(n_trials = 4, seed = 1)
mepAmplitude(pe, epoch_start_ms = -20)
```

mepLatency	<i>Estimate motor-evoked-potential onset latency</i>
------------	--

Description

Detects the first persistent signed deviation from the baseline mean above a multiple of the baseline standard deviation.

Usage

```
mepLatency(
  x,
  response_window_ms = c(5, 50),
  epoch_start_ms = 0,
  baseline_window_ms = NULL,
  threshold_sd = 3,
  min_consecutive_ms = 1,
  channels = NULL,
  assay_name = NULL
)
```

Arguments

x	A PhysioExperiment with time x channels x trials MEP data.
response_window_ms	Search window relative to the TMS pulse.
epoch_start_ms	Time of the first epoch sample relative to the pulse.
baseline_window_ms	Optional baseline interval. The default uses all pre-stimulus samples.
threshold_sd	Baseline standard-deviation multiplier.
min_consecutive_ms	Required duration of a threshold crossing.
channels	Optional channel labels or 1-based indices.
assay_name	Optional assay name.

Value

A data frame containing onset sample and latency for each selected channel and trial.

Examples

```
pe <- make_mep(n_trials = 4, intensities = rep(65, 4), seed = 2)
mepLatency(pe, epoch_start_ms = -20)
```

pairedPulse	<i>Summarize paired-pulse MEP responses</i>
-------------	---

Description

Compares conditioned motor-evoked-potential amplitudes with the aggregate unconditioned test response at each interstimulus interval (ISI).

Usage

```
pairedPulse(
  x,
  condition,
  isi_ms,
  response_window_ms = c(10, 60),
  epoch_start_ms = 0,
  channel = 1,
  assay_name = NULL,
  aggregate = c("mean", "median")
)
```

Arguments

x	An epoched PhysioExperiment containing MEP trials.
condition	Per-trial labels, exactly "test" or "conditioned".
isi_ms	Per-trial interstimulus interval in milliseconds. Use NA for test trials and a positive finite value for conditioned trials.
response_window_ms	MEP response window relative to the test pulse.
epoch_start_ms	Time of the first epoch sample relative to the test pulse.
channel	One channel label or 1-based index.
assay_name	Optional assay name.
aggregate	Whether to summarize amplitudes by the mean or median.

Value

A data frame with one row per conditioned ISI and conditioned/test amplitudes, their ratio, inhibition, and facilitation.

References

Kujirai T, Caramia MD, Rothwell JC, et al. (1993). Corticocortical inhibition in human motor cortex. *Journal of Physiology*, 471:501-519. doi:[10.1113/jphysiol.1993.sp019912](https://doi.org/10.1113/jphysiol.1993.sp019912)

Examples

```
pe <- make_mep(
  n_trials = 6,
  intensities = rep(50, 6),
  baseline_sd = 0,
  seed = 1
)
pairedPulse(
  pe,
  condition = c("test", "test", rep("conditioned", 4)),
  isi_ms = c(NA, NA, 2, 2, 10, 10),
  epoch_start_ms = -20
)
```

```
prep2
```

Apply the PREP2 upper-limb prognosis algorithm

Description

Implements the day-3 PREP2 decision tree from SAFE score, age, motor-evoked potential status, and NIH Stroke Scale score.

Usage

```
prep2(safe_score, age, mep_status = NULL, nihss = NULL)
```

Arguments

safe_score	Shoulder Abduction and Finger Extension MRC sum, an integer from 0 to 10.
age	Age in years.
mep_status	Optional MEP status: logical, "present"/"MEP+", or "absent"/"MEP-".
nihss	Optional day-3 NIHSS total, an integer from 0 to 42.

Value

A prep2_result containing category, decision pathway, inputs, and a clinical description.

References

Stinear CM, Byblow WD, Ackerley SJ, Smith MC, Stinear JW, Barber PA (2017). PREP2: A biomarker-based algorithm for predicting upper limb function after stroke. *Annals of Clinical and Translational Neurology*, 4:811-820. doi:[10.1002/acn3.488](https://doi.org/10.1002/acn3.488)

Examples

```
prep2(safe_score = 8, age = 65)
prep2(2, 70, mep_status = "absent", nihss = 5)
```

recruitmentCurve	<i>Fit a Boltzmann MEP recruitment curve</i>
------------------	--

Description

Fits peak-to-peak MEP amplitude against stimulator intensity with a three-parameter logistic curve.

Usage

```
recruitmentCurve(
  x,
  channel = 1,
  response_window_ms = c(10, 60),
  epoch_start_ms = 0,
  intensity = NULL,
  assay_name = NULL
)
```

Arguments

x	An epoched MEP PhysioExperiment.
channel	One channel label or 1-based index.
response_window_ms	MEP response window in milliseconds.
epoch_start_ms	Time of the first epoch sample relative to the pulse.
intensity	Optional per-trial stimulation intensity in %MSO.
assay_name	Optional assay name.

Value

A recruitment_curve object with fitted parameters, predictions, fit quality, and the underlying nls model.

References

Devanne H, Lavoie BA, Capaday C (1997). Input-output properties and gain changes in the human corticospinal pathway. *Experimental Brain Research*, 114:329-338. doi:[10.1007/PL00005641](https://doi.org/10.1007/PL00005641)

Examples

```
pe <- make_mep(n_trials = 15, baseline_sd = 0.001, seed = 3)
recruitmentCurve(pe, epoch_start_ms = -20)
```

removeTMSpulse	<i>Remove TMS pulse and recharge intervals</i>
----------------	--

Description

Replaces sample-exact closed pulse/recharge intervals by a linear or cubic Hermite bridge, or blanks them to zero or a trial-specific baseline. The selected input assay is preserved unless `overwrite = TRUE`.

Usage

```
removeTMSpulse(
  x,
  pulse_window_ms = c(-2, 10),
  recharge_windows_ms = NULL,
  method = c("cubic", "linear", "blank"),
  support_ms = 2,
  blank_value = c("baseline", "zero"),
  baseline_window_ms = c(-200, -20),
  epoch_start_ms = 0,
  assay_name = NULL,
  output_assay = "tms_pulse_clean",
  overwrite = FALSE
)
```

Arguments

<code>x</code>	A <code>PhysioExperiment</code> with time x channel or time x channel x trial data.
<code>pulse_window_ms</code>	Increasing pulse-window limits in milliseconds.
<code>recharge_windows_ms</code>	Optional increasing pair or $n \times 2$ matrix.
<code>method</code>	Exactly "cubic", "linear", or "blank".
<code>support_ms</code>	One positive derivative-support duration for cubic interpolation, in milliseconds.
<code>blank_value</code>	Exactly "baseline" or "zero".
<code>baseline_window_ms</code>	Closed baseline interval in milliseconds.
<code>epoch_start_ms</code>	Time of the first sample relative to the pulse.
<code>assay_name</code>	Optional input assay name.
<code>output_assay</code>	Output assay name.
<code>overwrite</code>	Whether to overwrite the selected input assay.

Details

Closed intervals use $\text{round}((\text{time_ms} - \text{epoch_start_ms}) / 1000 * \text{sampling_rate}) + 1$. Overlapping or sample-adjacent pulse/recharge intervals are merged. Linear and cubic methods require real samples on both sides and never bridge across a second removed interval. Baseline settings do not affect interpolation or zero blanking. Baseline blanking requires at least two samples wholly outside every removed interval. The audit metadata contains the complete altered mask, merged sample ranges, continuity jumps, and robust baseline noise.

Value

A modified `PhysioExperiment` with an appended TMS-EEG audit step.

References

Rogasch NC, Sullivan C, Thomson RH, et al. (2017). Analysing concurrent transcranial magnetic stimulation and electroencephalographic data. *NeuroImage*, 147:934-951. doi:10.1016/j.neuroimage.2016.10.031

setTMSpulses	<i>Store TMS pulse metadata</i>
--------------	---------------------------------

Description

Stores one pulse row per trial without replacing other experiment metadata. Intensity and resting motor threshold are expressed as percent of maximum stimulator output (%MSO).

Usage

```
setTMSpulses(
  x,
  intensity_pct_mso,
  target = NA_character_,
  coil = NA_character_,
  rmt_pct_mso = NA_real_,
  onset_sec = NA_real_
)
```

Arguments

<code>x</code>	A <code>PhysioExperiment</code> with a 2-D or epoched 3-D assay.
<code>intensity_pct_mso</code>	Numeric stimulation intensity, one value per trial.
<code>target</code>	Cortical target or target-muscle label.
<code>coil</code>	Coil descriptor.
<code>rmt_pct_mso</code>	Resting motor threshold in %MSO.
<code>onset_sec</code>	Pulse onset in the source continuous recording, in seconds.

Value

The modified PhysioExperiment.

Examples

```
pe <- make_mep(n_trials = 3, intensities = c(40, 50, 60))
pe <- setTMSpulses(pe, c(40, 50, 60), target = "M1_FDI")
getTMSpulses(pe)
```

siciIcf

Summarize short-interval inhibition and intracortical facilitation

Description

Summarize short-interval inhibition and intracortical facilitation

Usage

```
siciIcf(paired, sici_range_ms = c(1, 5), icf_range_ms = c(7, 20))
```

Arguments

paired	A table returned by <code>pairedPulse()</code> containing <code>isi_ms</code> , <code>n_conditioned</code> , and <code>ratio</code> .
sici_range_ms	Closed SICI ISI range in milliseconds.
icf_range_ms	Closed ICF ISI range in milliseconds.

Value

A one-row data frame with conditioned-trial-weighted SICI and ICF ratios, percentages, and trial counts.

Examples

```
paired <- data.frame(
  isi_ms = c(2, 3, 10, 15),
  n_conditioned = rep(2L, 4),
  ratio = c(0.4, 0.5, 1.5, 1.4)
)
siciIcf(paired)
```

soundClean

Clean TMS-EEG sensor noise with SOUND

Description

Implements simultaneous leave-one-sensor noise estimation followed by the source-space Wiener reconstruction of the SOUND algorithm.

Usage

```
soundClean(
    x,
    forward_model,
    lambda = 0.1,
    iterations = 10L,
    tolerance = 0.01,
    reference = "average",
    analysis_window_ms = NULL,
    epoch_start_ms = 0,
    assay_name = NULL,
    output_assay = "tms_sound",
    overwrite = FALSE
)
```

Arguments

x	A pulse-cleaned PhysioExperiment.
forward_model	A list containing a finite channel-matched leadfield.
lambda	Positive source-reconstruction regularization.
iterations	Maximum number of complete simultaneous updates.
tolerance	Non-negative maximum relative noise change for convergence.
reference	Currently exactly "average".
analysis_window_ms	Optional closed noise-estimation interval. NULL uses all samples except recorded pulse/recharge gaps.
epoch_start_ms	Time of the first epoch sample relative to the pulse.
assay_name	Optional pulse-cleaned input assay.
output_assay	Output assay name.
overwrite	Whether to overwrite the selected input assay.

Details

SOUND assumes diagonal sensor noise, an approximate channel-matched lead field, and i.i.d. source amplitudes for its regularized reconstruction. All channel noise estimates are updated simultaneously from the preceding round, and one final cleaning matrix is applied to every sample and trial. Pulse samples are excluded from noise estimation. Regularization is not a significance threshold and is not optimized against the reported TEP peaks.

Value

A modified `PhysioExperiment` with the fixed SOUND cleaning matrix, complete noise history, and convergence diagnostics.

References

Mutanen TP, Metsomaa J, Liljander S, Ilmoniemi RJ (2018). Automatic and robust noise suppression in EEG and MEG: The SOUND algorithm. *NeuroImage*, 166:135-151. doi:10.1016/j.neuroimage.2017.10.021

tepAverage	<i>Average TMS-evoked potentials and measure canonical peaks</i>
------------	--

Description

Baseline-corrects every trial and channel before a mean or trimmed mean, then finds signed peaks independently in each requested channel.

Usage

```
tepAverage(
  x,
  components = c("N15", "P30", "N45", "P60", "N100", "P180"),
  windows_ms = NULL,
  channels = NULL,
  baseline_window_ms = c(-200, -20),
  epoch_start_ms = 0,
  average = c("mean", "trimmed"),
  trim = 0.2,
  assay_name = NULL
)
```

Arguments

<code>x</code>	A <code>PhysioExperiment</code> containing epoched TMS-EEG.
<code>components</code>	Exact canonical component names in requested order.
<code>windows_ms</code>	Optional named component x 2 override matrix.
<code>channels</code>	Optional exact labels or 1-based indices.

baseline_window_ms Closed baseline interval.

epoch_start_ms Time of the first sample relative to the pulse.

average Exactly "mean" or "trimmed".

trim Trim fraction in $[\emptyset, \emptyset.5)$.

assay_name Optional assay name.

Details

Default signed peak windows are N15 (10–20 ms), P30 (20–40 ms), N45 (35–55 ms), P60 (50–75 ms), N100 (80–140 ms), and P180 (140–220 ms). Exact ties use the earliest sample and a peak on a window endpoint is marked as a boundary diagnostic. Canonical names define measurement windows only. Auditory and somatosensory responses can remain, and no component is evidence of a verified cortical source.

Value

A tms_tep list with waveform, component, and settings tables.

References

Rogasch NC, Sullivan C, Thomson RH, et al. (2017). Analysing concurrent transcranial magnetic stimulation and electroencephalographic data. *NeuroImage*, 147:934-951. doi:10.1016/j.neuroimage.2016.10.031

tmsSSPSIR

Clean TMS-EEG muscle artifact with SSP-SIR

Description

Estimates one deterministic artifact subspace across trials and reconstructs the retained activity through a channel-matched lead field.

Usage

```
tmsSSPSIR(
  x,
  forward_model,
  artifact_window_ms = c(5, 50),
  n_artifact = NULL,
  variance_fraction = 0.9,
  lambda = 0.05,
  reference = "average",
  epoch_start_ms = 0,
  assay_name = NULL,
  output_assay = "tms_sspsir",
  overwrite = FALSE
)
```

Arguments

<code>x</code>	A pulse-cleaned <code>PhysioExperiment</code> .
<code>forward_model</code>	A list containing a finite channel-matched leadfield.
<code>artifact_window_ms</code>	Closed artifact-training interval.
<code>n_artifact</code>	Optional exact number of artifact components.
<code>variance_fraction</code>	Cumulative artifact variance target when <code>n_artifact</code> is NULL.
<code>lambda</code>	Positive source-reconstruction regularization.
<code>reference</code>	Currently exactly "average".
<code>epoch_start_ms</code>	Time of the first epoch sample relative to the pulse.
<code>assay_name</code>	Optional pulse-cleaned input assay.
<code>output_assay</code>	Output assay name.
<code>overwrite</code>	Whether to overwrite the selected input assay.

Details

The pulse must already be removed or hardware absence must be explicitly declared in `metadata(x)$tms_eeg$pulse_absent`. Both data and lead field are average referenced with the same matrix. The returned data use the fixed source-informed reconstruction $Lr = G^T P$, not the plain SSP projection P . SSP-SIR can attenuate neural signal when the artifact and neural subspaces overlap; a lead field is an approximate physical model, not proof that a retained deflection is cortical.

Value

A modified `PhysioExperiment` with fixed SSP-SIR reconstruction metadata.

References

Mutanen TP, Kukkonen M, Nieminen JO, et al. (2016). Recovering TMS-evoked EEG responses masked by muscle artifacts. *NeuroImage*, 139:157-166. doi:10.1016/j.neuroimage.2016.05.028

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