Package: PhysioECG (via r-universe)

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Title ECG Analysis Functions for PhysioExperiment Objects

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Description Provides electrocardiography (ECG) analysis functions for PhysioExperiment objects. Includes R-peak detection (adaptive Pan-Tompkins), RR interval computation, HRV time-domain metrics (SDNN, RMSSD, pNN50), HRV frequency-domain analysis (VLF, LF, HF power), nonlinear HRV (Poincare, Sample Entropy, DFA), ECG morphology analysis (QRS boundaries, QT/QTc intervals), and signal quality assessment with ectopic beat correction.

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Contents

`ecgBaselineCorrect` *Correct Baseline Wander in ECG Signals*

Description

Removes low-frequency baseline drift from ECG data using either a high-pass moving-average subtraction or a running-median subtraction.

Usage

```
ecgBaselineCorrect(
  x,
  method = c("highpass", "median"),
  cutoff = 0.5,
  assay_name = NULL,
  output_assay = "baseline_corrected"
)
```

Arguments

`x`	A PhysioExperiment object with ECG data.
`method`	Correction method: `"highpass"` (default) subtracts a moving average; `"median"` subtracts a running median.
`cutoff`	Approximate cutoff frequency in Hz (default: 0.5). Controls the window size of the moving average or median filter.

assay_name	Name of the input assay. If NULL the default assay is used.
output_assay	Name of the assay in which to store the corrected signal (default: "baseline_corrected").

Value

A PhysioExperiment with the corrected signal stored in output_assay.

References

Clifford, G.D., Azuaje, F. & McSharry, P.E. (2006). *Advanced Methods and Tools for ECG Data Analysis*. Artech House.

See Also

ecgSignalQuality for signal quality assessment, ecgDetectRpeaks for R-peak detection, ecgQualityCheck for ectopic beat detection.

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ecgDelineate *Delineate ECG Waveform Morphology*

Description

For each detected R-peak, identifies QRS complex boundaries (onset and offset) and P-wave and T-wave peaks. QRS boundaries are detected using a gradient-based search from the R-peak, while P and T waves are found as local maxima in physiologically plausible time windows.

Usage

```
ecgDelineate(x, peaks, assay_name = NULL)
```

Arguments

x	A PhysioExperiment object with ECG data.
peaks	A data.frame of detected R-peaks as returned by ecgDetectRpeaks, with columns channel and sample.
assay_name	Name of the assay to use. If NULL, the default assay is used.

Value

A data.frame with one row per beat and the following columns:

channel Integer channel index (1-based).

beat Integer beat number within the channel (1-based).

r_peak Sample index of the R-peak.

qrs_onset Sample index of QRS complex onset.

qrs_offset Sample index of QRS complex offset (J-point).

qrs_duration_ms QRS complex duration in milliseconds.

p_peak Sample index of P-wave peak, or NA if not found in the search window (300–80 ms before R-peak).

t_peak Sample index of T-wave peak, or NA if not found in the search window (80–500 ms after R-peak).

t_end Sample index of T-wave end estimated by tangent-intercept method, or NA if T-wave not found.

Returns a zero-row data.frame with the same column structure if no beats are delineated.

References

Goldberger, A.L., et al. (2000). "PhysioBank, PhysioToolkit, and PhysioNet: Components of a new research resource for complex physiologic signals." *Circulation*, 101(23), e215–e220. doi:10.1161/01.CIR.101.23.e215

See Also

ecgDetectRpeaks for R-peak detection, ecgIntervals for computing clinical ECG intervals from delineation results, ecgSignalQuality for signal quality assessment.

Examples

```
## Not run:
pe <- make_ecg(n_time = 5000, sr = 500, heart_rate = 72)
peaks <- ecgDetectRpeaks(pe)
delin <- ecgDelineate(pe, peaks)
head(delin)

## End(Not run)
```

---

ecgDetectRpeaks *Detect R-Peaks in ECG Signal Using Pan-Tompkins Algorithm*

Description

Identifies R-peaks in ECG data using an adaptive dual-threshold Pan-Tompkins detector. The algorithm applies bandpass filtering (5-15 Hz), differentiation, squaring, and moving-window integration followed by adaptive thresholding with running signal and noise level estimates. Automatically detects and handles inverted ECG signals.

Usage

```
ecgDetectRpeaks(
  x,
  method = "pan_tompkins",
  threshold_factor = 0.6,
  refractory_ms = 200,
  assay_name = NULL
)
```

Arguments

x	A PhysioExperiment object with ECG data.
method	Detection method. Currently only "pan_tompkins" is supported.
threshold_factor	Fraction of the peak integrated signal used as the detection threshold (default: 0.6).
refractory_ms	Refractory period in milliseconds. No two peaks can be closer than this (default: 200).
assay_name	Name of the assay to use. If NULL, the default assay is used.

Value

A data.frame with one row per detected R-peak and the following columns:

channel Integer channel index (1-based).

sample Integer sample index of the R-peak within the assay matrix.

time_sec Time of the R-peak in seconds from signal onset.

amplitude Amplitude of the raw signal at the R-peak location (in original units, not inverted).

Returns a zero-row data.frame with the same column structure if no peaks are detected.

References

Pan, J. & Tompkins, W.J. (1985). "A real-time QRS detection algorithm." *IEEE Transactions on Biomedical Engineering*, 32(3), 230–236. doi:10.1109/TBME.1985.325532

See Also

ecgRRintervals for computing RR intervals from detected peaks, ecgDelineate for full waveform morphology analysis, ecgSignalQuality for signal quality assessment.

Examples

```
## Not run:
pe <- make_ecg(n_time = 5000, sr = 500, heart_rate = 72)
peaks <- ecgDetectRpeaks(pe)
head(peaks)

## End(Not run)
```

ecgDFA *Detrended Fluctuation Analysis of RR Intervals*

Description

Performs detrended fluctuation analysis (DFA) on RR interval data to characterize fractal scaling properties. Computes alpha1 (short-range correlations, 4–16 beats) and alpha2 (long-range correlations, 16–64 beats).

Usage

```
ecgDFA(rr, short_range = c(4, 16), long_range = c(16, 64))
```

Arguments

rr	A data.frame with columns channel, rr_ms, and time_sec, as returned by ecgRRintervals.
short_range	Numeric vector of length 2 defining the scale range (in beats) for alpha1 (default: c(4, 16)).
long_range	Numeric vector of length 2 defining the scale range (in beats) for alpha2 (default: c(16, 64)).

Value

A data.frame with one row per channel and the following columns:

channel Integer channel index.

alpha1 Short-range scaling exponent. Values near 1.0 indicate fractal-like (healthy) correlations; values near 0.5 indicate uncorrelated (random) behavior; values near 1.5 suggest Brownian noise. NA if the series is too short.

alpha2 Long-range scaling exponent with the same interpretation as alpha1 but over larger time scales. NA if the series is too short.

References

Peng, C.-K., et al. (1994). "Mosaic organization of DNA nucleotides." *Physical Review E*, 49(2), 1685–1689. doi:10.1103/PhysRevE.49.1685

See Also

ecgHRVnonlinear for the combined nonlinear analysis wrapper, ecgSampleEntropy for sample entropy, ecgHRVpoincare for Poincare plot descriptors.

`ecgHRVfreq` *HRV Frequency-Domain Analysis*

Description

Computes heart rate variability frequency-domain metrics from RR interval data using Welch's method or Lomb-Scargle periodogram.

Usage

```
ecgHRVfreq(
  rr,
  method = c("welch", "lomb"),
  vlf_band = c(0.003, 0.04),
  lf_band = c(0.04, 0.15),
  hf_band = c(0.15, 0.4)
)
```

Arguments

`rr`	A data.frame with columns `channel`, `rr_ms`, and `time_sec`, as returned by `ecgRRintervals`.
`method`	Spectral estimation method: `"welch"` (default) for uniformly resampled FFT-based PSD, or `"lomb"` for Lomb-Scargle periodogram on unevenly sampled data.
`vlf_band`	Numeric vector of length 2 defining VLF band in Hz (default: c(0.003, 0.04)).
`lf_band`	Numeric vector of length 2 defining LF band in Hz (default: c(0.04, 0.15)).
`hf_band`	Numeric vector of length 2 defining HF band in Hz (default: c(0.15, 0.4)).

Value

A data.frame with one row per channel and the following columns:

channel Integer channel index.

vlf Absolute power in the very-low-frequency band (ms^2).

lf Absolute power in the low-frequency band (ms^2), associated with sympathetic and parasympathetic modulation.

hf Absolute power in the high-frequency band (ms^2), associated with parasympathetic (vagal) modulation.

lf_hf_ratio Ratio of LF to HF power, or `NA` if HF power is zero.

total_power Sum of VLF, LF, and HF power (ms^2).

References

Task Force of the European Society of Cardiology and the North American Society of Pacing and Electrophysiology (1996). "Heart rate variability: Standards of measurement, physiological interpretation and clinical use." *Circulation*, 93(5), 1043–1065.

See Also

`ecgRRintervals` for computing RR intervals, `ecgHRVtime` for time-domain HRV metrics, `ecgHRVnonlinear` for nonlinear HRV analysis, `ecgRRcorrect` for ectopic beat correction before analysis.

Examples

```
n <- 300
time_sec <- cumsum(rep(0.85, n))
rr_ms <- 850 + 30 * sin(2 * pi * 0.1 * time_sec)
rr <- data.frame(channel = rep(1L, n), rr_ms = rr_ms, time_sec = time_sec)
result <- ecgHRVfreq(rr, method = "welch")
```

---

ecgHRVnonlinear *Nonlinear HRV Analysis (Convenience Wrapper)*

Description

Computes all nonlinear HRV metrics by calling `ecgHRVpoincare`, `ecgSampleEntropy`, and `ecgDFA`, and merging the results into a single data.frame.

Usage

```
ecgHRVnonlinear(
  rr,
  m = 2L,
  r_factor = 0.2,
  short_range = c(4, 16),
  long_range = c(16, 64)
)
```

Arguments

`rr`	A data.frame with columns `channel`, `rr_ms`, and `time_sec`, as returned by `ecgRRintervals`.
`m`	Embedding dimension for sample entropy (default: 2).
`r_factor`	Tolerance factor for sample entropy (default: 0.2).
`short_range`	Scale range for DFA alpha1 (default: c(4, 16)).
`long_range`	Scale range for DFA alpha2 (default: c(16, 64)).

Value

A data.frame with columns: channel, sd1, sd2, sd1_sd2_ratio, sample_entropy, m, r, alpha1, alpha2.

References

Shaffer, F. & Ginsberg, J.P. (2017). "An overview of heart rate variability metrics and norms." *Frontiers in Public Health*, 5, 258. doi:10.3389/fpubh.2017.00258

Task Force of the European Society of Cardiology and the North American Society of Pacing and Electrophysiology (1996). "Heart rate variability: Standards of measurement, physiological interpretation and clinical use." *Circulation*, 93(5), 1043–1065.

See Also

`ecgHRVpoincare` for Poincare plot descriptors, `ecgSampleEntropy` for sample entropy, `ecgDFA` for detrended fluctuation analysis, `ecgHRVtime` for time-domain HRV metrics, `ecgHRVfreq` for frequency-domain HRV analysis.

---

ecgHRVpoincare *Poincare Plot Descriptors for HRV Analysis*

Description

Computes Poincare plot descriptors (SD1, SD2, SD1/SD2 ratio) from RR interval data. SD1 reflects short-term variability (perpendicular to the identity line), while SD2 reflects long-term variability (along the identity line).

Usage

```
ecgHRVpoincare(rr)
```

Arguments

`rr`	A data.frame with columns `channel`, `rr_ms`, and `time_sec`, as returned by `ecgRRintervals`.

Value

A data.frame with one row per channel and the following columns:

channel Integer channel index.

sd1 Standard deviation perpendicular to the identity line (ms), reflecting beat-to-beat (short-term) variability.

sd2 Standard deviation along the identity line (ms), reflecting long-term variability.

sd1_sd2_ratio Ratio of SD1 to SD2, or `NA` if SD2 is zero.

References

Task Force of the European Society of Cardiology and the North American Society of Pacing and Electrophysiology (1996). "Heart rate variability: Standards of measurement, physiological interpretation and clinical use." *Circulation*, 93(5), 1043–1065.

See Also

`ecgHRVnonlinear` for the combined nonlinear analysis wrapper, `ecgSampleEntropy` for sample entropy, `ecgDFA` for detrended fluctuation analysis.

`ecgHRVtime` *HRV Time-Domain Metrics*

Description

Compute standard heart rate variability (HRV) time-domain metrics from RR interval data. Calculates SDNN, RMSSD, pNN50, mean RR interval, and mean heart rate for each channel.

Usage

```
ecgHRVtime(rr)
```

Arguments

`rr`	A data.frame with columns `channel`, `rr_ms`, and `time_sec`, as returned by `ecgRRintervals`.

Value

A data.frame with one row per channel and the following columns:

channel Integer channel index.

mean_rr Mean RR interval in milliseconds.

sdnn Standard deviation of all RR intervals (ms), reflecting overall HRV.

rmssd Root mean square of successive RR interval differences (ms), reflecting short-term vagal modulation.

pnn50 Percentage of successive RR intervals differing by more than 50 ms.

mean_hr Mean heart rate in beats per minute (60000 / mean_rr).

References

Task Force of the European Society of Cardiology and the North American Society of Pacing and Electrophysiology (1996). "Heart rate variability: Standards of measurement, physiological interpretation and clinical use." *Circulation*, 93(5), 1043–1065.

See Also

ecgRRintervals for computing RR intervals, ecgHRVfreq for frequency-domain HRV analysis, ecgHRVnonlinear for nonlinear HRV metrics, ecgQualityCheck for ectopic beat detection before analysis.

---

ecgIntervals *Compute ECG Intervals from Delineation*

Description

Calculates standard clinical ECG intervals from the waveform delineation produced by ecgDelineate: PR interval, QT interval, QTc (Bazett correction), QRS duration, and RR interval.

Usage

```
ecgIntervals(delineation, sr)
```

Arguments

delineation	A data.frame as returned by ecgDelineate, with columns channel, beat, r_peak, qrs_onset, qrs_offset, p_peak, t_peak, t_end.
sr	Sampling rate in Hz.

Value

A data.frame with one row per beat and the following columns:

channel Integer channel index (1-based).

beat Integer beat number within the channel.

pr_ms PR interval in milliseconds (P-wave peak to QRS onset), or NA if the P wave was not detected.

qt_ms QT interval in milliseconds (QRS onset to T-wave end), or NA if the T wave was not detected.

qtc_ms Corrected QT interval using Bazett's formula (QT / sqrt(RR_sec)), or NA if QT or RR is unavailable.

qrs_ms QRS complex duration in milliseconds.

rr_ms RR interval in milliseconds to the next beat, or NA for the last beat in each channel.

Returns a zero-row data.frame with the same column structure if no beats are present.

References

Goldberger, A.L., et al. (2000). "PhysioBank, PhysioToolkit, and PhysioNet: Components of a new research resource for complex physiologic signals." *Circulation*, 101(23), e215–e220. doi:10.1161/01.CIR.101.23.e215

See Also

ecgDelineate for waveform delineation, ecgDetectRpeaks for R-peak detection, ecgRRintervals for RR interval computation.

Examples

```
## Not run:
pe <- make_ecg(n_time = 5000, sr = 500, heart_rate = 72)
peaks <- ecgDetectRpeaks(pe)
delin <- ecgDelineate(pe, peaks)
intervals <- ecgIntervals(delin, samplingRate(pe))
head(intervals)

## End(Not run)
```

---

ecgQualityCheck *Detect Ectopic Beats in RR Interval Data*

Description

Identifies ectopic (abnormal) beats by comparing each RR interval to the local median computed over a sliding window of 5 beats. Beats with deviation exceeding the threshold are marked as ectopic.

Usage

```
ecgQualityCheck(rr, threshold_ms = 300)
```

Arguments

rr	A data.frame with columns channel, rr_ms, and time_sec, as returned by ecgRRintervals.
threshold_ms	Maximum allowed deviation from local median in milliseconds (default: 300).

Value

The input data.frame with an additional logical column is_ectopic.

References

Clifford, G.D., Azuaje, F. & McSharry, P.E. (2006). *Advanced Methods and Tools for ECG Data Analysis*. Artech House.

Task Force of the European Society of Cardiology and the North American Society of Pacing and Electrophysiology (1996). "Heart rate variability: Standards of measurement, physiological interpretation and clinical use." *Circulation*, 93(5), 1043–1065.

See Also

ecgRRcorrect for correcting detected ectopic beats, ecgRRintervals for computing RR intervals, ecgHRVtime for time-domain HRV analysis, ecgSignalQuality for signal quality assessment.

`ecgRRcorrect` *Correct Ectopic Beats in RR Interval Data*

Description

Replaces or removes ectopic beats identified by ecgQualityCheck. The "interpolate" method uses linear interpolation from surrounding non-ectopic intervals, while "remove" simply drops ectopic rows.

Usage

```
ecgRRcorrect(rr, method = c("interpolate", "remove"))
```

Arguments

rr	A data.frame with an is_ectopic logical column, as returned by ecgQualityCheck.
method	Correction method: "interpolate" (default) replaces ectopic values with linear interpolation; "remove" drops ectopic rows.

Value

A data.frame with corrected RR intervals. The is_ectopic column is removed from the output.

References

Clifford, G.D., Azuaje, F. & McSharry, P.E. (2006). *Advanced Methods and Tools for ECG Data Analysis*. Artech House.

See Also

ecgQualityCheck for detecting ectopic beats, ecgRRintervals for computing RR intervals, ecgHRVtime for time-domain HRV analysis.

`ecgRRintervals` *Compute RR Intervals from Detected R-Peaks*

Description

Calculates the time intervals between consecutive R-peaks for each channel. The resulting RR interval series is the standard input for all HRV analysis functions in this package.

Usage

```
ecgRRintervals(x, peaks)
```

Arguments

`x`	A PhysioExperiment object.
`peaks`	A data.frame of detected peaks as returned by `ecgDetectRpeaks`, with columns `channel`, `sample`, and `time_sec`.

Value

A data.frame with one row per consecutive beat pair and the following columns:

channel Integer channel index (1-based).

rr_ms RR interval in milliseconds (time between successive R-peaks).

time_sec Time of the first beat in each pair (seconds from signal onset).

Returns a zero-row data.frame with the same column structure if fewer than two peaks are available.

References

Pan, J. & Tompkins, W.J. (1985). "A real-time QRS detection algorithm." *IEEE Transactions on Biomedical Engineering*, 32(3), 230–236. doi:10.1109/TBME.1985.325532

See Also

`ecgDetectRpeaks` for R-peak detection, `ecgHRVtime` for time-domain HRV metrics, `ecgHRVfreq` for frequency-domain HRV analysis, `ecgQualityCheck` for ectopic beat detection.

Examples

```
## Not run:
pe <- make_ecg(n_time = 5000, sr = 500, heart_rate = 60)
peaks <- ecgDetectRpeaks(pe)
rr <- ecgRRintervals(pe, peaks)
head(rr)

## End(Not run)
```

`ecgSampleEntropy` *Sample Entropy of RR Intervals*

Description

Computes sample entropy (SampEn) from RR interval data. Sample entropy measures the regularity or predictability of a time series. Lower values indicate more regular (predictable) signals, while higher values indicate more complex (irregular) signals.

Usage

```
ecgSampleEntropy(rr, m = 2L, r_factor = 0.2)
```

Arguments

`rr`	A data.frame with columns `channel`, `rr_ms`, and `time_sec`, as returned by `ecgRRintervals`.
`m`	Embedding dimension (default: 2). Length of template patterns to compare.
`r_factor`	Tolerance factor (default: 0.2). The tolerance `r` is computed as `r_factor * sd(rr_ms)`.

Value

A data.frame with one row per channel and the following columns:

channel Integer channel index.

sample_entropy Sample entropy value (nats). Lower values indicate more regular signals; higher values indicate more complex signals. `NA` if the series is too short or constant.

m Embedding dimension used.

r Tolerance threshold (ms) computed as `r_factor * sd(rr_ms)`.

References

Richman, J.S. & Moorman, J.R. (2000). "Physiological time-series analysis using approximate entropy and sample entropy." *American Journal of Physiology-Heart and Circulatory Physiology*, 278(6), H2039–H2049. doi:10.1152/ajpheart.2000.278.6.H2039

See Also

`ecgHRVnonlinear` for the combined nonlinear analysis wrapper, `ecgHRVpoincare` for Poincare plot descriptors, `ecgDFA` for detrended fluctuation analysis.

`ecgSignalQuality` *Assess ECG Signal Quality Per Channel*

Description

Computes per-channel signal quality metrics for ECG data stored in a PhysioExperiment object. When detected R-peak locations are provided the signal-to-noise ratio is estimated from QRS vs.\ baseline power; otherwise a variance-based estimate is used.

Usage

```
ecgSignalQuality(x, peaks = NULL, assay_name = NULL)
```

Arguments

`x`	A PhysioExperiment object with ECG data.
`peaks`	Optional data.frame of detected R-peaks as returned by `ecgDetectRpeaks`, with at least columns `channel` and `sample`.
`assay_name`	Name of the assay to use. If `NULL` the default assay is used.

Value

A data.frame with one row per channel and columns:

channel Integer channel index.

snr_db Signal-to-noise ratio in decibels.

baseline_wander RMS amplitude of the low-frequency drift.

saturation_ratio Fraction of samples within 1\ min or max.

quality_score Composite quality score in the range [0, 1], where 1 indicates excellent quality.

References

Clifford, G.D., Azuaje, F. & McSharry, P.E. (2006). *Advanced Methods and Tools for ECG Data Analysis*. Artech House.

Shaffer, F. & Ginsberg, J.P. (2017). "An overview of heart rate variability metrics and norms." *Frontiers in Public Health*, 5, 258. doi:10.3389/fpubh.2017.00258

See Also

`ecgDetectRpeaks` for R-peak detection, `ecgBaselineCorrect` for baseline wander correction, `ecgQualityCheck` for ectopic beat detection.

make_ecg *Create Simulated ECG PhysioExperiment*

Description

Generates a PhysioExperiment object containing synthetic ECG data with Gaussian-shaped R-peaks at regular intervals. The resulting object is suitable for testing R-peak detection, RR interval computation, and HRV analysis pipelines.

Usage

```
make_ecg(n_time = 5000, n_channels = 1, sr = 500, heart_rate = 72)
```

Arguments

n_time	Number of time points (default: 5000).
n_channels	Number of ECG channels (default: 1).
sr	Sampling rate in Hz (default: 500).
heart_rate	Heart rate in beats per minute (default: 72).

Value

A PhysioExperiment object with a single "raw" assay containing the simulated ECG signal.

References

Pan, J. & Tompkins, W.J. (1985). "A real-time QRS detection algorithm." *IEEE Transactions on Biomedical Engineering*, 32(3), 230–236. doi:10.1109/TBME.1985.325532

Clifford, G.D., Azuaje, F. & McSharry, P.E. (2006). *Advanced Methods and Tools for ECG Data Analysis*. Artech House.

See Also

make_ecg_irregular for ECG with ectopic beats, make_ecg_pqrst for ECG with full PQRST morphology, make_ecg_noisy for ECG with noise artifacts, ecgDetectRpeaks for R-peak detection.

Examples

```
pe <- make_ecg(n_time = 5000, sr = 500, heart_rate = 72)
pe
```

make_ecg_irregular *Create Simulated ECG with Irregular R-R Intervals*

Description

Generates a PhysioExperiment object containing synthetic ECG data with irregular beat timing. Every 5th beat is premature (60\ interval), followed by a compensatory pause (140\ Useful for testing ectopic beat detection and RR interval correction.

Usage

```
make_ecg_irregular(n_time = 5000, sr = 500, heart_rate = 72)
```

Arguments

n_time	Number of time points (default: 5000).
sr	Sampling rate in Hz (default: 500).
heart_rate	Base heart rate in beats per minute (default: 72).

Value

A PhysioExperiment object with a single "raw" assay containing the simulated ECG signal with irregular beats.

References

Clifford, G.D., Azuaje, F. & McSharry, P.E. (2006). *Advanced Methods and Tools for ECG Data Analysis*. Artech House.

Task Force of the European Society of Cardiology and the North American Society of Pacing and Electrophysiology (1996). "Heart rate variability: Standards of measurement, physiological interpretation and clinical use." *Circulation*, 93(5), 1043–1065.

See Also

make_ecg for regular ECG data, ecgQualityCheck for ectopic beat detection, ecgRRcorrect for ectopic beat correction, ecgRRintervals for RR interval computation.

Examples

```
pe <- make_ecg_irregular(n_time = 5000, sr = 500, heart_rate = 72)
pe
```

`make_ecg_noisy` *Create Simulated ECG with Noise Artifacts*

Description

Generates a PhysioExperiment object containing synthetic ECG data contaminated with multiple noise sources: baseline wander (0.3 Hz sinusoidal drift), powerline interference (50 Hz), and broadband Gaussian noise. Useful for testing signal quality assessment, baseline correction, and filtering pipelines.

Usage

```
make_ecg_noisy(
  n_time = 5000,
  n_channels = 1,
  sr = 500,
  heart_rate = 72,
  baseline_amp = 0.3,
  powerline_amp = 0.1,
  noise_sd = 0.15
)
```

Arguments

`n_time`	Number of time points (default: 5000).
`n_channels`	Number of ECG channels (default: 1).
`sr`	Sampling rate in Hz (default: 500).
`heart_rate`	Heart rate in beats per minute (default: 72).
`baseline_amp`	Amplitude of baseline wander in arbitrary units (default: 0.3).
`powerline_amp`	Amplitude of 50 Hz powerline noise (default: 0.1).
`noise_sd`	Standard deviation of broadband Gaussian noise (default: 0.15).

Value

A PhysioExperiment object with a single `"raw"` assay containing the noisy ECG signal.

References

Clifford, G.D., Azuaje, F. & McSharry, P.E. (2006). *Advanced Methods and Tools for ECG Data Analysis*. Artech House.

Shaffer, F. & Ginsberg, J.P. (2017). "An overview of heart rate variability metrics and norms." *Frontiers in Public Health*, 5, 258. doi:10.3389/fpubh.2017.00258

See Also

make_ecg for clean ECG data, ecgSignalQuality for signal quality assessment, ecgBaselineCorrect for baseline wander removal, ecgDetectRpeaks for R-peak detection.

Examples

```
pe <- make_ecg_noisy(n_time = 5000, sr = 500)
pe
```

---

make_ecg_pqrst *Create Simulated ECG with PQRST Morphology*

Description

Generates a PhysioExperiment object containing synthetic ECG data with physiologically realistic P, Q, R, S, and T wave components. Returns both the PhysioExperiment and a data.frame of known fiducial points for validation testing of waveform delineation algorithms.

Usage

```
make_ecg_pqrst(
  n_time = 10000,
  n_channels = 1,
  sr = 500,
  heart_rate = 72,
  noise_sd = 0.02
)
```

Arguments

n_time	Number of time points (default: 10000, i.e., 20 seconds at 500 Hz).
n_channels	Number of ECG channels (default: 1).
sr	Sampling rate in Hz (default: 500).
heart_rate	Heart rate in beats per minute (default: 72).
noise_sd	Standard deviation of baseline noise (default: 0.02).

Value

A list with two components:

pe PhysioExperiment object with the simulated ECG signal.

fiducials A data.frame with columns: beat, r_peak, p_peak, q_point, s_point, t_peak, qrs_onset, qrs_offset (all in sample indices).

References

Goldberger, A.L., et al. (2000). "PhysioBank, PhysioToolkit, and PhysioNet: Components of a new research resource for complex physiologic signals." *Circulation*, 101(23), e215–e220. doi:10.1161/01.CIR.101.23.e215

Clifford, G.D., Azuaje, F. & McSharry, P.E. (2006). *Advanced Methods and Tools for ECG Data Analysis*. Artech House.

See Also

`make_ecg` for basic ECG data, `ecgDelineate` for PQRST waveform delineation, `ecgIntervals` for computing clinical ECG intervals, `ecgDetectRpeaks` for R-peak detection.

Examples

```
result <- make_ecg_pqrst(n_time = 10000, sr = 500, heart_rate = 72)
pe <- result$pe
fiducials <- result$fiducials
head(fiducials)
```

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