ECG

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Main

ecg_process()

```
ecg_process(ecg_signal, sampling_rate=1000, method='neurokit',
**kwargs)
[source]
```

Automated pipeline for preprocessing an ECG signal

This function runs different preprocessing steps: Cleaning (using ecg_clean()), peak detection (using ecg_peaks()), heart rate calculation (using signal_rate()), signal quality assessment (using ecg_quality()), QRS complex delineation (using ecg_delineate()), and cardiac phase determination (using ecg_phase()).

Help us improve the documentation of this function by making it more tidy and useful!

Parameters:

- ecg_signal (Union[list, np.array, pd.Series]) The raw single-channel ECG signal.
- **sampling_rate** (*int*) The sampling frequency of ecg_signal (in Hz, i.e., samples/second). Defar Back to top
- **method** (*str*) The processing method used for signal cleaning (using ecg_clean()) and peak detection (using ecg_peaks()). Defaults to

'neurokit'. Available methods are 'neurokit', 'pantompkins1985', 'hamilton2002', 'elgendi2010', 'engzeemod2012'. We aim at improving this aspect to make the available methods more transparent, and be able to generate specific reports. Please get in touch if you are interested in helping out with this.

Returns:

- **signals** (*DataFrame*) A DataFrame of the same length as the ecg_signal containing the following columns:
 - [ECG_Raw]: The raw signal.
 - ECG_Clean: The cleaned signal.
 - [ECG_Rate]: Heart rate interpolated between R-peaks.
 - ECG_Quality: The quality of the cleaned signal.
 - ECG_R_Peaks: The R-peaks marked as "1" in a list of zeros.
 - ECG R Onsets: The R-onsets marked as "1" in a list of zeros.
 - ECG R Offsets: The R-offsets marked as "1" in a list of zeros.
 - [ECG_P_Peaks]: The P-peaks marked as "1" in a list of zeros.
 - ECG_P_Onsets: The P-onsets marked as "1" in a list of zeros.
 - [ECG_P_Offsets]: The P-offsets marked as "1" in a list of zeros.
 - ECG_Q_Peaks: The Q-peaks marked as "1" in a list of zeros.
 - ECG S Peaks: The S-peaks marked as "1" in a list of zeros.
 - ECG_T_Peaks: The T-peaks marked as "1" in a list of zeros.
 - ECG T Onsets: The T-onsets marked as "1" in a list of zeros.
 - ECG T Offsets: The T-offsets marked as "1" in a list of zeros.
 - ECG_Phase_Atrial: Cardiac phase, marked by "1" for systole and "0" for diastole.
 - ECG_Phase_Completion_Atrial: Cardiac phase (atrial) completion, expressed in percentage (from 0 to 1), representing the stage of the current cardiac phase.
 - ECG_Phase_Completion_Ventricular: Cardiac phase (ventricular)
 completion, expressed in percentage (from 0 to 1), representing the stage of the current cardiac phase.
- rpeaks (dict) A dictionary containing the samples at which the R-peaks occur, accessible with the key "ECG_R_Peaks", as well as the signals' sampling rate.

```
See also

ecg_clean, ecg_peaks, ecg_quality, ecg_delineate, ecg_phase,
ecg_plot, signal_rate
```

Examples

```
In [1]: import neurokit2 as nk

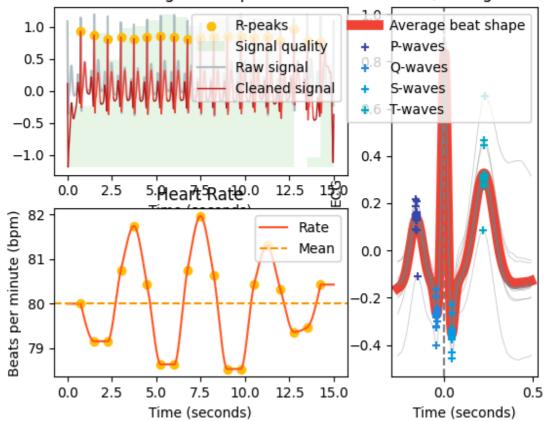
# Simulate ECG signal
In [2]: ecg = nk.ecg_simulate(duration=15, sampling_rate=1000, heart_rat

# Preprocess ECG signal
In [3]: signals, info = nk.ecg_process(ecg, sampling_rate=1000)

# Visualize
In [4]: nk.ecg_plot(signals, info)
```

Electrocardiogram (ECG)

ECG signal and pedkadual Heart Beats (average heart rate:



ecg_analyze()

ecg_analyze(data, sampling_rate=1000, method='auto')

[source]

Performs ECG analysis by computing relevant features and indices on either epochs (event-related analysis) or on longer periods of data (interval-related analysis), such as resting-state data.

Parameters:

- data (Union[dict, pd.DataFrame]) A dictionary of epochs, containing one
 DataFrame per epoch, usually obtained via epochs_create(), or a
 DataFrame containing all epochs, usually obtained via epochs_to_df(). Can
 also take a DataFrame of processed signals from a longer period of data,
 typically generated by ecg_process() or bio_process(). Can also take a
 dict containing sets of separate periods of data.
- **sampling_rate** (*int*) The sampling frequency of the signal (in Hz, i.e., samples/second). Defaults to 1000Hz.
- **method** (*str*) Can be one of "event-related" for event-related analysis on epochs, or "interval-related" for analysis on longer periods of data.

 Defaults to auto, where the method will be chosen based on the mean duration of the data ("event-related" for duration under 10s).

Returns:

DataFrame – A dataframe containing the analyzed ECG features. If event-related analysis is conducted, each epoch is indicated by the Label column. See ecg_eventrelated() and ecg_intervalrelated() docstrings for details.

```
bio_process, ecg_process, epochs_create, ecg_eventrelated,
ecg_intervalrelated
```

Examples

• Example 1: Event-related analysis

```
In [1]: import neurokit2 as nk
# Download the data
In [2]: data = nk.data("bio eventrelated 100hz")
# Process the data for event-related analysis
In [3]: df, info = nk.bio_process(ecg=data["ECG"], sampling_rate=100)
In [4]: events = nk.events_find(data["Photosensor"], threshold_keep='bel
                                event conditions=["Negative", "Neutral",
   . . . :
   . . . :
In [5]: epochs = nk.epochs create(df, events, sampling rate=100, epochs
# Analyze
In [6]: analyze_epochs = nk.ecg_analyze(epochs, sampling_rate=100)
# Get a dataframe with all the results
In [7]: analyze epochs
Out[7]:
  Label Condition ...
                        ECG_Phase_Completion_Ventricular ECG_Quality_Me
1
      1 Negative ...
                                                 0.400000
                                                                   0.9521
2
      2
         Neutral ...
                                                 0.553846
                                                                   0.9236
3
      3
         Neutral
                                                 0.133333
                                                                   0.9302
      4 Negative
                                                 0.575342
                                                                   0.9557
[4 rows x 18 columns]
```

• Example 2: Interval-related analysis

ecg_simulate()

Generate an artificial (synthetic) ECG signal of a given duration and sampling rate using either the ECGSYN dynamical model (McSharry et al., 2003) or a simpler model based on Daubechies wavelets to roughly approximate cardiac cycles.

Parameters:

- **duration** (*int*) Desired recording length in seconds.
- **sampling_rate** (*int*) The desired sampling rate (in Hz, i.e., samples/second).
- **length** (*int*) The desired length of the signal (in samples).
- **noise** (*float*) Noise level (amplitude of the laplace noise).
- heart_rate (int) Desired simulated heart rate (in beats per minute). The default is 70. Note that for the "ECGSYN" method, random fluctuations are to be expected to mimick a real heart rate. These fluctuations can cause some slight discrepancies between the requested heart rate and the empirical heart rate, especially for shorter signals.
- heart_rate_std (int) Desired heart rate standard deviation (beats per minute).
- method (str) The model used to generate the signal. Can be "simple" for a simulation based on Daubechies wavelets that roughly approximates a single cardiac cycle. If "ecgsyn" (default), will use the model desbribed McSharry et al. (2003). If "multileads", will return a DataFrame containing 12-leads (see 12-leads ECG simulation).
- random_state (None, int, numpy.random.RandomState or numpy.random.Generator) – Seed for the random number generator. See for misc.check_random_state for further information.
- random_state_distort ({'legacy', 'spawn'}, None, int, numpy.random.RandomState or numpy.random.Generator) Random state to be used to distort the signal. If "legacy", use the same random state used to generate the signal (discouraged as it creates dependent random streams). If "spawn", spawn independent children random number generators from the random_state argument. If any of the other types, generate independent children random number generators from the random_state_distort provided

(this allows generating multiple version of the same signal distorted by different random noise realizations).

• **kwargs – Other keywords parameters for ECGSYN algorithm, such as "lfhfratio", "ti", "ai", "bi".

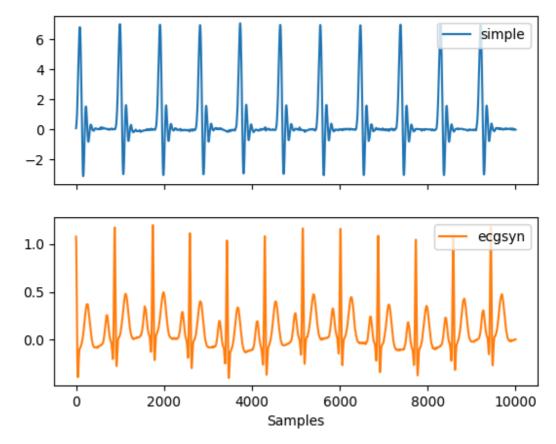
Returns:

array - Vector containing the ECG signal.

Examples

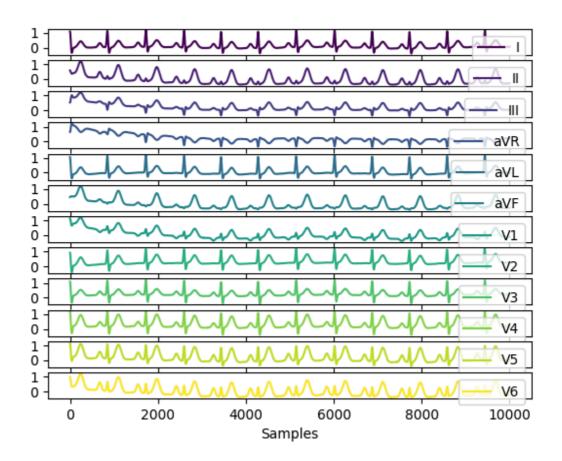
• Example 1: Simulate single lead ECG

```
In [1]: import neurokit2 as nk
In [2]: ecg1 = nk.ecg_simulate(duration=10, method="simple")
In [3]: ecg2 = nk.ecg_simulate(duration=10, method="ecgsyn")
# Visualize result
In [4]: nk.signal_plot([ecg1, ecg2], labels=["simple", "ecgsyn"], subplo
```



• Example 2: Simulate 12-leads ECG

```
In [5]: ecg12 = nk.ecg_simulate(duration=10, method="multileads")
# Visualize result
In [6]: nk.signal_plot(ecg12, subplots=True)
```



References

• McSharry, P. E., Clifford, G. D., Tarassenko, L., & Smith, L. A. (2003). A dynamical model for generating synthetic electrocardiogram signals. IEEE transactions on biomedical engineering, 50 (3), 289-294.

ecg_plot()

ecg_plot(ecg_signals, info=None)

[source]

Visualize ECG data

Plot ECG signals and R-peaks.

Parameters:

- ecg_signals (DataFrame) DataFrame obtained from ecg_process().
- **info** (*dict*) The information Dict returned by ecg_process(). Defaults to None.

```
See also

ecg_process
```

Returns:

- Though the function returns nothing, the figure can be retrieved and saved as follows
- .. code-block:: python # To be run after ecg_plot() fig = plt.gcf()
 fig.set_size_inches(10, 12, forward=True) fig.savefig("myfig.png")

Examples

```
In [1]: import neurokit2 as nk

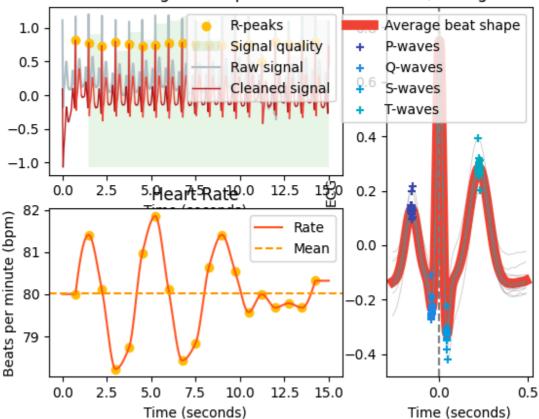
# Simulate data
In [2]: ecg = nk.ecg_simulate(duration=15, sampling_rate=1000, heart_rat

# Process signal
In [3]: signals, info = nk.ecg_process(ecg, sampling_rate=1000)

# Plot
In [4]: nk.ecg_plot(signals, info)
```

Electrocardiogram (ECG)

ECG signal and pedkedual Heart Beats (average heart rate:



Preprocessing

ecg_clean()

ecg_clean(ecg_signal, sampling_rate=1000, method='neurokit',
**kwargs)
[source]

ECG Signal Cleaning

Clean an ECG signal to remove noise and improve peak-detection accuracy. Different cleaning methods are implemented.

- 'neurokit' (default): 0.5 Hz high-pass butterworth filter (order = 5), followed by powerline filtering (see signal_filter()). By default, powerline = 50.
- 'biosppy': Method used in the BioSPPy package. A FIR filter ([0.67, 45] Hz; order = 1.5 * SR). The 0.67 Hz cutoff value was selected based on the fact that there are no morphological features below the heartrate (assuming a minimum heart rate of 40 bpm).

- 'pantompkins1985': Method used in Pan & Tompkins (1985). Please help providing a better description!
- <u>'hamilton2002'</u>: Method used in Hamilton (2002). **Please help providing a** better description!
- <u>'elgendi2010'</u>: Method used in Elgendi et al. (2010). **Please help providing a** better description!
- 'engzeemod2012': Method used in Engelse & Zeelenberg (1979). Please help providing a better description!
- 'vg': Method used in Visibility Graph Based Detection Emrich et al. (2023) and Koka et al. (2022). A 4.0 Hz high-pass butterworth filter (order = 2).

Parameters:

- ecg_signal (Union[list, np.array, pd.Series]) The raw ECG channel.
- **sampling_rate** (*int*) The sampling frequency of ecg_signal (in Hz, i.e., samples/second). Defaults to 1000.
- method (str) The processing pipeline to apply. Can be one of "neurokit" (default), "biosppy", "pantompkins1985", "hamilton2002", "elgendi2010", "engzeemod2012", 'vg'.
- **kwargs Other arguments to be passed to specific methods.

Returns:

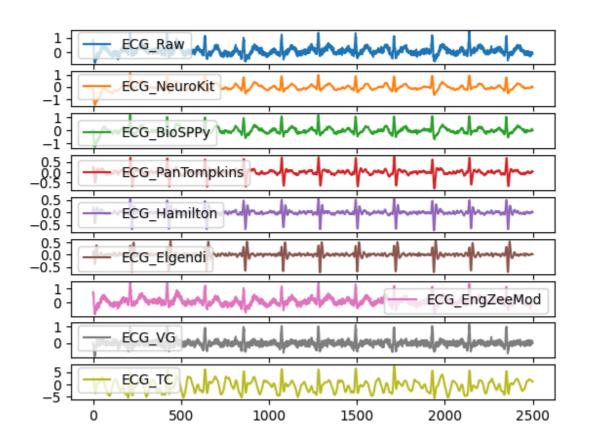
array - Vector containing the cleaned ECG signal.

```
See also

ecg_peaks, ecg_process, ecg_plot, signal_rate, signal_filter
```

Examples

```
In [1]: import pandas as pd
In [2]: import numpy as np
In [3]: import neurokit2 as nk
In [4]: ecg = nk.ecg_simulate(duration=10, sampling_rate=250, noise=0.2)
In [5]: ecg += np.random.normal(0, 0.1, len(ecg)) # Add Gaussian noise
In [6]: signals = pd.DataFrame({
            "ECG_Raw" : ecg,
            "ECG NeuroKit": nk.ecg clean(ecg, sampling rate=250, method
            "ECG_BioSPPy": nk.ecg_clean(ecg, sampling_rate=250, method=
            "ECG_PanTompkins" : nk.ecg_clean(ecg, sampling_rate=250, met
   . . . :
            "ECG_Hamilton" : nk.ecg_clean(ecg, sampling_rate=250, method
            "ECG_Elgendi": nk.ecg_clean(ecg, sampling_rate=250, method=
            "ECG_EngZeeMod" : nk.ecg_clean(ecg, sampling_rate=250, metho
            "ECG VG": nk.ecg clean(ecg, sampling rate=250, method="vg")
            "ECG_TC": nk.ecg_clean(ecg, sampling_rate=250, method="temp
   ...: })
   . . . :
In [7]: signals.plot(subplots=True)
Out [7]:
array([<Axes: >, <Axes: >, <Axes: >, <Axes: >, <Axes: >,
       <Axes: >, <Axes: >], dtype=object)
```



References

- Engelse, W. A., & Zeelenberg, C. (1979). A single scan algorithm for QRS-detection and feature extraction. Computers in cardiology, 6(1979), 37-42.
- Pan, J., & Tompkins, W. J. (1985). A real-time QRS detection algorithm. IEEE transactions on biomedical engineering, (3), 230-236.
- Hamilton, P. (2002). Open source ECG analysis. In Computers in cardiology (pp. 101-104). IEEE.
- Elgendi, M., Jonkman, M., & De Boer, F. (2010). Frequency Bands Effects on QRS
 Detection. Biosignals, Proceedings of the Third International Conference on Bioinspired Systems and Signal Processing, 428-431.
- Emrich, J., Koka, T., Wirth, S., & Muma, M. (2023), Accelerated Sample-Accurate R-Peak Detectors Based on Visibility Graphs. 31st European Signal Processing Conference (EUSIPCO), 1090-1094, doi: 10.23919/EUSIPCO58844.2023.10290007

ecg_quality()

ecg_quality(ecg_cleaned, rpeaks=None, sampling_rate=1000,
method='averageQRS', approach=None)
[source]

ECG Signal Quality Assessment

Assess the quality of the ECG Signal using various methods:

- The "averageQRS" method computes a continuous index of quality of the ECG signal, by interpolating the distance of each QRS segment from the average QRS segment present in the * data. This index is therefore relative: 1 corresponds to heartbeats that are the closest to the average sample and 0 corresponds to the most distant heartbeat from that average sample. Note that 1 does not necessarily means "good": if the majority of samples are bad, then being close to the average will likely mean bad as well. Use this index with care and plot it alongside your ECG signal to see if it makes sense.
- The "zhao2018" method (Zhao et al., 2018) extracts several signal quality indexes (SQIs): QRS wave power spectrum distribution pSQI, kurtosis kSQI, and baseline relative power basSQI. An additional R peak detection match qSQI was originally computed in the paper but left out in this algorithm. The indices were originally weighted with a ratio of [0.4, 0.4, 0.1, 0.1] to generate the final

classification outcome, but because qSQI was dropped, the weights have been rearranged to [0.6, 0.2, 0.2] for pSQI, kSQI and basSQI respectively.

Parameters:

- ecg_cleaned (Union[list, np.array, pd.Series]) The cleaned ECG signal in the form of a vector of values.
- **rpeaks** (*tuple or list*) The list of R-peak samples returned by ecg_peaks(). If None, peaks is computed from the signal input.
- **sampling_rate** (*int*) The sampling frequency of the signal (in Hz, i.e., samples/second).
- **method** (*str*) The method for computing ECG signal quality, can be "averageQRS" (default) or "zhao2018".
- approach (str) The data fusion approach as documented in Zhao et al. (2018). Can be "simple" or "fuzzy". The former performs simple heuristic fusion of SQIs and the latter performs fuzzy comprehensive evaluation. If
 None (default), simple heuristic fusion is used.
- **kwargs Keyword arguments to be passed to signal_power() in the computation of basSQI and pSQI.

Returns:

```
array or str – Vector containing the quality index ranging from 0 to 1 for "averageQRS" method, returns string classification (Unacceptable), Barely acceptable or Excellent) of the signal for "zhao2018" method.
```

```
See also
    ecg_segment, ecg_delineate
```

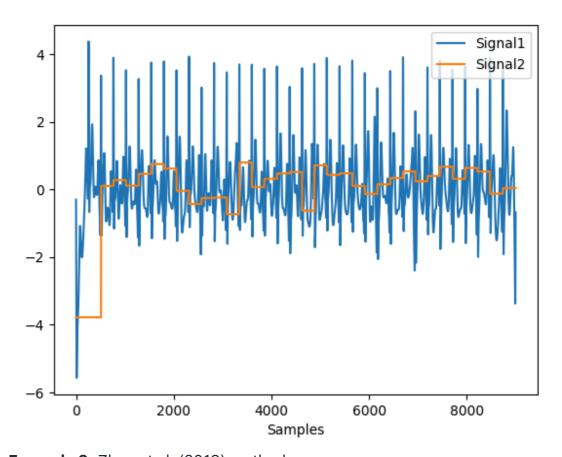
References

• Zhao, Z., & Zhang, Y. (2018). "SQI quality evaluation mechanism of single-lead ECG signal based on simple heuristic fusion and fuzzy comprehensive evaluation". Frontiers in Physiology, 9, 727.

Examples

• Example 1: 'averageQRS' method

```
In [1]: import neurokit2 as nk
In [2]: ecg = nk.ecg_simulate(duration=30, sampling_rate=300, noise=0.2)
In [3]: ecg_cleaned = nk.ecg_clean(ecg, sampling_rate=300)
In [4]: quality = nk.ecg_quality(ecg_cleaned, sampling_rate=300)
In [5]: nk.signal_plot([ecg_cleaned, quality], standardize=True)
```



• Example 2: Zhao et al. (2018) method

```
ecg_rsp()
```

```
ecg_rsp(ecg_rate, sampling_rate=1000, method='vangent2019')

ECG-Derived Respiration (EDR)
[source]
```

Extract ECG-Derived Respiration (EDR), a proxy of a respiratory signal based on heart rate.

Different methods include:

- vangent2019: 0.1-0.4 Hz filter.
- soni2019: 0-0.5 Hz filter.
- charlton2016: 0.066-1 Hz filter.
- sarkar2015: 0.1-0.7 Hz filter.

Warning

Help is required to double-check whether the implementation match the papers.

Parameters:

- ecg_rate (array) The heart rate signal as obtained via ecg_rate().
- sampling rate (int) The sampling frequency of the signal that contains the R-peaks (in Hz, i.e., samples/second). Defaults to 1000Hz.
- method (str) Can be one of "vangent2019" (default), "soni2019", "charlton2016" or "sarkar2015".

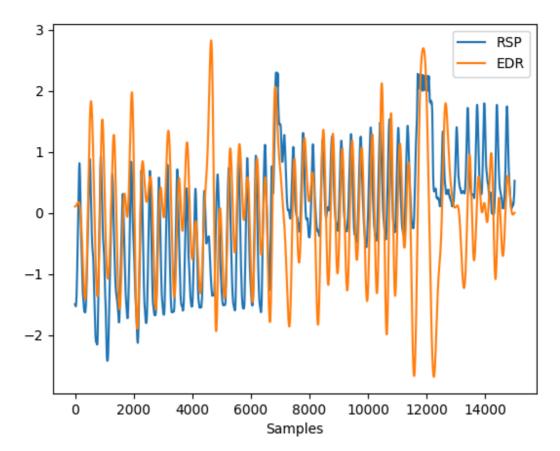
Returns:

array – A Numpy array containing the ECG-Derived Respiration signal.

Examples

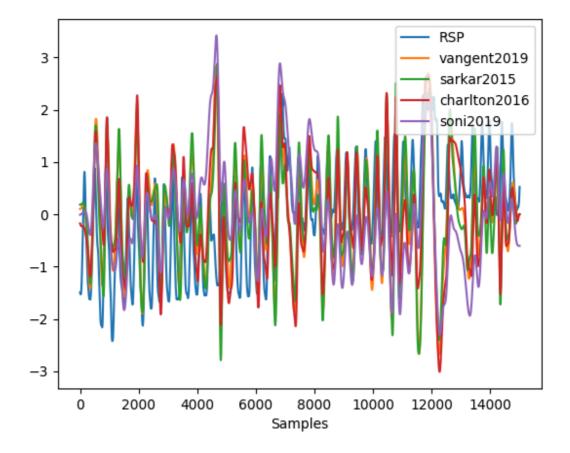
• Example 1: Compare to real RSP signal

```
In [1]: import neurokit2 as nk
# Get heart rate
In [2]: data = nk.data("bio_eventrelated_100hz")
In [3]: rpeaks, info = nk.ecg_peaks(data["ECG"], sampling_rate=100)
In [4]: ecg_rate = nk.signal_rate(rpeaks, sampling_rate=100, desired_len
# Get ECG Derived Respiration (EDR) and add to the data
In [5]: data["EDR"] = nk.ecg_rsp(ecg_rate, sampling_rate=100)
# Visualize result
In [6]: nk.signal_plot([data["RSP"], data["EDR"]], standardize = True)
```



• Example 2: Methods comparison

```
In [7]: data["vangent2019"] = nk.ecg_rsp(ecg_rate, sampling_rate=100, me
In [8]: data["sarkar2015"] = nk.ecg_rsp(ecg_rate, sampling_rate=100, met
In [9]: data["charlton2016"] = nk.ecg_rsp(ecg_rate, sampling_rate=100, m
In [10]: data["soni2019"] = nk.ecg_rsp(ecg_rate, sampling_rate=100, meth
# Visualize results
In [11]: nk.signal_plot([data["RSP"], data["vangent2019"], data["sarkar2"], data["charlton2016"], data["soni2019"]], standa....:
```



References

- van Gent, P., Farah, H., van Nes, N., & van Arem, B. (2019). HeartPy: A novel heart rate algorithm for the analysis of noisy signals. Transportation research part F: traffic psychology and behaviour, 66, 368-378.
- Sarkar, S., Bhattacherjee, S., & Pal, S. (2015). Extraction of respiration signal from ECG for respiratory rate estimation.
- Charlton, P. H., Bonnici, T., Tarassenko, L., Clifton, D. A., Beale, R., & Watkinson, P. J. (2016). An assessment of algorithms to estimate respiratory rate from the electrocardiogram and photoplethysmogram. Physiological measurement, 37(4), 610.
- Soni, R., & Muniyandi, M. (2019). Breath rate variability: a novel measure to study the meditation effects. International Journal of Yoga, 12(1), 45.

ecg_peaks()

ecg_peaks(ecg_cleaned, sampling_rate=1000, method='neurokit',
correct_artifacts=False, show=False, **kwargs)
[source]

Find R-peaks in an ECG signal

Find R-peaks in an ECG signal using the specified method. You can pass an unfiltered ECG signals as input, but typically a filtered ECG (cleaned using ecg_clean()) will result in better results.

Different algorithms for peak-detection include:

- neurokit (default): QRS complexes are detected based on the steepness of the absolute gradient of the ECG signal. Subsequently, R-peaks are detected as local maxima in the QRS complexes. The method is unpublished, but see: (i)

 neuropsychology/NeuroKit#476 for discussion of this algorithm; and (ii)
 https://doi.org/10.21105/joss.02621 for the original validation of this algorithm.
- pantompkins1985: Algorithm by Pan & Tompkins (1985).
- hamilton2002: Algorithm by Hamilton (2002).
- zong2003: Algorithm by Zong et al. (2003).
- martinez2004: Algorithm by Martinez et al (2004).
- **christov2004**: Algorithm by Christov (2004).
- gamboa2008: Algorithm by Gamboa (2008).
- elgendi2010: Algorithm by Elgendi et al. (2010).
- engzeemod2012: Original algorithm by Engelse & Zeelenberg (1979) modified by Lourenço et al. (2012).
- manikandan2012: Algorithm by Manikandan & Soman (2012) based on the Shannon energy envelope (SEE).
- kalidas2017: Algorithm by Kalidas et al. (2017).
- **nabian2018**: Algorithm by Nabian et al. (2018) based on the Pan-Tompkins algorithm.
- rodrigues2021: Adaptation of the work by Sadhukhan & Mitra (2012) and Gutiérrez-Rivas et al. (2015) by Rodrigues et al. (2021).
- emrich2023: FastNVG Algorithm by Emrich et al. (2023) based on the visibility graph detector of Koka et al. (2022). Provides fast and sample-accurate R-peak detection. The algorithm transforms the ecg into a graph representation and extracts exact R-peak positions using graph metrics.
- promac: ProMAC combines the result of several R-peak detectors in a probabilistic way. For a given peak detector, the binary signal representing the peak locations is convolved with a Gaussian distribution, resulting in a probabilistic representation of each peak location. This procedure is repeated for all selected methods and the resulting signals are accumulated. Finally, a threshold is used to accept or reject the peak locations. See this discussion for more information on the origins of the method: neuropsychology/NeuroKit#222



Please help us improve the methods' documentation by adding a small description.

Parameters:

- **ecg_cleaned** (*Union[list, np.array, pd.Series]*) The cleaned ECG channel as returned by **ecg_clean()**.
- **sampling_rate** (*int*) The sampling frequency of ecg_cleaned (in Hz, i.e., samples/second). Defaults to 1000.
- **method** (*string*) The algorithm to be used for R-peak detection.
- **correct_artifacts** (*bool*) Whether or not to identify and fix artifacts, using the method by Lipponen & Tarvainen (2019).
- **show** (*bool*) If True, will show a plot of the signal with peaks. Defaults to False.
- **kwargs Additional keyword arguments, usually specific for each method.

Returns:

- **signals** (*DataFrame*) A DataFrame of same length as the input signal in which occurrences of R-peaks marked as 1 in a list of zeros with the same length as ecg_cleaned. Accessible with the keys "ECG_R_Peaks".
- **info** (*dict*) A dictionary containing additional information, in this case the samples at which R-peaks occur, accessible with the key "ECG_R_Peaks", as well as the signals' sampling rate, accessible with the key "sampling_rate".

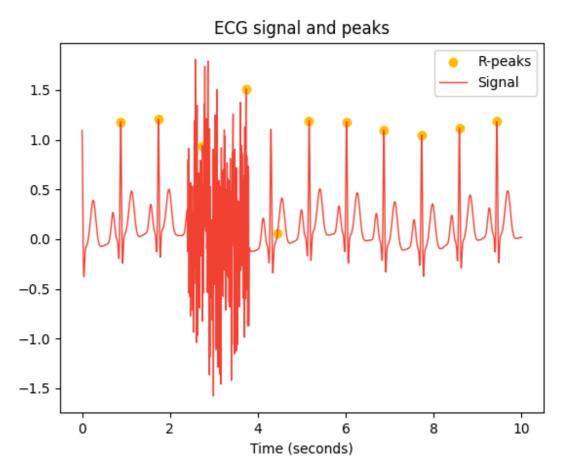
```
See also

ecg_clean, ecg_findpeaks, signal_fixpeaks
```

Examples

• **Example 1**: Find R-peaks using the default method ("neurokit").

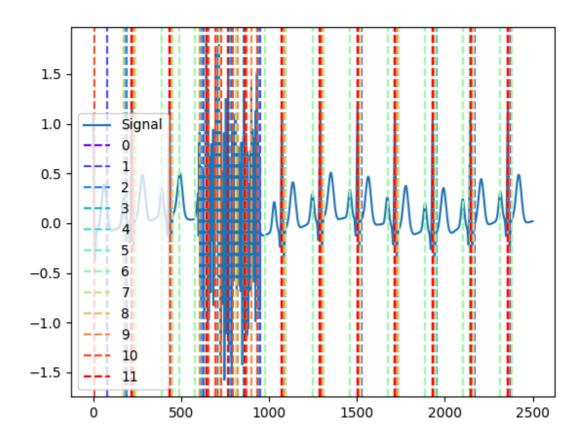
```
In [1]: import neurokit2 as nk
In [2]: import numpy as np
In [3]: ecg = nk.ecg_simulate(duration=10, sampling_rate=250)
In [4]: ecg[600:950] = ecg[600:950] + np.random.normal(0, 0.6, 350)
In [5]: signals, info = nk.ecg_peaks(ecg, sampling_rate=250, correct_art
```



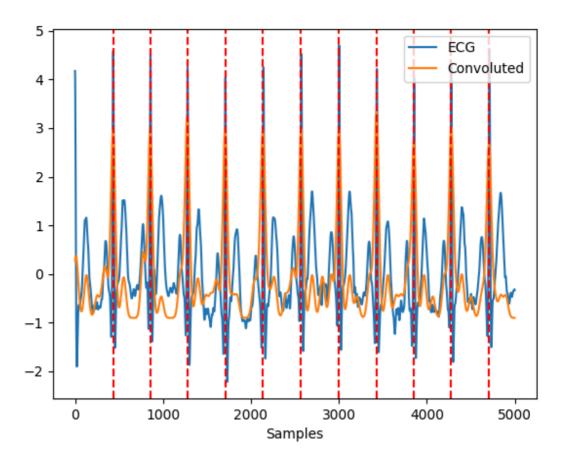
• Example 2: Compare different methods

```
# neurokit (default)
In [6]: cleaned = nk.ecg_clean(ecg, sampling_rate=250, method="neurokit"
In [7]: _, neurokit = nk.ecg_peaks(cleaned, sampling_rate=250, method="n
# pantompkins1985
In [8]: cleaned = nk.ecg_clean(ecg, sampling_rate=250, method="pantompki")
In [9]: _, pantompkins1985 = nk.ecg_peaks(cleaned, sampling_rate=250, me
# hamilton2002
In [10]: cleaned = nk.ecg_clean(ecg, sampling_rate=250, method="hamilton")
In [11]: _, hamilton2002 = nk.ecg_peaks(cleaned, sampling_rate=250, meth
# zong2003
In [12]: _, zong2003 = nk.ecg_peaks(ecg, sampling_rate=250, method="zong")
# martinez2004
In [13]: _, martinez2004 = nk.ecg_peaks(ecg, sampling_rate=250, method="
# christov2004
In [14]: _, christov2004 = nk.ecg_peaks(cleaned, sampling_rate=250, meth
# gamboa2008
In [15]: cleaned = nk.ecg_clean(ecg, sampling_rate=250, method="gamboa20")
In [16]: _, gamboa2008 = nk.ecg_peaks(cleaned, sampling_rate=250, method
# elgendi2010
In [17]: cleaned = nk.ecg_clean(ecg, sampling_rate=250, method="elgendi2")
In [18]: _, elgendi2010 = nk.ecg_peaks(cleaned, sampling_rate=250, methol
# engzeemod2012
In [19]: cleaned = nk.ecg_clean(ecg, sampling_rate=250, method="engzeemo")
In [20]: _, engzeemod2012 = nk.ecg_peaks(cleaned, sampling_rate=250, met
# Manikandan (2012)
In [21]: _, manikandan2012 = nk.ecg_peaks(ecg, sampling_rate=250, method
# kalidas2017
In [22]: cleaned = nk.ecg_clean(ecg, sampling_rate=250, method="kalidas2")
In [23]: _, kalidas2017 = nk.ecg_peaks(cleaned, sampling_rate=250, methor
# nabian2018
In [24]: _, nabian2018 = nk.ecg_peaks(ecg, sampling_rate=250, method="na
# rodrigues2021
In [25]: _, rodrigues2021 = nk.ecg_peaks(ecg, sampling_rate=250, method=
# emrich2023
In [26]: cleaned = nk.ecg_clean(ecg, sampling_rate=250, method="emrich20")
In [27]: _, emrich2023 = nk.ecg_peaks(cleaned, sampling_rate=250, method
```

```
# Collect all R-peak lists by iterating through the result dicts
In [28]: rpeaks = [
             i["ECG_R_Peaks"]
             for i in [
                 neurokit,
                 pantompkins1985,
                 nabian2018,
                 hamilton2002,
                 martinez2004,
                 christov2004,
                 gamboa2008,
                 elgendi2010,
                 engzeemod2012,
                 kalidas2017,
                 rodrigues2021,
                 emrich2023
             ]
# Visualize results
In [29]: nk.events_plot(rpeaks, ecg)
Out[29]: <Figure size 640x480 with 1 Axes>
```



• **Example 3**: Method-agreement procedure ('promac')



References

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- promac
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ecg_delineate()

ecg_delineate(ecg_cleaned, rpeaks=None, sampling_rate=1000,
method='dwt', show=False, show_type='peaks', check=False, **kwargs)
Delineate QRS complex
[source]

Function to delineate the QRS complex, i.e., the different waves of the cardiac cycles. A typical ECG heartbeat consists of a P wave, a QRS complex and a T wave. The P wave represents the wave of depolarization that spreads from the SA-node throughout the atria. The QRS complex reflects the rapid depolarization of the right and left ventricles. Since the ventricles are the largest part of the heart, in terms of mass, the QRS complex usually has a much larger amplitude than the P-wave. The T wave represents the ventricular repolarization of the ventricles. On rare occasions, a U wave can be seen following the T wave. The U wave is believed to be related to the last remnants of ventricular repolarization.

Parameters:

- **ecg_cleaned** (*Union[list, np.array, pd.Series]*) The cleaned ECG channel as returned by **ecg_clean()**.
- **rpeaks** (*Union[list, np.array, pd.Series]*) The samples at which R-peaks occur. Accessible with the key "ECG_R_Peaks" in the info dictionary returned by ecg_findpeaks().
- **sampling_rate** (*int*) The sampling frequency of ecg_signal (in Hz, i.e., samples/second). Defaults to 1000.

- method (str) Can be one of "peak" for a peak-based method,

 "prominence" for a peak-prominence-based method (Emrich et al., 2024),

 "cwt" for continuous wavelet transform or "dwt" (default) for discrete

 wavelet transform. The "prominence" method might be useful to detect the

 waves, allowing to set individual physiological limits (see kwargs), while the

 "dwt" method might be more precise for detecting the onsets and offsets of
 the waves (but might exhibit lower accuracy when there is significant variation
 in wave morphology). The "peak" method, which uses the zero-crossings of
 the signal derivatives, works best with very clean signals.
- **show** (*bool*) If True, will return a plot to visualizing the delineated waves information.
- **show_type** (*str*) The type of delineated waves information showed in the plot. Can be "peaks", "bounds_R", "bounds_T", "bounds_P" or "all".
- **check** (*bool*) Defaults to False. If True, replaces the delineated features with np.nan if its standardized distance from R-peaks is more than 3.
- **kwargs Other optional arguments: If using the "prominence" method, additional parameters (in milliseconds) can be passed to set individual physiological limits for the search boundaries: max_qrs_interval: The maximum allowable QRS complex interval. Defaults to 180 ms. max_pr_interval: The maximum PR interval duration. Defaults to 300 ms. max_r_rise_time: Maximum duration for the R-wave rise. Defaults to 120 ms. typical_st_segment: Typical duration of the ST segment. Defaults to 150 ms. max_p_basepoint_interval: The maximum interval between P-wave on- and offset. Defaults to 100 ms. max_r_basepoint_interval: The maximum interval between R-wave on- and offset. Defaults to 100 ms. max_t_basepoint_interval: The maximum interval between T-wave on- and offset. Defaults to 200 ms.

Returns:

waves (dict) – A dictionary containing additional information. For derivative method, the dictionary contains the samples at which P-peaks, Q-peaks, S-peaks, T-peaks, P-onsets and T-offsets occur, accessible with the keys "ECG_P_Peaks", "ECG_Q_Peaks", "ECG_S_Peaks", "ECG_T_Peaks", "ECG_T_Peaks", "ECG_P_Onsets", "ECG_T_Offsets", respectively.
 For the wavelet and prominence methods, in addition to the above information, the dictionary contains the samples at which QRS-onsets and QRS-offsets occur, accessible with the key "ECG_P_Peaks", "ECG_T_Peaks",

"ECG_P_Onsets", ["ECG_P_Offsets"], ["ECG_Q_Peaks"], ["ECG_S_Peaks"],

```
"ECG_T_Onsets", "ECG_T_Offsets", "ECG_R_Onsets", "ECG_R_Offsets", respectively.
```

 signals (DataFrame) – A DataFrame of same length as the input signal in which occurrences of peaks, onsets and offsets marked as "1" in a list of zeros.

```
See also

ecg_clean, signal_fixpeaks, ecg_peaks, signal_rate, ecg_process,
ecg_plot
```

Examples

• Step 1. Delineate

```
In [1]: import neurokit2 as nk

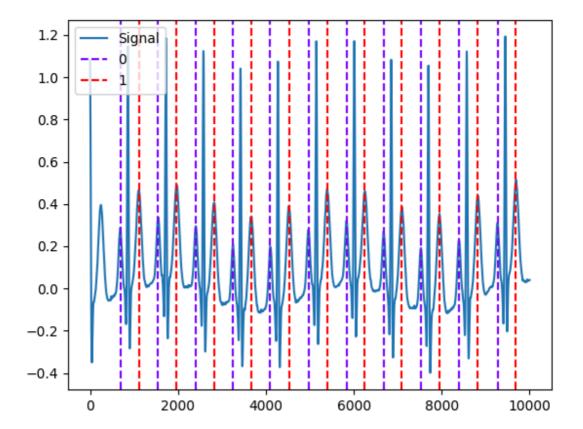
# Simulate ECG signal
In [2]: ecg = nk.ecg_simulate(duration=10, sampling_rate=1000)

# Get R-peaks location
In [3]: _, rpeaks = nk.ecg_peaks(ecg, sampling_rate=1000)

# Delineate cardiac cycle
In [4]: signals, waves = nk.ecg_delineate(ecg, rpeaks, sampling_rate=100)
```

Step 2. Plot P-Peaks and T-Peaks

```
In [5]: nk.events_plot([waves["ECG_P_Peaks"], waves["ECG_T_Peaks"]], ecg
Out[5]: <Figure size 640x480 with 1 Axes>
```



References

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ecg_phase()

ecg_phase(ecg_cleaned, rpeaks=None, delineate_info=None,
sampling_rate=None)

[source]

Find the Cardiac Phase

Compute cardiac phase (for both atrial and ventricular), labelled as 1 for systole and 0 for diastole.

Parameters:

- **ecg_cleaned** (*Union[list, np.array, pd.Series]*) The cleaned ECG channel as returned by <code>ecg_clean()</code>.
- **rpeaks** (*list or array or DataFrame or Series or dict*) The samples at which the different ECG peaks occur. If a dict or a DataFrame is passed, it is assumed that these containers were obtained with ecg_findpeaks() or ecg_peaks().
- **delineate_info** (*dict*) A dictionary containing additional information of ecg delineation and can be obtained with ecg_delineate().
- **sampling_rate** (*int*) The sampling frequency of ecg_signal (in Hz, i.e., samples/second). Defaults to None.

Returns:

signals (*DataFrame*) – A DataFrame of same length as ecg_signal containing the following columns:

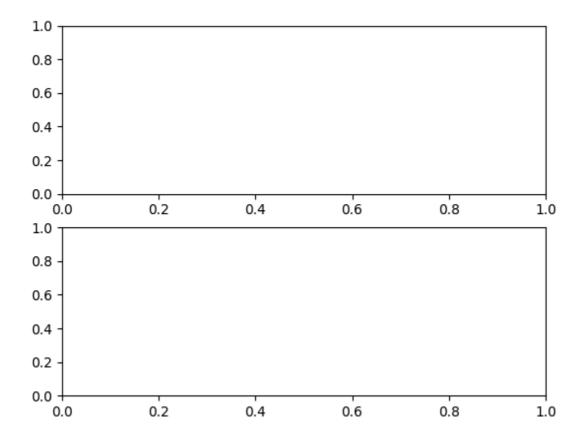
- "ECG_Phase_Atrial": cardiac phase, marked by "1" for systole and "0" for diastole.
- "ECG_Phase_Completion_Atrial": cardiac phase (atrial) completion, expressed in percentage (from 0 to 1), representing the stage of the current cardiac phase.
- "ECG_Phase_Ventricular": cardiac phase, marked by "1" for systole and "0" for diastole.
- "ECG_Phase_Completion_Ventricular": cardiac phase (ventricular) completion, expressed in percentage (from 0 to 1), representing the stage of the current cardiac phase.

```
See also

ecg_clean, ecg_peaks, ecg_delineate, ecg_process, ecg_plot
```

Examples

```
In [1]: import neurokit2 as nk
In [2]: ecg = nk.ecg_simulate(duration=6, sampling rate=1000)
In [3]: _, rpeaks = nk.ecg_peaks(ecg)
In [4]: signals, waves = nk.ecg_delineate(ecg, rpeaks, sampling_rate=100
In [5]: cardiac_phase = nk.ecg_phase(ecg_cleaned=ecg, rpeaks=rpeaks,
                                     delineate info=waves, sampling rate
   . . . :
In [6]: , ax = plt.subplots(nrows=2)
In [7]: ax[0].plot(nk.rescale(ecg), label="ECG", color="red", alpha=0.3)
Out[7]: [<matplotlib.lines.Line2D at 0x1dc4fbbad50>]
In [8]: ax[0].plot(cardiac_phase["ECG_Phase_Atrial"], label="Atrial Phas
Out[8]: [<matplotlib.lines.Line2D at 0x1dc4fbbac10>]
In [9]: ax[0].plot(cardiac_phase["ECG_Phase_Completion_Atrial"],
                   label="Atrial Phase Completion", linestyle="dotted")
   . . . :
Out[9]: [<matplotlib.lines.Line2D at 0x1dc4fbbaad0>]
In [10]: ax[0].legend(loc="upper right")
Out[10]: <matplotlib.legend.Legend at 0x1dc4fbb8cd0>
In [11]: ax[1].plot(nk.rescale(ecg), label="ECG", color="red", alpha=0.3
Out[11]: [<matplotlib.lines.Line2D at 0x1dc4fbb8910>]
In [12]: ax[1].plot(cardiac_phase["ECG_Phase_Ventricular"], label="Ventr
Out[12]: [<matplotlib.lines.Line2D at 0x1dc4fbba350>]
In [13]: ax[1].plot(cardiac_phase["ECG_Phase_Completion_Ventricular"],
                    label="Ventricular Phase Completion", linestyle="dot
   . . . . :
   . . . . :
Out[13]: [<matplotlib.lines.Line2D at 0x1dc4fbb8f50>]
In [14]: ax[1].legend(loc="upper right")
Out[14]: <matplotlib.legend.Legend at 0x1dc4fbb87d0>
```



ecg_rate()

ecg_rate(peaks, sampling_rate=1000, desired_length=None, interpolation_method='monotone_cubic', show=False)

Compute Signal Rate

Calculate signal rate (per minute) from a series of peaks. It is a general function that works for any series of peaks (i.e., not specific to a particular type of signal). It is computed as 60 / period, where the period is the time between the peaks (see func:.signal_period).

Note

This function is implemented under signal rate(), but it also re-exported under different names, such as ecg_rate(), or rsp_rate(). The aliases are provided for consistency.

Parameters:

- **peaks** (*Union[list, np.array, pd.DataFrame, pd.Series, dict]*) The samples at which the peaks occur. If an array is passed in, it is assumed that it was obtained with **signal_findpeaks()**. If a DataFrame is passed in, it is assumed it is of the same length as the input signal in which occurrences of R-peaks are marked as "1", with such containers obtained with e.g., :func:. `ecg_findpeaks` or **rsp_findpeaks()**.
- **sampling_rate** (*int*) The sampling frequency of the signal that contains peaks (in Hz, i.e., samples/second). Defaults to 1000.
- **desired_length** (*int*) If left at the default None, the returned rated will have the same number of elements as peaks. If set to a value larger than the sample at which the last peak occurs in the signal (i.e., peaks [-1]), the returned rate will be interpolated between peaks over desired_length samples. To interpolate the rate over the entire duration of the signal, set desired_length to the number of samples in the signal. Cannot be smaller than or equal to the sample at which the last peak occurs in the signal. Defaults to None.
- interpolation_method (str) Method used to interpolate the rate between peaks. See signal_interpolate().

"monotone_cubic" is chosen as the default interpolation method since it ensures monotone interpolation between data points (i.e., it prevents physiologically implausible "overshoots" or "undershoots" in the y-direction). In contrast, the widely used cubic spline interpolation does not ensure monotonicity.

show: bool

If True, shows a plot. Defaults to False.

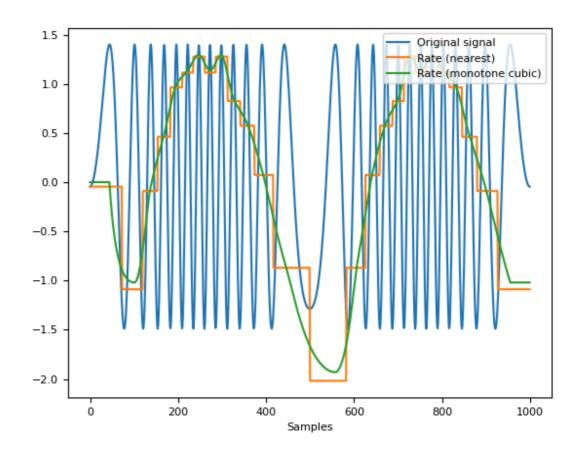
Returns:

array – A vector containing the rate (peaks per minute).

```
    See also
    signal_period, signal_findpeaks, signal_fixpeaks, signal_plot
```

Examples

```
In [1]: import neurokit2 as nk
# Create signal of varying frequency
In [2]: freq = nk.signal_simulate(1, frequency = 1)
In [3]: signal = np.sin((freq).cumsum() * 0.5)
# Find peaks
In [4]: info = nk.signal_findpeaks(signal)
# Compute rate using 2 methods
In [5]: rate1 = nk.signal_rate(peaks=info["Peaks"],
                                 desired length=len(signal),
   . . . :
                                 interpolation method="nearest")
   . . . :
   . . . :
In [6]: rate2 = nk.signal_rate(peaks=info["Peaks"],
                                desired length=len(signal),
                                 interpolation_method="monotone_cubic")
   . . . :
   . . . :
# Visualize signal and rate on the same scale
In [7]: nk.signal_plot([signal, rate1, rate2],
                        labels = ["Original signal", "Rate (nearest)", "R
                        standardize = True)
   . . . :
   . . . :
```



ecg_segment()

```
ecg_segment(ecg_cleaned, rpeaks=None, sampling_rate=1000,
show=False, **kwargs)
[source]
```

Segment an ECG signal into single heartbeats

Segment an ECG signal into single heartbeats. Convenient for visualizing all the heart beats.

Parameters:

- **ecg_cleaned** (*Union[list, np.array, pd.Series]*) The cleaned ECG channel as returned by <code>ecg_clean()</code>.
- **rpeaks** (*dict*) The samples at which the R-peaks occur. Dict returned by ecg_peaks(). Defaults to None.
- **sampling_rate** (*int*) The sampling frequency of ecg_cleaned (in Hz, i.e., samples/second). Defaults to 1000.
- **show** (*bool*) If True, will return a plot of heartbeats. Defaults to False. If "return", returns the axis of the plot.
- **kwargs Other arguments to be passed.

Returns:

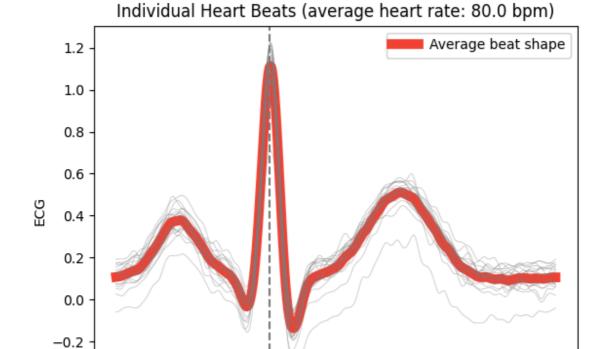
dict – A dict containing DataFrames for all segmented heartbeats.

```
See also

ecg_clean, ecg_plot
```

Examples

```
In [1]: import neurokit2 as nk
In [2]: ecg = nk.ecg_simulate(duration=15, sampling_rate=1000, heart_rat
In [3]: qrs_epochs = nk.ecg_segment(ecg, rpeaks=None, sampling_rate=1000)
```



Analysis

-0.4

ecg_eventrelated()

ecg_eventrelated(epochs, silent=False)

-0.2

-0.1

0.0

0.1

Time (seconds)

0.2

0.3

0.4

0.5

[source]

Event-related analysis of ECG

Performs event-related ECG analysis on epochs containing ECG signals.

Parameters:

- **epochs** (*Union[dict, pd.DataFrame]*) A dict containing one DataFrame per event/trial, usually obtained via epochs_create()), or a DataFrame containing all epochs, usually obtained via epochs_to_df()).
- **silent** (bool) If True, silence possible warnings.

Returns:

DataFrame – A dataframe containing the analyzed ECG features for each epoch, with each epoch indicated by the Label column (if not present, by the Index column). The analyzed features consist of the following:

- [ECG_Rate_Max]: The maximum heart rate after stimulus onset.
- ECG_Rate_Min: The minimum heart rate after stimulus onset.
- [ECG_Rate_Mean]: The mean heart rate after stimulus onset.
- [ECG_Rate_SD]: The standard deviation of the heart rate after stimulus onset.
- [ECG_Rate_Max_Time]: The time at which maximum heart rate occurs.
- [ECG_Rate_Min_Time]: The time at which minimum heart rate occurs.
- ECG_Phase_Atrial: Indication of whether the onset of the event concurs with respiratory systole (1) or diastole (0).
- ECG_Phase_Ventricular: Indication of whether the onset of the event concurs with respiratory systole (1) or diastole (0).
- ECG_Phase_Atrial_Completion: Indication of the stage of the current cardiac (atrial) phase (0 to 1) at the onset of the event.
- ECG_Phase_Ventricular_Completion: Indication of the stage of the current cardiac (ventricular) phase (0 to 1) at the onset of the event.

We also include the following *experimental* features related to the parameters of a quadratic model:

- [ECG_Rate_Trend_Linear]: The parameter corresponding to the linear trend.
- [ECG_Rate_Trend_Quadratic]: The parameter corresponding to the curvature.
- ECG_Rate_Trend_R2: The quality of the quadratic model. If too low, the parameters might not be reliable or meaningful.

```
See also
    events_find, epochs_create, bio_process
```

Examples

• Example 1: Simulated Data

```
In [1]: import neurokit2 as nk
# Simulate ECG signal
In [2]: signal = nk.ecg simulate(duration=20)
# Preprocess
In [3]: ecg, info = nk.ecg_process(signal)
# Create epochs
In [4]: epochs = nk.epochs_create(ecg, events=[5000, 10000, 15000],
   . . . :
                                   epochs_start=-0.1, epochs_end=1.9)
   . . . :
In [5]: nk.ecg_eventrelated(epochs)
Out[5]:
  Label Event Onset
                            ECG_Phase_Completion_Ventricular ECG_Quality
                      . . .
1
      1
                5000
                                                                        0.9
                                                     0.714286
2
      2
               10000
                                                     0.462656
                                                                        0.9
                      . . .
3
      3
               15000
                                                     0.156057
                                                                        0.9
[3 rows x 17 columns]
```

• Example 2: Real Data

```
# Download real dataset
In [6]: data = nk.data("bio_eventrelated_100hz")
# Process the data
In [7]: df, info = nk.bio process(ecg=data["ECG"], sampling rate=100)
In [8]: events = nk.events_find(data["Photosensor"],
                                 threshold_keep='below',
                                 event_conditions=["Negative", "Neutral",
   ...:
                                                    "Neutral", "Negative"]
   . . . :
   . . . :
In [9]: epochs = nk.epochs_create(df, events, sampling_rate=100,
   . . . :
                                   epochs_start=-0.1, epochs_end=1.9)
   . . . :
In [10]: nk.ecg_eventrelated(epochs)
Out [10]:
  Label Condition ...
                         ECG_Phase_Completion_Ventricular
                                                            ECG_Quality_Me
1
      1 Negative ...
                                                  0.400000
                                                                    0.9521
         Neutral ...
2
      2
                                                  0.553846
                                                                    0.9236
3
      3
          Neutral
                                                  0.133333
                                                                    0.9302
      4 Negative
                                                  0.575342
                                                                    0.9557
[4 rows x 18 columns]
```

ecg_intervalrelated()

ecg_intervalrelated(data, sampling_rate=1000)

[source]

Interval-related analysis of ECG

Performs ECG analysis on longer periods of data (typically > 10 seconds), such as resting-state data.

Parameters:

- **data** (*Union[dict, pd.DataFrame]*) A DataFrame containing the different processed signal(s) as different columns, typically generated by ecg_process()) or bio_process()). Can also take a dict containing sets of separately processed DataFrames.
- **sampling_rate** (*int*) The sampling frequency of the signal (in Hz, i.e., samples/second). Defaults to 1000Hz.

Returns:

DataFrame – A dataframe containing the analyzed ECG features. The analyzed features consist of the following:

- ECG_Rate_Mean: The mean heart rate.
- ECG HRV: the different heart rate variability metrices.

See hrv_summary() docstrings for details.

Examples

```
In [1]: import neurokit2 as nk
# Download data
In [2]: data = nk.data("bio resting 5min 100hz")
# Process the data
In [3]: df, info = nk.ecg_process(data["ECG"], sampling_rate=100)
# Single dataframe is passed
In [4]: nk.ecg_intervalrelated(df, sampling_rate=100)
Out [4]:
  ECG_Rate_Mean
                                     HRV_LZC
     86.392105
                [[0.8731238852455482]]
[1 rows x 92 columns]
In [5]: epochs = nk.epochs_create(df, events=[0, 15000], sampling_rate=1
In [6]: nk.ecg intervalrelated(epochs)
Out[6]:
  Label ECG_Rate_Mean
                                           HRV KFD
                                                                   HRV L
1
      1
             86.389814
                             [[2.336829556302458]]
                                                    [[0.8288764443746864
                       . . .
2
             86.394396 ...
                             [[3.094110204759245]] [[0.9730288694833277
[2 rows x 93 columns]
```

Miscellaneous

ecg_findpeaks()

```
ecg_findpeaks(ecg_cleaned, sampling_rate=1000, method='neurokit',
show=False, **kwargs)
[source]
```

Locate R-peaks

Low-level function used by <u>ecg_peaks()</u> to identify R-peaks in an ECG signal using a different set of algorithms. Use the main function and see its documentation for details.

Parameters:

- ecg_cleaned (Union[list, np.array, pd.Series]) See ecg_peaks().
- sampling_rate (int) See ecg_peaks().
- method (string) See ecg_peaks()
- **show** (*bool*) If True, will return a plot to visualizing the thresholds used in the algorithm. Useful for debugging.

• **kwargs – Additional keyword arguments, usually specific for each method.

Returns:

info (*dict*) – A dictionary containing additional information, in this case the samples at which R-peaks occur, accessible with the key "ECG_R_Peaks".

```
See also

ecg_peaks, <a href="mailto:signal_fixpeaks">signal_fixpeaks</a>
```

ecg_invert()

```
ecg_invert(ecg_signal, sampling_rate=1000, force=False,
show=False)
[source]
```

ECG signal inversion

Checks whether an ECG signal is inverted, and if so, corrects for this inversion. To automatically detect the inversion, the ECG signal is cleaned, the mean is subtracted, and with a rolling window of 2 seconds, the original value corresponding to the maximum of the squared signal is taken. If the median of these values is negative, it is assumed that the signal is inverted.

Parameters:

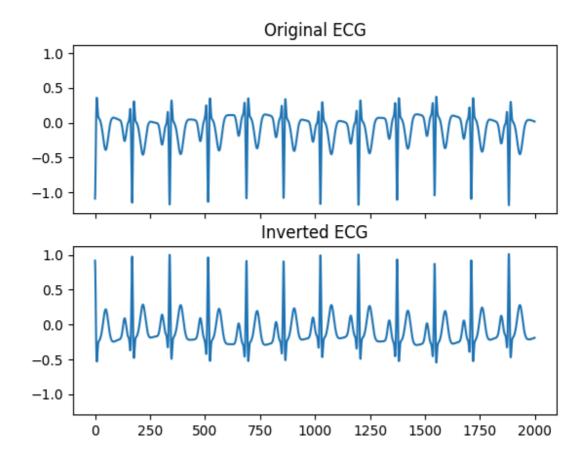
- ecg_signal (Union[list, np.array, pd.Series]) The raw ECG channel.
- **sampling_rate** (*int*) The sampling frequency of ecg_signal (in Hz, i.e., samples/second). Defaults to 1000.
- **force** (*bool*) Whether to force inversion of the signal regardless of whether it is detected as inverted. The default is False.
- **show** (bool) Shows a plot of the original and inverted signal.

Returns:

- array Vector containing the corrected ECG signal.
- bool Whether the inversion was performed.

Examples

```
In [1]: import neurokit2 as nk
In [2]: ecg = -1 * nk.ecg_simulate(duration=10, sampling_rate=200, heart
# Invert if necessary
In [3]: ecg_fixed, is_inverted = nk.ecg_invert(ecg, sampling_rate=200, s
```



Any function appearing below this point is not explicitly part of the documentation and should be added. Please open an issue if there is one.

Submodule for NeuroKit.