NeuroKit2: A Python Toolbox for Neurophysiological Signal Processing

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18   Abstract

19   NeuroKit2 is an open-source, community-driven, and user-centered Python package for

20   neurophysiological signal processing. It provides a comprehensive suite of processing

21   routines for a variety of bodily signals (e.g., ECG, PPG, EDA, EMG, RSP). These

22   processing routines include high-level functions that enable data processing in a few lines

23   of code using validated pipelines, which we illustrate in two examples covering the most

24   typical scenarios, such as an event-related paradigm and an interval-related analysis. The

25   package also includes tools for specific processing steps such as rate extraction and

26   filtering methods, offering a trade-off between high-level convenience and fine-tuned

27   control. Its goal is to improve transparency and reproducibility in neurophysiological

28   research, as well as foster exploration and innovation. Its design philosophy is centred on

29   user-experience and accessibility to both novice and advanced users.

30   *Keywords:* Neurophysiology, Biosignals, Python, ECG, EDA, EMG

31   Word count: 2513

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Neurophysiological measurements increasingly gain popularity in the study of cognition and behavior. These measurements include electroencephalography (EEG), electrocardiography (ECG), electromyography (EMG) and electrodermal activity (EDA). Their popularity is driven by theoretical motivations (e.g., the growth of embodied or affective neuroscience; Kiverstein & Miller, 2015) as well as practical reasons. The latter include low costs (especially compared with other imaging techniques, such as MRI or MEG), ease of use (e.g., portability, setup speed), and the increasing availability of recording devices (e.g., wearables; Yuehong, Zeng, Chen, & Fan, 2016). Moreover, the extraction of meaningful information from neurophysiological signals is facilitated by current advances in signal processing algorithms (Clifton, Gibbons, Davies, & Tarassenko, 2012; Roy et al., 2019). Unfortunately, these algorithms are often not distributed in a usable way (i.e., in the form of packaged code) which makes them inaccessible to researchers who do not have the time or experience to implement them. Moreover, many software tools for neurophysiological analyses are limited to a single type of signal (for instance ECG). This makes it inconvenient for researchers who might have to concurrently rely on a number of software packages to process and analyze multimodal data.

Additionally, psychology and neuroscience face a "reproducibility crisis" (Maizey & Tzavella, 2019; Miłkowski, Hensel, & Hohol, 2018; Nosek, Cohoon, Kidwell, & Spies, 2015; Topalidou, Leblois, Boraud, & Rougier, 2015) which has lead to a profound reassessment of research practices (by researchers, publishers, funding agencies, etc.). The opacity of data processing, such as ill-specified, or inaccessible analysis pipelines, plays a major role in the crisis. This issue could in part be alleviated by making analyses code an integral part of scientific publications, rather than treating a paper as the sole and most important part of the research project. However, distributing the analysis script alongside the paper poses new challenge: Scripts must be shareable (not always feasible with closed-source and proprietary software

or programming languages), accessible (well-documented and organized scripts) and repro-
ducible (which is difficult for software relying on a graphical user interfaces - GUI - in which
the manual point-and-click sequence can be hard to automate).

NeuroKit2, addresses these challenges by offering a free, user-centered, and comprehensive so-
lution for neurophysiological data processing, with an initial focus on bodily signals including
ECG (electrocardiography is used to measure cardiac activity), PPG (photoplethysmogram
is an optical measurement of blood flow), RSP (respiration measures), EDA (electroder-
mal activity measuring the electrical conductance of the skin), EMG (electromyography
measuring muscular activity) and EOG (electrooculography measuring eye movements). It
also provides modality-independent functions that can be used for other modalities such
as EEG (electroencephalography measuring electrical activity of the brain), for which more
specific support is in development. The open-source Python package is developed by a multi-
disciplinary team that actively invites new collaborators. The target audience of *NeuroKit2*
includes both experienced and novice programmers. Although being a programming-based
tool, users not familiar with Python or other languages can start using the software (and
improve their programming skills along the way) by following our step-by-step examples.
Moreover, we also include a thorough tutorial on Python installation, as well as a "10 minutes
introduction to Python" in the documentation. While many of the existing software caters
to a singe signal modality (e.g., *KUBIOS*©(Tarvainen, Niskanen, Lipponen, Ranta-Aho, &
Karjalainen, 2014), *HeartPy* (Gent, Farah, Nes, & Arem, 2019) and *pyHRV* (Gomes, Mar-
garitoff, & Silva, 2019) for ECG, *cvxEDA* (Greco, Valenza, Lanata, Scilingo, & Citi, 2015),
Ledalab (Benedek & Kaernbach, 2010), and *SCRalyze* (Bach, 2014) for EDA), *NeuroKit2*
provides support for various signals and allows its users to process signals from multiple
physiological modalities with a uniform application programming interface (API). It aims
at being accessible, well-documented, well-tested, cutting-edge, flexible and efficient. The
library allows users to select from a wide range of validated analysis pipelines and to create
custom pipelines tailored to specific analyses requirements. Historically, *NeuroKit2* is the

⁸⁵ re-forged successor of *NeuroKit1* (Makowski, 2020), taking over its most successful features
⁸⁶ and design choices, and re-implementing them in a way that adheres to current best practices
⁸⁷ in open source software development.

⁸⁸ *NeuroKit2* offers a breadth of functionalities which includes, but is not limited to signal
⁸⁹ simulation; data management (e.g., downloading existing datasets, reading and formatting
⁹⁰ files into a dataframe); event extraction from signals; epoch extraction, signal processing
⁹¹ (e.g., filtering, resampling, rate computation using different published algorithms detailed
⁹² in the package's documentation); spectral analyses; complexity and entropy analyses; and
⁹³ convenient statistical methods (e.g., K-means clustering, ICA or PCA). A variety of plot-
⁹⁴ ting functions allow for quick and expressive visualization of the signal processing and the
⁹⁵ resulting features.

⁹⁶ The package is implemented in Python 3 (Van Rossum & Drake, 2009), which means that
⁹⁷ *NeuroKit2's* users benefit from an large number of learning resources and a vibrant commu-
⁹⁸ nity. The package depends on relatively few, well established and robust packages from the
⁹⁹ numeric Python ecosystem such as *NumPy* (Van Der Walt, Colbert, & Varoquaux, 2011),
¹⁰⁰ *pandas* (McKinney & others, 2010), *SciPy* (Virtanen et al., 2020), *scikit-learn* (Pedregosa et
¹⁰¹ al., 2011) and *MatplotLib* (Hunter, 2007) (with an additional system of optional dependen-
¹⁰² cies), making *NeuroKit2* a viable dependency for other packages.

¹⁰³ *NeuroKit2's* source code is available under the MIT license on GitHub (*https://github.com/*
¹⁰⁴ *neuropsychology/NeuroKit*). Its documentation (*https://neurokit2.readthedocs.io/*) is auto-
¹⁰⁵ matically built and rendered from the code and includes guides for installation and contri-
¹⁰⁶ bution, a description of the package's functions, as well as several "hands-on" examples and
¹⁰⁷ tutorials (e.g., how to extract and visualize individual heartbeats, how to analyze event-
¹⁰⁸ related data etc.). Importantly, users can add new examples by simply submitting a Jupyter
¹⁰⁹ notebook (Kluyver et al., 2016) to the GitHub repository. The notebook will automatically
¹¹⁰ be displayed on the website, ensuring easily accessible and evolving documentation. More-

over, users can try out the example notebooks directly in their browser via a cloud-based *Binder* environment (Jupyter et al., 2018). Finally, the issue tracker on GitHub offers a convenient and public forum that allows users to report bugs, get help and gain insight into the development of the package. Our collaborators from academia and industry have diverse backgrounds in the life sciences and engineering fields (See the "authors" section on the package's documentation). *NeuroKit2* has attracted users of different profiles, ranging from those who are new to signal processing and programming to more experienced users.

NeuroKit2 aims at being reliable and trustworthy, including implementations of processing pipelines that have been described in peer-reviewed publications. Details and references regarding those pipelines are available in the package's documentation. Many pipelines have been tested against established software such as *BioSPPy* (Carreiras et al., 2015), *hrv* (Bartels & Pecanha, 2020), *PySiology* (Gabrieli, Azhari, & Esposito, 2019), *HeartPy* (Gent et al., 2019), *systole* (Legrand & Allen, 2020) or *nolds* (Schölzel, 2019). Additionally, the repository leverages a comprehensive test suite (using *pytest*) and continuous integration (using Travis-CI and GitHub actions) to ensure software stability and quality. The test coverage and build status can transparently be tracked via the GitHub repository. Thanks to its collaborative and open development, *NeuroKit2* can remain cutting-edge and continuously evolve, adapt, and integrate new methods as they are emerging.

Finally, we believe that the design philosophy of *NeuroKit2* contributes to an efficient (i.e., allowing to achieve a lot with few functions) yet flexible (i.e., enabling fine control and precision over what is done) API. We will illustrate these claims with two examples of common use-cases (the analysis of event-related and resting state data), and will conclude by discussing how *NeuroKit2* contributes to neurophysiological research by raising the standards for validity, reproducibility and accessibility.

135 **Design Philosophy**

136 *NeuroKit2* aims at being accessible to beginners and, at the same time, offering a maximal

137 level of control to experienced users. This is achieved by allowing beginning users to im-

138 plement complex processing pipelines with a few functions, while still providing experienced

139 users with fine-tuned control over arguments and parameters. In concrete terms, this trade-

140 off is enabled by an API structure organized in three layers.

141 **Low-level: Base Utilities for Signal Processing**

142 The basic building blocks are functions for general signal processing, i.e., filtering, resam-

143 pling, interpolation, peak detection, etc. These functions are modality-independent, and

144 include several parameters (e.g., one can change the filtering method, frequencies, and or-

145 der, by overwriting the default arguments). Most of these functions are based on established

146 algorithms implemented in *scipy* (Virtanen et al., 2020). Examples of such functions include

147 `signal_filter()`, `signal_interpolate()`, `signal_resample()`, `signal_detrend()`, and

148 `signal_findpeaks()`.

149 **Mid-level: Neurophysiological Processing Steps**

150 The base utilities are used by mid-level functions specific to the different physiological modal-

151 ities (i.e., ECG, RSP, EDA, EMG, PPG). These functions carry out modality-specific signal

152 processing steps, such as cleaning, peak detection, phase classification or rate computa-

153 tion. Critically, for each type of signal, uniform function names are used (in the form

154 `signaltype_functiongoal()`) to achieve equivalent goals, e.g., `*_clean()`, `*_findpeaks()`,

155 `*_process()`, `*_plot()`, making the implementation intuitive and consistent across differ-

156 ent modalities.

157 For example, the `rsp_clean()` function uses `signal_filter()` and `signal_detrend()`,

158 with different sets of default parameters that can be switched with a "method" argu-

159 ment (corresponding to different published or established pipelines). For instance, setting

160 `method="khodadad2018"` will use the cleaning workflow described in Khodadad et al. (2018).

161 However, if a user wants to build their own custom cleaning pipeline, they can use the clean-

162 ing function as a template, and tweak the parameters to their desires in the low-level signal

163 processing operations.

High-level Wrappers for Processing and Analysis
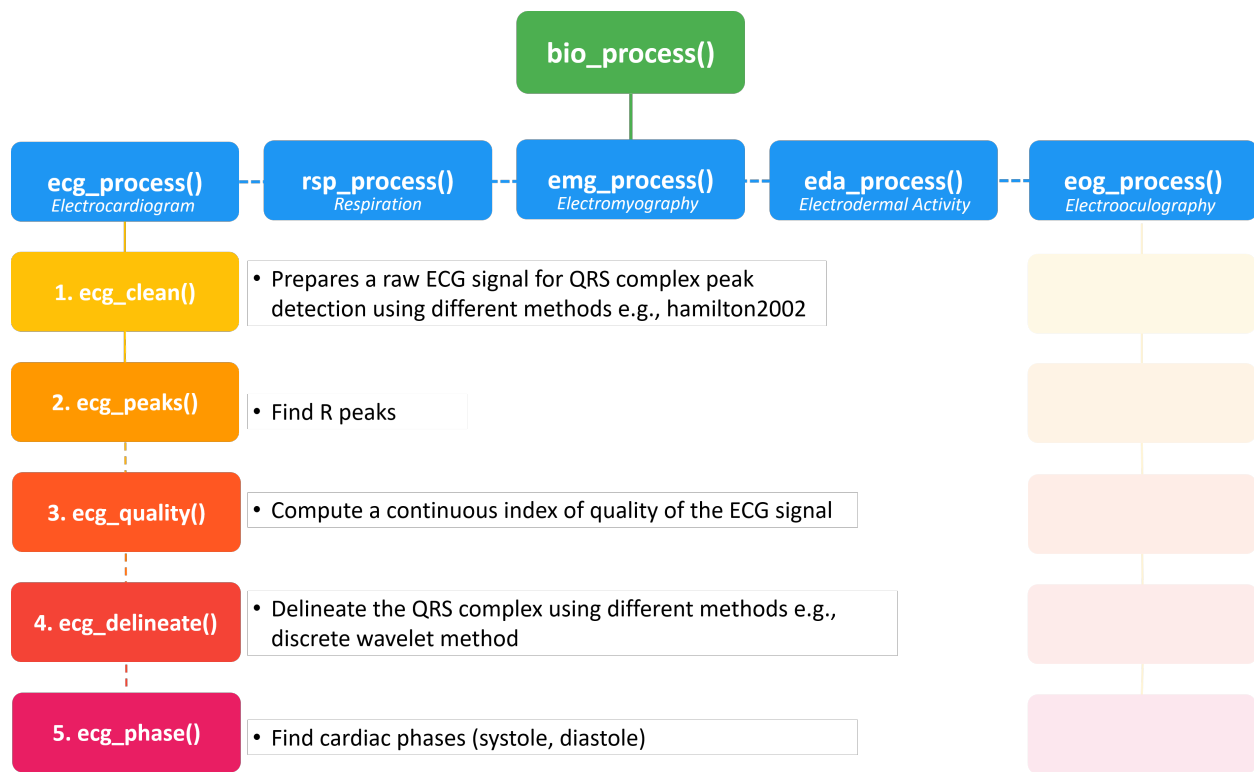
Figure 1. Illustration of the NeuroKit2 package architecture, in the case of ECG signal process-
ing.

165 The mid-level functions are assembled in high-level wrappers, that are convenient entry

166 points for new users. For instance, the `ecg_process()` function internally chains the

167 mid-level functions `ecg_clean()`, `ecg_peaks()`, `ecg_quality()`, `ecg_delineate()`, and

168 `ecg_phase()`, as shown in **Figure 1**. A specific processing pipeline can be selected with the

169 `method` argument that is then propagated throughout the internal functions. Easily switch-

¹⁷⁰ ing between processing pipelines allows for the comparison of different methods, and stream-
¹⁷¹ lines critical but time-consuming steps in reproducible research, such as the validation of data
¹⁷² preparation and quality control (Quintana, Alvares, & Heathers, 2016). Finally, the package
¹⁷³ includes convenience-functions (e.g., `bio_process`) that enable the combined processing of
¹⁷⁴ multiple types of signals at once (e.g., `bio_process(ecg=ecg_signal, eda=eda_signal)`).

¹⁷⁵ Performing an entire set of operations with sensible default parameters in one function can
¹⁷⁶ be rewarding, especially for beginners, allowing them to perform cutting-edge processing or
¹⁷⁷ replication of research steps without requiring much programming expertise. Moreover, it
¹⁷⁸ contributes to the demystification of the usage of programming tools (as opposed to GUI-
¹⁷⁹ based software such as *SPSS*, *Kubios*, or *Acqknowledge*), providing a welcoming framework
¹⁸⁰ to further explore physiological data processing. Importantly, more advanced users can build
¹⁸¹ custom analysis pipelines by using the low- and mid-level functions, allowing for finer control
¹⁸² over the processing parameters. We believe that this implementation is a well-calibrated
¹⁸³ trade-off between flexibility and user-friendliness.

Installing NeuroKit2

¹⁸⁵ *NeuroKit2* is available on PyPI and can be installed using pip (via '*pip install neurokit2*'
¹⁸⁶ command). Detailed instructions on how to install Python are also available in the *installa-*
¹⁸⁷ *tion* section of the package's documentation.

Examples

¹⁸⁹ In this section, we present two examples that illustrate the most common use-cases. Both
¹⁹⁰ examples can be accessed in an interactive format (without any prior installation) via a
¹⁹¹ *Binder environment*. The first example shows how to extract the characteristics of physio-
¹⁹² logical activity during a certain time interval (not necessarily tied to a specific and sudden
¹⁹³ event). The second example presents an event-related paradigm, in which the interest lies

194 in shorter-term physiological changes related to specific events (see **Figure 1** and **Table**

195 **1**). The example datasets are available with the package and can be downloaded using the

196 `data()` function. This utility reads comma separated values files (*.csv*) with the Pandas

197 function *pd.read_csv()*, where each column is a different biosignal. Each row is a sample

198 that correspond to signals' value at a given point in time. All examples use the 0.0.40 version

199 release of *NeuroKit2.*
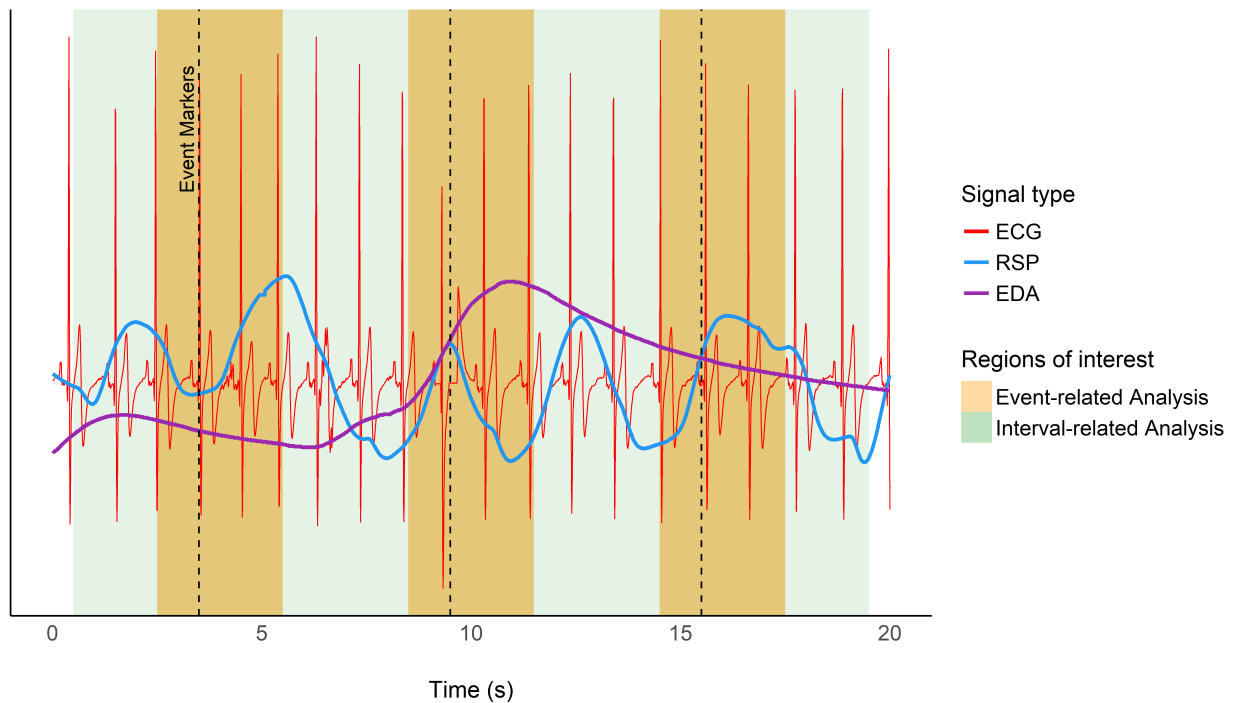
Figure 2. Illustration of the difference between event-related analysis, focusing on activity changes in short windows (the orange rectangles), and interval-related analysis, pertaining to features of large areas, or the entire signal (e.g., the green rectangle).

Resting-state Features

201 The first dataset corresponds to 5 minutes of physiological activity of a human participant

202 at rest (eyes-closed in a seated position), with no specific instructions. It contains three

203 channels (ECG, PPG and RSP) sampled at a frequency of 100Hz.

Table 1

Examples of features computed in different domains.

Event-related Features	Interval-related Features
ECG Rate Changes (Min, Mean, Max, Time of Min, Max, Trend)	ECG Rate Characteristics (Mean, Amplitude)
RSP Rate Changes (Min, Mean, Max, Time of Min, Max)	Heart Rate Variability (HRV) indices
RSP Amplitude Measures (Min, Mean, Max)	Respiratory Rate Variability (RRV) indices
ECG and RSP Phase (Inspiration/Expiration, Systole/Diastole, Completion)	Respiratory Sinus Arrhythmia (RSA) indices
SCR peak and its characteristics (amplitude, rise time, recovery time)	Number of SCR Peaks and mean amplitude

```python
# Load the package
import neurokit2 as nk


# Download the example dataset
data = nk.data("bio_resting_5min_100hz")


# Process the data
df, info = nk.bio_process(ecg=data["ECG"],
                          rsp=data["RSP"],
                          sampling_rate=100)


# Extract features
results = nk.bio_analyze(df, sampling_rate=100)


# Show subset of results
results[["ECG_Rate_Mean", "HRV_RMSSD", "RSP_Rate_Mean", "RSA_P2T_Mean"]]
```

Table 2

Subset of properties characterizing the physiological activity over a period of 5 minutes of resting-state.

ECG_Rate_Mean	HRV_RMSSD	RSP_Rate_Mean	RSA_P2T_Mean
86.39	38.84	15.74	0.07

Here, the aim was to illustrate a type of physiological analysis that we refer to as interval-related (or resting-state paradigm, as opposed to an event-related paradigm). After loading the package and the example dataset, each physiological signal is processed using `bio_process()`. As we want to compute features related to the entire dataset (see **Table 2**), we can directly pass the whole dataframe to `bio_analyze()`, and compute the interval-related features. Users can choose a specific time interval from their dataset.

Interval-related analyses compute features of signal variability and activation patterns over a given period of time, including average heart and breathing rate, as well as indices of heart rate variability (HRV) and respiratory sinus arrhythmia (RSA). *NeuroKit2* allows for the fast creation of standardized and reproducible pipelines to describe this kind of physiological activity.

Event-related Paradigm

This example dataset contains ECG, RSP and EDA signals of one participant who was presented with four emotional images (from the NAPS database; Marchewka, Żurawski, Jednoróg, & Grabowska, 2014) in a typical (albeit shortened) experimental psychology paradigm.

The signals are 2.5 minutes long and are recorded at a frequency of 100Hz (note that the sampling rate is lower than usually required, see Quintana et al., 2016, in order to be able to include the example data in the *NeuroKit2* distribution). It has 4 channels including three

₂₂₃ physiological signals, and one corresponding to events marked with a photosensor (signal
₂₂₄ strength decreases when a stimulus appears on the screen).

```python
# Load the package
import neurokit2 as nk


# Download the example dataset
data = nk.data("bio_eventrelated_100hz")


# Process the data
df, info = nk.bio_process(ecg=data["ECG"],
                          rsp=data["RSP"],
                          eda=data["EDA"],
                          sampling_rate=100)


# Find events
conditions = ["Negative", "Neutral", "Neutral", "Negative"]
events = nk.events_find(event_channel=data["Photosensor"],
                        threshold_keep='below',
                        event_conditions=conditions)


# Epoch the data
epochs = nk.epochs_create(data=df,
                          events=events,
                          sampling_rate=100,
                          epochs_start=-0.1,
                          epochs_end=4)
```

```python
# Extract event related features
results = nk.bio_analyze(epochs, sampling_rate=100)


# Show subset of results
results[["Condition", "ECG_Rate_Mean", "RSP_Rate_Mean", "EDA_Peak_Amplitude"]]
```

Table 3

Subset of the ouput related to event-related analysis characterizing the pattern of physiological changes related to specific stimuli.

Condition	ECG_Rate_Mean	RSP_Rate_Mean	EDA_Peak_Amplitude
Negative	-2.01	-0.15	0.93
Neutral	-3.13	1.40	0.41
Neutral	1.34	-0.34	0.02
Negative	-3.55	1.97	1.06

In this example, the steps of the analysis are identical to the previous example, including loading the package, the dataset and processing the data. The difference is that stimulus onsets in the photosensor are detected separately with `events_find()`. Once we have the preprocessed signals and the location of events, we use `epochs_create()` to slice the data into segments corresponding to a time window (ranging from -0.1 to 4 seconds) around each stimulus. Finally, relevant features are computed for each epoch (i.e., each stimulus) by passing them to `bio_analyze()`.

Notably, the features include the changes in rate of ECG and RSP signals (e.g. maximum, minimum and mean rate after stimulus onset, and the time at which they occur), and the peak characteristics of the EDA signal (e.g., occurrence of skin conductance response (SCR), and if SCR is present, its corresponding peak amplitude, time of peak, rise and recovery time). In addition, respiration and cardiac cycle phases are extracted (i.e., the respiration

phase - inspiration/expiration - and cardiac phase - systole/diastole - occurring at the onset of event).

We hope that these examples demonstrate how straightforward the process of extracting features of physiological responses can be with *NeuroKit2*. This pipeline can easily scale up to group-level analyses by aggregating the average of features across participants. In addition to streamlining data analyses, *NeuroKit2* aims to allow researchers to extract an extensive suite of features that can be linked to neurocognitive processes. In this example (see **Table 3**), exposure to negative stimuli, as compared to neutral stimuli, is related to stronger cardiac deceleration, higher skin conductance response, and accelerated breathing rate (note that this descriptive interpretation is given solely for illustrative purposes).

Discussion

NeuroKit2 is a neurophysiological signal processing library accessible to people across different levels of programming experience and backgrounds. For users who are novice programmers or are new to neurophysiology, the package presents an ideal opportunity for exploration and learning. The experienced programmer is encouraged to choose and validate the preprocessing and analysis pipelines most appropriate for their data. Suggestions for improvements or additions to the library are welcome and openly discussed in the community. Overall, the development of *NeuroKit2* is focused on creating an intuitive user-experience, as well as building a collaborative community. Its modular structure and organization not only facilitate the use of existing and validated processing pipelines, but also create a fertile ground for experimentation and innovation.

The library is also a pragmatic answer to the broader need for transparent and reproducible methods in neurophysiology. The impact of our package on reproducibility in research is two-fold: firstly, while black-box software can be easy and convenient to use, users do not have access to the source code, making processing results subject to unknown idiosyncrasies

of the underlying implementation of processing routines. This makes it difficult to identify the source of potential discrepancies in results obtained with other software and can lead to irreproducible findings. In contrast, *NeuroKit2* documents each step of the implementation along with the analysis method, allowing users to pin-point the analysis steps where differences might arise. While maintaining a focus on overall user-experience, the open-source nature of *NeuroKit2* encourages independent researchers to cross-validate research findings. Secondly, not only does *NeuroKit2* implement several methods for analysis, it also allows for the comparison of different algorithms. For instance, using a suite of open-source databases, different algorithms for ECG R-peak detection have been compared for their robustness (number of errors encountered), efficiency (computation time) and accuracy (absolute distance from true R-peak location), documented in the "Studies" section of the package's documentation. As *NeuroKit2* continues to work on benchmarking, we hope to support users in making more informed decisions regarding which method is most suited for their specific requirements.

NeuroKit2 also prioritizes a high standard of quality control during code development. This is done through automated testing using continuous integration, as well as striving for code simplicity and readability. The API is thoroughly documented, including working examples. We ensure that the documentation evolves alongside the code by including it in our continuous integration. While *NeuroKit2* currently has a fairly comprehensive documentation, more examples and tutorials will be added as the package grows and expands. Additionally, we provide thorough guidelines for new contributors who wish to contribute code or documentation.

We expect the package's future evolution to be driven by the communities' needs and the advances in related fields. For instance, although *NeuroKit2* already implements a lot of useful functions for EEG processing (such as entropy and fractal dimensions quantification), its support could be further improved (for example with high-level functions built on top of utilities provided by the leading EEG Python software, namely *MNE*; Gramfort et al.,

2013). Additionally, in the future we strive to support other types of bodily signals (e.g., electrogastrography - EGG, electrooculography - EOG) and plan to optimize computational efficiency on large datasets. We also plan to further validate the available processing pipelines using public databases. In line with this objective, the support of standardized data structure formats (e.g. WFDB, BIDS, …) could be extended.

In conclusion, we believe that *NeuroKit2* provides useful tools for anyone who is interested in analyzing physiological data collected with research-grade hardware or wearable "smart health devices". By increasing the autonomy of researchers and practitioners, and by shortening the delay between data collection and results acquisition, *NeuroKit2* could be useful beyond academic research in neuroscience and psychology, including applications such as personal physiological monitoring and exercise science. Finally, we hope that *NeuroKit2* encourages users to become part of a supportive open-science community with diverse areas of expertise rather than relying on closed-source and proprietary software, thus shaping the future of neurophysiology and its related fields.

Conflict of Interest

The authors declare that the research was conducted in the absence of commercial or financial relationships that could constitute a conflict of interest.

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