NeuroKit2: A Python Toolbox for Neurophysiological Signal Processing

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15   Abstract

16   NeuroKit2 is an open-source, community-driven, and user-friendly Python package

17   dedicated to neurophysiological signal processing (e.g., ECG, EDA, EMG, …). Its design

18   philosophy is centred on user-experience and accessibility to both novice and advanced

19   users. The package provides general functions that enable data processing in a few lines of

20   code using validated pipelines, as well as tools dedicated to specific processing steps,

21   offering a trade-off between efficiency and fine-tuned control. NeuroKit2 aims at improving

22   transparency and reproducibility in neurophysiological research, as well as fostering

23   exploration and innovation.

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

25   Word count: 2270

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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 mostly inaccessible to researchers without experience in programming and signal processing. Moreover, many software tools for neurophysiological analyses are limited to one type of signal (for instance, focused on ECG). This makes it inconvenient for researchers who might have to learn and concurrently rely on different software to process multimodal data.

Another important issue existing in psychology and neuroscience has been coined as the "reproducibility crisis" (**???**; Collaboration & others, 2015; Miłkowski, Hensel, & Hohol, 2018; Topalidou, Leblois, Boraud, & Rougier, 2015), and has lead to a profound questioning and reassessment from different actors involved (researchers, publishers, fund agencies, …). One of the main identified contributing factor is the actual opacity of data processing, where analysis pipelines are not described in enough details to ensure a full and exact reproduction. One of the suggested response to that issue has been to provide, alongside the study, the analysis script, which in turns opens new challenges. Indeed, these scripts must be shareable (not always feasible with closed-source and proprietary software or programming languages), accessible (enticing documented and well-organized scripts) and reproducible (which is in-

52 herently difficult for many software relying on a graphical user interface - GUI - in which

53 the manual point-and-click sequence is hard to automate).

54 *NeuroKit2* addresses these challenges by offering a free, user-friendly, and comprehensive

55 solution for neurophysiological data processing. It is an open-source Python package, devel-

56 oped by a multi-disciplinary team that actively invites new collaborators. It aims at being

57 accessible, well-documented, well-tested, cutting-edge, flexible and efficient, allowing users

58 to select from a wide range of validated analysis pipelines as well as creating their own.

59 Historically, *NeuroKit2* is the re-forged successor *NeuroKit1* (Makowski, 2020), taking on its

60 most successful features and design choices, and re-implementing them in a professional and

61 well-thought way.

62 The package is implemented in Python 3 (Van Rossum & Drake, 2009), which means that

63 *NeuroKit2's* users benefit from an large amount of learning resources and a vibrant com-

64 munity. The package depends on relatively few, well established and robust packages from

65 the Python data analysis ecosystem (Virtanen et al., 2020) such as *NumPy*, *pandas*, *SciPy*,

66 *scikit-learn* and *MatplotLib* (with an additional system of optional dependencies), making

67 *NeuroKit2* itself a viable dependency in other software.

68 *NeuroKit2's* source code is available under the permissive MIT license on GitHub (*https://*

69 *github.com/neuropsychology/NeuroKit*). Its documentation (*https://neurokit2.readthedocs.*

70 *io/*) is automatically built and rendered from the code and includes guides for installation

71 and contribution, a description of the package's functions, as well as several "hands-on"

72 examples and tutorials (e.g., how to extract and visualize individual heartbeats, how to ana-

73 lyze event-related data etc.). Importantly, users can add new examples by simply uploading

74 a Python notebook (Kluyver et al., 2016) to the GitHub repository. The notebook will

75 automatically be displayed on the website, ensuring easily accessible and evolving documen-

76 tation. Moreover, users can try out the example notebooks directly in their browser via a

77 cloud-based *Binder* environment (Jupyter et al., 2018). Finally, the issue tracker on GitHub

78 offers a convenient and public forum that allows newcomers and potential collaborators to
79 report bugs, get help and gain insight into the development of the package.

80 *NeuroKit2* aims at being reliable and trustworthy, including peer-reviewed processing pipelines
81 and functions tested against established software such as *BioSPPy* (Carreiras et al., 2015),
82 *hrv under review*, *PySiology* (Gabrieli, Azhari, & Esposito, 2019), *HeartPy* (Gent, Farah,
83 Nes, & Arem, 2019), *systole* (Legrand & Allen, 2020) or *nolds* (Schölzel, 2020). The repos-
84 itory leverages a comprehensive test suite and continuous integration to ensure stability
85 and prevent errors. Thanks to its collaborative and open development, *NeuroKit2* can re-
86 main cutting-edge and continuously evolve, adapt, and integrate new methods as they are
87 emerging.

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

Design Philosophy

95 As stated above, *NeuroKit2* aims at being accessible to beginners and, at the same time,
96 offering a maximal level of control to experienced users. This is achieved by allowing begin-
97 ning users to implement complex processing and analyses pipelines with very few functions,
98 while still enabling fine-tuned control and precision over arguments and parameters to more
99 experienced users. In concrete terms, this trade-off is allowed by a API structure organized
100 in three three layers of abstraction.

Low-level: Base Utilities for Signal Processing

The basic building blocks are functions for general signal processing, i.e., filtering, resampling, interpolation, peak detection, etc. These functions are signal-agnostic, and include a lot of parameters (e.g., one can change the filtering method, frequencies, and order, by overwriting the default arguments). Most of these functions are based on established algorithms implemented in *scipy* (Virtanen et al., 2020). Examples of such functions include `signal_filter()`, `signal_interpolate()`, `signal_resample()`, `signal_detrend()`, and `signal_findpeaks()`.

Mid-level: Neurophysiological Processing Steps

The base utilities are used by mid-level functions specific to the different physiological modalities (i.e., ECG, RSP, EDA, EMG, PPG). These functions carry out modality-specific signal processing steps, such as cleaning, peak detection, phase classification or rate computation. Critically, for each type of signal, the same function names are called (in the form `signaltype_functiongoal()`) to achieve equivalent goals, e.g., `*_clean()`, `*_findpeaks()`, `*_process()`, `*_plot()`, making the implementation intuitive and consistent across different modalities.

For example, the `rsp_clean()` function uses `signal_filter()` and `signal_detrend()`, with different sets of default parameters that can be switched with a "method" argument (corresponding to different published or established pipelines). For instance, setting `method="khodadad2018"` will use the cleaning workflow described in Khodadad et al. (2018). However, if a user wants to build their own custom cleaning pipeline, they can use the cleaning function as a template, and tweak the parameters to their desires in the low-level signal processing operations.

High-level Wrappers for Processing and Analysis

The mid-level functions are assembled in high-level "master" functions, that are convenient entry points for new users. For instance, the `ecg_process()` function internally chains the mid-level functions `ecg_clean()`, `ecg_findpeaks()`, `ecg_rate()`. A specific processing pipeline can be selected with the `method` argument, that is then propagated throughout the internal functions. Easily switching between processing pipelines allows for the comparison of different methods, and streamlines critical but time-consuming steps in reproducible research, such as the validation of data preparation and quality control (Quintana, Alvares, & Heathers, 2016). Finally, the package includes convenience meta-functions (e.g., `bio_process`) that enable the combined processing of multiple types of signals at once (e.g., `bio_process(ecg=ecg_signal, eda=eda_signal)`).

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

Examples

In this section, we present two examples that illustrate the most common use-cases. The first example is an event-related paradigm, in which the interest lies in short-term physiological changes related to specific events. The second example shows how to extract the characteristics of physiological activity during a longer period of time (not necessarily tied

149 to a specific and sudden event). The example datasets are made available with the package

150 and can be downloaded using the `data()` function.

Event-related Paradigm

152 This example dataset contains ECG, RSP and EDA signals of one participant who was

153 presented with four emotional images (from the NAPS database; Marchewka, Żurawski,

154 Jednoróg, & Grabowska, 2014), in a typical (albeit highly shortened) experimental psychol-

155 ogy paradigm.

156 Signals are 2.5 minutes long and are recorded at a frequency of 100Hz (note that the sampling

157 rate is low for storage purposes and should be higher in actual recordings, see Quintana et

158 al., 2016). It has 4 channels including three physiological signals, and one corresponding to

159 the marking of events with a photosensor (which signal decreases when a stimulus appeared

160 on the screen).

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


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


# Figure 1. Visualize 10 seconds of data (on the same scale)
nk.signal_plot(data[900:1900], standardize=True)


# 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)


# Extract event related features

results = nk.bio_analyze(epochs)


# Show subset of results

results[["Condition", "ECG_Rate_Mean", "RSP_Rate_Mean", "EDA_Peak_Amplitude"]]
```

161 In this example, after loading the package and the example dataset, each physiological

162 signal is processed using `bio_process()`. Stimulus onsets in the photosensor are detected

163 separately with `events_find()`. Once we have the preprocessed signals and the location of

164 events, we can slice the data into segments corresponding to a time window (ranging from

165 -0.1 to 4 seconds) around each stimulus with `epochs_create()`. Finally, relevant features

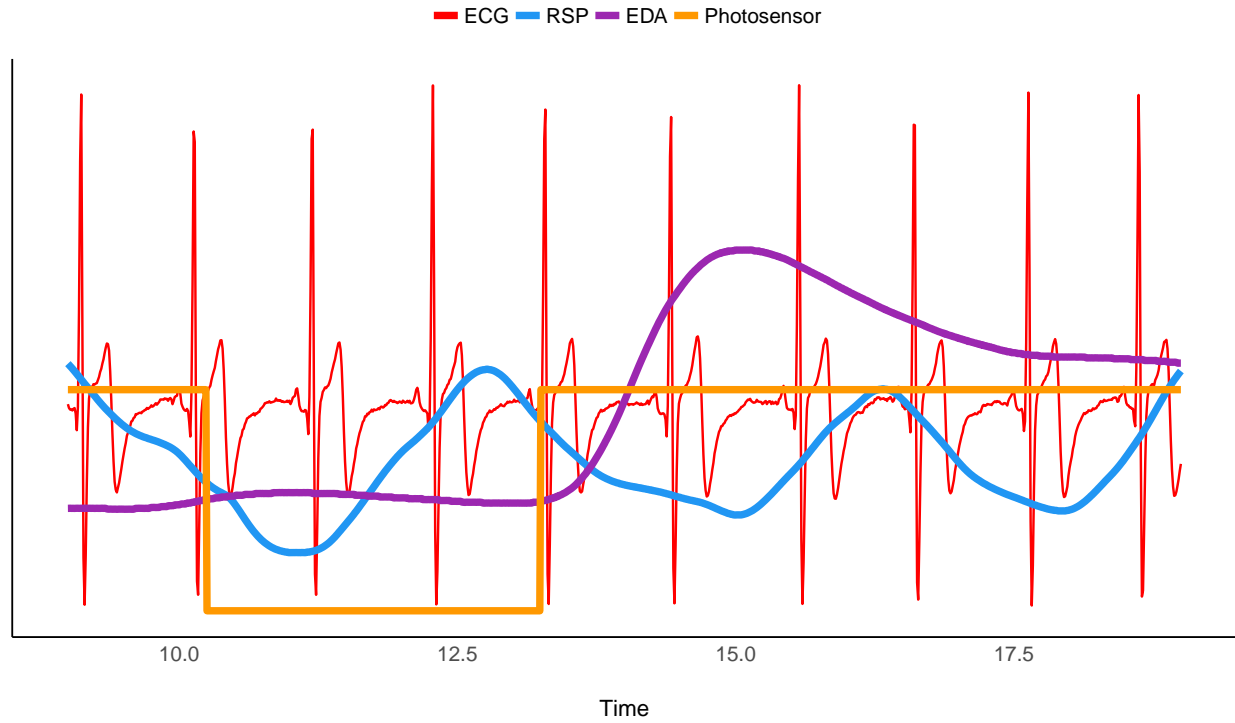166 are computed for each epoch (i.e., each stimulus) by passing them to `bio_analyze()`.

Figure 1. Subset of the dataset showing one event (in orange) and the other physiological signals.

Table 1

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	-1.94	-0.22	None
Neutral	-4.36	1.57	None
Neutral	1.02	-0.30	None
Negative	-3.61	2.22	1.68

167 The features include for example the changes in rate of ECG and RSP signals (e.g. maximum,

168 minimum and mean rate after stimulus onset, and the time at which they occur), and the

169 peak characteristics of the EDA signal (e.g., occurrence of skin conductance response (SCR),

¹⁷⁰ and if SCR is present, its corresponding peak amplitude, time of peak, rise and recovery

¹⁷¹ time). In addition, respiration and cardiac cycle phases are extracted (i.e., the respiration

¹⁷² phase - inspiration/expiration - and cardiac phase - systole/diastole - occurring at the onset

¹⁷³ of event).

¹⁷⁴ This example shows the straightforward process of extracting features of physiological re-

¹⁷⁵ sponses. This pipeline can easily scale up to group-level analysis by aggregating the average

¹⁷⁶ of features across participants. In addition to streamlining data analyses, *NeuroKit2* aims

¹⁷⁷ to provide researchers an extensive suite of signal features, allowing for precise interpreta-

¹⁷⁸ tions in terms of relationship between physiological activity and neurocognitive processes.

¹⁷⁹ In this example (see **Table 1**), exposure to negative stimuli, as compared to neutral stimuli,

¹⁸⁰ is related to stronger cardiac deceleration, higher skin conductance response, and acceler-

¹⁸¹ ated breathing rate (note that this descriptive interpretation is given solely for illustrative

¹⁸² purposes).

¹⁸³ **Resting-state Features**

¹⁸⁴ The second dataset corresponds to 5 minutes of physiological activity of a human participant

¹⁸⁵ at rest (eyes-closed in a seated position), under no specific set of instructions. It contains

¹⁸⁶ three channels (ECG, PPG and RSP) sampled at a frequency of 100Hz.

```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)


# Show subset of results
results[["ECG_Rate_Mean", "ECG_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	ECG_HRV_RMSSD	RSP_Rate_Mean	RSA_P2T_Mean
86.42	4.28	15.86	0.01

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 there is no epoching, as we want to compute features related to the whole dataset. Thus, we can directly pass the dataframe to `bio_analyze()`, which will detect that these are not epochs, and compute the appropriate features accordingly. These include for instance the average heart and breathing rate, as well as indices of heart rate variability (HRV) and respiratory sinus arrhythmia (RSA).

This example illustrates a second type of physiological analysis, that we refer to as interval-related (as opposed to event-related). Interval-related analyses compute features of signal variability and activation patterns over a longer-term period of time (typically minutes). *NeuroKit2* allows for the fast creation of a standardized and reproducible pipeline to describe this kind of physiological activity, which can be beneficial for a wide variety of applications.

Discussion

NeuroKit2 is a neurophysiological signal processing software accessible to people with all levels of programming experience and background. Its development is focused on creating an intuitive user-experience, as well as building a collaborative community. It is also a pragmatic answer to the broader need for transparent and reproducible methods in neurophysiology. Its modular structure and organization not only facilitates the use of existing and validated processing pipelines, but also creates a fertile ground for experimentation and innovation.

We expect the package's future evolution to be driven by the communities' needs and the advances in related fields. Possible directions include extending the support for other types of bodily signals (e.g., electrogastrography - EGG, electrooculography - EOG) and achieving performance gains for large datasets by using efficient algorithms. Further validation of the available processing pipelines could be made through the (re)analysis of 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 from research-grade hardware as well as 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 biofeedback, 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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References

Carreiras, C., Alves, A. P., Lourenço, A., Canento, F., Silva, H., Fred, A., & others. (2015). BioSPPy: Biosignal processing in Python. Retrieved from https://github.com/PIA-Group/BioSPPy/

Clifton, D. A., Gibbons, J., Davies, J., & Tarassenko, L. (2012). Machine learning and software engineering in health informatics. In *2012 first international workshop on realizing ai synergies in software engineering (raise)* (pp. 37–41). IEEE.

Collaboration, O. S., & others. (2015). Estimating the reproducibility of psychological science. *Science, 349*(6251), aac4716.

Gabrieli, G., Azhari, A., & Esposito, G. (2019). PySiology: A python package for physiological feature extraction. In *Neural approaches to dynamics of signal exchanges* (pp. 395–402). Springer Singapore. https://doi.org/10.1007/978-981-13-8950-4_35

Gent, P. van, Farah, H., Nes, N. van, & Arem, B. van. (2019). HeartPy: A novel heart rate algorithm for the analysis of noisy signals. *Transportation Research Part F: Traffic Psychology and Behaviour, 66*, 368–378. https://doi.org/10.1016/j.trf.2019.09.015

Jupyter, Bussonnier, Forde, Freeman, Granger, Head, … Willing. (2018). Binder 2.0 - Reproducible, interactive, sharable environments for science at scale. In Fatih Akici, David Lippa, Dillon Niederhut, & M. Pacer (Eds.), *Proceedings of the 17th Python in Science Conference* (pp. 113–120). https://doi.org/%2010.25080/Majora-4af1f417-011%20

Khodadad, D., Nordebo, S., Mueller, B., Waldmann, A., Yerworth, R., Becher, T., … others. (2018). Optimized breath detection algorithm in electrical impedance tomography. *Physiological Measurement, 39*(9), 094001.

Kiverstein, J., & Miller, M. (2015). The embodied brain: Towards a radical embodied cognitive neuroscience. *Frontiers in Human Neuroscience, 9*, 237.

Kluyver, T., Ragan-Kelley, B., Pérez, F., Granger, B. E., Bussonnier, M., Frederic, J., … others. (2016). Jupyter notebooks-a publishing format for reproducible computational workflows. In *ELPUB* (pp. 87–90).

Legrand, N., & Allen, M. (2020). Systole: A python toolbox for preprocessing, analyzing, and synchronizing cardiac data. Retrieved from https://github.com/embodied-computation-group/systole

Makowski, D. (2020). Neurokit: A python toolbox for statistics and neurophysiological signal processing (eeg, eda, ecg, emg...). *GitHub*. Retrieved from https://github.com/neuropsychology/NeuroKit.py

Marchewka, A., Żurawski, Ł., Jednoróg, K., & Grabowska, A. (2014). The nencki affective picture system (naps): Introduction to a novel, standardized, wide-range, high-quality, realistic picture database. *Behavior Research Methods*, *46*(2), 596–610.

Miłkowski, M., Hensel, W. M., & Hohol, M. (2018). Replicability or reproducibility? On the replication crisis in computational neuroscience and sharing only relevant detail. *Journal of Computational Neuroscience*, *45*(3), 163–172.

Quintana, D., Alvares, G. A., & Heathers, J. (2016). Guidelines for reporting articles on psychiatry and heart rate variability (graph): Recommendations to advance research communication. *Translational Psychiatry*, *6*(5), e803–e803.

Roy, Y., Banville, H., Albuquerque, I., Gramfort, A., Falk, T. H., & Faubert, J. (2019). Deep learning-based electroencephalography analysis: A systematic review. *Journal of Neural Engineering*, *16*(5), 051001.

Schölzel, C. (2020). NOnLinear measures for dynamical systems (nolds). Retrieved from https://github.com/CSchoel/nolds

Topalidou, M., Leblois, A., Boraud, T., & Rougier, N. P. (2015). A long journey into reproducible computational neuroscience. *Frontiers in Computational Neuroscience*,

278   *9*, 30.

279   Van Rossum, G., & Drake, F. L. (2009). *Python 3 reference manual.* Scotts Valley, CA:
280   CreateSpace.

281   Virtanen, P., Gommers, R., Oliphant, T. E., Haberland, M., Reddy, T., Cournapeau, D.,
282   … Contributors, S. 1. 0. (2020). SciPy 1.0: Fundamental Algorithms for Scientific
283   Computing in Python. *Nature Methods*, *17*, 261–272. https://doi.org/https://doi.
284   org/10.1038/s41592-019-0686-2

285   Yuehong, Y., Zeng, Y., Chen, X., & Fan, Y. (2016). The internet of things in healthcare:
286   An overview. *Journal of Industrial Information Integration*, *1*, 3–13.