
TruScanEEGpy Documentation

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CHAPTER 1

TruScanEEGpy

Utility functions to work with Deymed's TruScan EEG system.

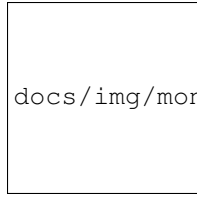
1.1 Installation

To install TruScanEEGpy, run this command in your terminal:

```
$ pip install TruScanEEGpy
```

1.2 Documentation

```
> import TruScanEEGpy
> import mne
>
> layout = TruScanEEGpy.layout_128('10-5')
> montage = TruScanEEGpy.montage_mne_128(layout)
> mne.viz.plot_montage(montage)
```



docs/img/montage_128.png

2.1 Stable release

To install TruScanEEGpy, run this command in your terminal:

```
$ pip install TruScanEEGpy
```

This is the preferred method to install TruScanEEGpy, as it will always install the most recent stable release. It is also possible to install it directly from github:

```
$ pip install https://github.com/neuropsychology/TruScanEEGpy/zipball/master
```

If you don't have `pip` installed, this [Python installation guide](#) can guide you through the process.

2.2 From sources

The sources for TruScanEEGpy can be downloaded from the [Github repo](#).

You can either clone the public repository:

```
$ git clone git://github.com/neuropsychology/TruScanEEGpy
```

Or download the [tarball](#):

```
$ curl -OL https://github.com/neuropsychology/TruScanEEGpy/tarball/master
```

Once you have a copy of the source, you can install it with:

```
$ python setup.py install
```


This part of the documentation details the complete TruScanEEGpy for python API.

Submodule.

layout_128 (*names='index'*)

Create layout file

Parameters **names** (*str*) – Can be ‘index’ or ‘10-5’ for the ‘mak-128’ (an adapted version of 10-5) layout.

Examples

```
>>> import TruScanEEGpy
>>>
>>> layout = TruScanEEGpy.layout_128()
>>> layout = TruScanEEGpy.layout_128('10-5')
```

Submodule.

montage_mne_128 (*layout*)

Create MNE montage

Examples

```
>>> import TruScanEEGpy
>>> import mne
>>>
>>> layout = TruScanEEGpy.layout_128('10-5')
>>> montage = TruScanEEGpy.montage_mne_128(layout)
>>> mne.viz.plot_montage(montage)
>>> mne.viz.plot_montage(montage, kind = "3d")
>>>
```

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```
>>> # Compare to other standard montages
>>> montage = mne.channels.make_standard_montage('standard_1005')
>>> montage.get_positions()
>>> montage.get_positions()['ch_pos']["TP9"]
>>> mne.viz.plot_montage(montage)
>>>
>>> montage = mne.channels.make_standard_montage('biosemi128')
>>> montage.get_positions()
>>> mne.viz.plot_montage(montage)
>>>
>>> montage = mne.channels.make_standard_montage('GSN-HydroCel-128')
>>> montage.get_positions()
>>> mne.viz.plot_montage(montage)
>>>
>>> montage = mne.channels.make_standard_montage('easycap-M1')
>>> mne.viz.plot_montage(montage)
```

CHAPTER 4

Indices and tables

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- `modindex`
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