

# *Analyse des séquences de potentiels d'action* tutorial

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## Data used

We are going to use spike trains obtained from the antennal lobe–first olfactory relay–of locust, *Schistocerca americana*. These spike trains can be found on the [zenodo-locust-datasets-analysis](https://github.com/christophe-pouzat/zenodo-locust-datasets-analysis) GitHub repository. You can also find there a complete description of the sorting procedure used to go from the raw data, that are available on [zenodo](https://zenodo.org), to the spike trains. We will mostly use the spike trains from experiment locust20010214 that can be found at the following address: [https://github.com/christophe-pouzat/zenodo-locust-datasets-analysis/tree/master/Locust\\_Analysis\\_with\\_R/locust20010214/locust20010214\\_spike\\_trains](https://github.com/christophe-pouzat/zenodo-locust-datasets-analysis/tree/master/Locust_Analysis_with_R/locust20010214/locust20010214_spike_trains).

## Getting a spike train

We will start by downloading the spike train from unit 1 from group Spontaneous\_1. This is done by typing in the shell:

```
wget https://raw.githubusercontent.com/christophe-pouzat/\
zenodo-locust-datasets-analysis/master/Locust_Analysis_with_R/\
locust20010214/locust20010214_spike_trains/\
locust20010214_Spontaneous_1_tetB_u1.txt
```