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🌐 Spike Detection

Bryan Yoo[1], Jessica Griffiths[1], Sarkis Mazmanian[1]

[1]California Institute of Technology

Nov 02, 2021

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dx.doi.org/10.17504/protocols.io.bzp9p5r6

Mazmanian Lab

Jessica Griffiths

Protocol for spike detection of GCaMP6F imaging data used in Yoo et al 2021

DOI

dx.doi.org/10.17504/protocols.io.bzp9p5r6

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Nov 02, 2021

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1   Data sets of fluorescent values recorded at a rate of 0.206 s from GCaMP6F-expressing unstimulated neurons in the myenteric plexus of the proximal large intestine and analyzed with the MLspike software for Matlab downloaded from GitHub (https://github.com/MLspike/spikes) (**Deneux et al., 2016**).

2   MLspike determines a new baseline to subtract from the raw fluorescence data to allow accurate modelling. The software uses a version of the Viterbi algorithm to obtain the most probable spike train. From the model, fluctuating baseline, model-estimated spike train, and most probable spike times were extracted. Polynomial coefficients (p_2) were changed from 0.5 to 0.55 and (p_3) from 0.01 to 0.03 for GCaMP6F fluorescence as recommended (**Deneux et al., 2016**). The minimum range for baseline (b_{min}) was changed from 0.7 to 0.5 as determined by observed fluorescence values.

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Citation: Bryan Yoo, Jessica Griffiths, Sarkis Mazmanian Spike Detection https://dx.doi.org/10.17504/protocols.io.bzp9p5r6

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