***eLife’s* transparent reporting form**

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**Sample-size estimation**

* You should state whether an appropriate sample size was computed when the study was being designed
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This information does not apply to our submission, as we built a data analysis method rather than designed a study.

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* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
* The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
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* Criteria for exclusion/inclusion of data should be clearly stated
* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

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Only simulation experiments were performed in this study. In the Results section, we analyze 1000 realizations of each noisy simulated signal. We note that we illustrate application of the method to *in vivo* data by considering a small number of illustrative examples, as described in Results. These are not considered experiments.

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* Statistical analysis methods should be described and justified
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* Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

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In the Methods section, we describe how we compute 95% confidence intervals for the measures, and how we arrive at both analytic and bootstrap p-values for both the produced measure and the modulation index. These p-values are reported in Results. Further, we indicate exact p-values when applying the proposed method to *in vivo* data examples.

(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

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* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
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* Include model definition files including the full list of parameters used
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Please indicate the figures or tables for which source data files have been provided:

*In vivo* rat data is available at <https://github.com/tne-lab/cl-example-data>

*In vivo* human data, along with all code used for data analysis, is available at <https://github.com/Eden-Kramer-Lab/GLM-CFC>