***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
* You should state the statistical method of sample size computation and any required assumptions
* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

Sample size was determined based on the similar experimental approaches performed previously. Thus, no explicit power analysis was performed in this study. All details related to sample sizes are explained in the methods section.

**Replicates**

* 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
* If you encountered any outliers, you should describe how these were handled
* 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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Replication information is included in the figures and/or legends with a few additional numbers provided in the results section when not included in figures.

As the study is based on computational modelling, yielding results devoid of ambiguities, most results depict single experiments. No outliers were encountered, and all data were included in the analysis.

**Statistical reporting**

* Statistical analysis methods should be described and justified
* Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
* For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
* 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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Raw data, precision, and distributions are depicted in all graphs from measurements. Statistical methods and significance are listed next to all p-values (in Figure Legends and Results). Data are reported as mean +/- SEM and stated so in the Figure Legends and Methods.

(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.)

**Group allocation**

* 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
* Indicate if masking was used during group allocation, data collection and/or data analysis

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

Samples were allocated into experimental groups based on modelling environment used for data generation or the neural net architecture that was employed.

**Additional data files (“source data”)**

* We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
* Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
* Include model definition files including the full list of parameters used
* Include code used for data analysis (e.g., R, MatLab)
* Avoid stating that data files are “available upon request”

Please indicate the figures or tables for which source data files have been provided:

All code used for simulating single and multicompartmental NEURON models, ANN benchmarking, ANN representations, and the layer 5 microcircuit are available on GitHub (<https://github.com/ViktorJOlah/Neuro_ANN>) (see github reference Olah 2022 in the main text) and Dryad (doi:10.5061/dryad.0cfxpnw60). To adhere with eLife data availability policies, we also uploaded all data points displayed in the text and figures, on Dryad (doi:10.5061/dryad.0cfxpnw60) in compliance with FAIR (Findable, Accessible, Interoperable, Reusable) principles.