Methods and simulation details

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1 Simulation of a divergent spiking sequence

In Figure 1A, we show a simulation of a divergent spiking sequence. The spiking sequence is defined as

$$\left\{ t_n = 1 - \frac{1}{\sqrt{n}} \middle| n = 1, 2, \cdots, N, \ N < \infty \right\}, \tag{1}$$

and is computed in the script `result_Figure1.m`.

2 Simulation of the biophysical model

Figure 1B and Figure 2 use simulations of the biophysical model developed in previous works Boerlin et al. (2013); Koren et al. (2025), consisting of an Excitatory-Inhibitory network of generalized integrate-and-fire neurons. The set of parameters necessary to replicate our simulations is specified in Table 1 and is the same as the default set of parameters in Koren et al. (2025).

Specification of model parameters

In what follows, we briefly describe how model parameters were chosen (for further details, see Koren et al. (2025)). The number of E neurons N^E, the number of input stimuli M, and the time constant of the stimuli τ and the standard deviation of the distribution of decoding weights of E neurons σ_w^E were chosen for their biological plausibility and computational simplicity. The ratio of the number of E to I neurons $N^E : N^I$, time constants of adaptation in E and I neurons τ_r^E and τ_r^I, the noise intensity σ, the metabolic constant μ and the ratio of standard deviations of decoding weights $\sigma_w^I : \sigma_w^E$ were chosen as parameters that minimize the time-averaged Loss. The time-averaged Loss is defined as the weighted sum of the time-averaged square root of the Squared error and the time-averaged square root of the Metabolic cost. The default weighting of these two variables in the average Loss is $g = 0.7$ in profit of the Squared error against $1 - g = 0.3$ for the Metabolic cost.

The decoding weights of population $y \in \{E, I\}$ are drawn from a normal distribution with mean μ_w^y and standard deviation σ_w^y specified in the Table 1. Decoding weights are then normalized for each neuron following the procedure described in Ref. Koren et al. (2025).

Numerical simulation of the biophysical model

Numerical integration of the membrane potential. We integrate stochastic differential equations describing the time-derivative of the membrane potential of each neuron using Euler integration scheme. When a neuron reaches the firing threshold, a spike is registered and the membrane potential is reset to the value of the reset potential. The synaptic transmission delay is homogeneous across synapses and is set to a single timestep.

Computation of the Squared error, Metabolic cost and Loss. Using the spiking activity of the network, we also compute the population readout of the neural activity $\hat{\boldsymbol{x}}^y(t)$ for $y \in \{E, I\}$. We then evaluate the Squared error of the Excitatory (E) population as the time-dependent squared distance between the target signal $\boldsymbol{x}(t)$ and the population readout of the activity of E neurons $\hat{\boldsymbol{x}}^E(t)$. Similarly, the Squared error of the Inhibitory (I) population is computed as the squared distance between the time-dependent population readout of E ($\hat{\boldsymbol{x}}^E(t)$) and I neurons ($\hat{\boldsymbol{x}}^I(t)$). The time-dependent Metabolic cost of population y is computed as the sum across neurons of the low-pass filtered spiking activity from the

parameter	notation	value
number of E neurons	N^E	400
ratio of E to I neuron numbers	$N^E : N^I$	4:1
number of the input features	M	3
time constant of the population readout (E and I)	τ	10 ms
time constant of the single neuron readout	$\tau_r^E = \tau_r^I$	10 ms
noise strength	σ	5.0 mV
mean of distribution of decoding weights in E and I	$\mu_w^E = \mu_w^I$	$0\ (\mathrm{mV})^{1/2}$
standard deviation of distribution of decoding weights in E	σ_w^E	$1.0\ (\mathrm{mV})^{1/2}$
ratio of standard deviations of decoding weights	$\sigma_w^I : \sigma_w^E$	3:1
metabolic constant	μ	14 mV
weighting of the Squared error vs the Metabolic cost	g	0.7
time step	dt	0.01 ms
stimulus time constant	τ_s	10 ms
stimulus variance	σ_s	$2\ (\mathrm{mV})^{1/2}$

Table 1. Table of default model and stimulus parameters
The metabolic constant μ and the noise strength σ are assumed to be the same across the E and I population, e.g., $\mu^E = \mu^I = \mu$ and $\sigma^E = \sigma^I = \sigma$.

notation	N^E	M	σ	μ	g	τ_s
range	$25 - 1600$	$1 - 50$	$0 - 16$ mV	$0 - 50$ mV	$0 - 1$	$5 - 50$ ms

Table 2. Parameter ranges used for parameter exploration
We vary the network size by varying the number of E neurons N^E and keeping constant the ratio of the number of E to I neurons at its default value of 4:1, thus jointly varying the number of E and I neurons in the network.

population $y \in \{E, I\}$. Finally, the time-dependent empirical Loss for populations of E and I neurons is computed as a weighted sum of the Squared error and Metabolic cost, using weighting g. The Squared error, Metabolic cost and Loss of E neurons were reported on Figure 2A, together with the sum (across neurons) of all spikes fired by the E population (computed with script `result_plot_Figure_2A.m`).

Spike-triggered averages. We evaluated the spike-triggered variables (Squared error, Metabolic cost and Loss) by computing the value of the respective variable shortly before and after each spiking event and averaging across spiking events. If the variable typically decreases at the time of a spike, its spike-triggered average has a negative jump at time lag of 0 milliseconds. This is typically the case of the Squared error and of the Loss. Conversely, if the variable increases at spike times, its spike-triggered average has a positive jump at zero time lag. This is always the case of the Metabolic cost. Spike-triggered averages were reported on Figure 2B (computed with script `result_plot_Figure_2B.m`).

Proportion of error-decreasing and loss-decreasing spikes. To compute the proportion of error-decreasing spikes, we evaluated the difference of the Squared error in a timestep before and after every spike. If the difference is negative, the spike decreased the Squared error and is counted as an error-decreasing spike. We measured the number of error-decreasing spikes over a (50 seconds) long simulation trial, and divided the number of such spikes with the number of all fired spikes, thus getting the proportion of error-decreasing spikes. The computation of the proportion of loss-decreasing spikes follows the same procedure, using the time-dependent Loss instead of the Squared error. We computed these measures for the E and I population.

The proportion of the error- and loss-decreasing spikes for the model with parameters in Table 1 is reported numerically in the Results and computed in script `result_proportion_good_spikes.m`.

Parameter exploration. Finally, we evaluated the proportion of loss-decreasing (efficient) spikes as we varied key model and stimulus parameters. We varied one parameter at the time, keeping other parameters at default values as specified in Table 1. The parameters were varied within ranges specified in Table 2. How the proportion of efficient spikes varies with parameters is shown on Figure 2 C and D. These results were computed with the scripts `result_Figure_2C_mu_sigma.m` (parameters μ and σ), `result_Figure_2C_g.m` (parameter g), `result_Figure_2C_network_size.m` (parameter N^E), and `result_Figure_2C_stimulus.m` (parameters M and τ_s).

Computation time

The simulation of the biophysical model including the computation of decoding weights, connectivity, stimulus, target signal and integration of the membrane potentials for 10 seconds of simulation time takes approximately 53 seconds on a laptop. Most of the computation time is spent integrating the membrane potentials.

References

Boerlin, M., Machens, C. K., and Denève, S. (2013). Predictive coding of dynamical variables in balanced spiking networks. *PLoS Comput Biol*, 9(11):e1003258.

Koren, V., Malerba, S. B., Schwalger, T., and Panzeri, S. (2025). Efficient coding in biophysically realistic excitatory-inhibitory spiking networks. *eLife*, 13:RP99545.