The Asynchronous State in the Cerebral Cortex

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1 Theory

Here, we present some aspects of the theory that we developed to describe asynchronous activity in densely connected, strongly coupled recurrent networks. Asynchronous states in recurrent networks have been studied analytically before (1–7). However, previous treatments lacked at least one of two features which are crucial for an accurate description of how recurrent circuits in the cortex operate: the networks studied so far were either sparsely connected or weakly coupled. In order to make these concepts precise, we adopt the large N limit, considering a series of models of increasing size, in which connection probabilities and strengths scale in a systematic manner with the size N of the network. In this approach, considering how dynamical properties of the network change with N allows one to make qualitative statements which are robust to the precise values of model parameters.

A network is said to have dense connectivity if the probability that two cells are connected does not decrease with the network size. In a random densely connected network with connection probability p, any pair of cells will therefore share a fraction p of their inputs, even in the limit of very large networks. Similarly, a network is said to have strong coupling if the number of inputs needed to make the neuron fire is a small fraction of the total number of inputs the cell receives; more precisely, this fraction should approach zero as network size increases. Thus, the connection strength has to decrease with the network size at a slower rate than $\sim O(1/N)$. For the current model, we considered the scaling introduced in (3), in which the synaptic couplings scale as $\sim O(1/\sqrt{N})$. With this scaling, the magnitude of temporal fluctuations in the synaptic input currents to the neurons in an asynchronous network saturates to a value of the order of the synaptic threshold in the limit of large networks (3). Thus, in a densely connected, strongly coupled network, neurons share inputs and synaptic currents display strong temporal fluctuations, even in the limit of very large networks.

1.1 Analytical Methods

1.1.1 Network Architecture

We consider a recurrent network composed of N excitatory and N inhibitory cells. The probability that a neuron of population $\alpha = E, I$ (where E and I denote the excitatory and inhibitory populations) receives input from a neuron of population $\beta = E, I$ is denoted by $p_{\alpha\beta}$. In addition to the cells in the recurrent network, we also consider input from an external population of neurons, which do not receive inputs from the recurrent network (see Fig. 2A main text). In
particular, we assume that there are $N$ excitatory cells in the external network and that the probability of a connection from an external cell to a cell in population $\alpha$ of the recurrent network is $p_{\alpha X}$.

The strength of the synaptic connection from cell $j$ in population $\beta$ to cell $i$ in population $\alpha$ is denoted as $J_{ij}^{\alpha \beta}$. We consider randomly connected networks in which

$$P(J_{ij}^{\alpha \beta} = \frac{j_{\alpha \beta}}{\sqrt{N}}) = p_{\alpha \beta}$$

$$P(J_{ij}^{\alpha \beta} = 0) = 1 - p_{\alpha \beta}$$

so that all connections between pairs of neurons belonging to the same populations have the same strength. The quantities $j_{\alpha \beta}$ are order unity (which we write as $\sim O(1)$), meaning that they are independent of the network size. Synaptic connections are thus strong, so that a change in the activity of only $\sim O(\sqrt{N})$ neurons is enough to provoke a change in the synaptic input to the neurons of order unity (of the order of the firing threshold).

This network architecture is similar to the one analyzed in (3), with an important difference. In that network, the average number of pre-synaptic inputs was held fixed independently of the network size, whereas in our network it is proportional to the total number of neurons per population $N$. Thus, in that network the fraction of shared input for any pair of cells vanishes in the limit of large networks, whereas in our network it is constant at $p_{\alpha \beta}$ independently of network size.

### 1.1.2 Dynamics

We use the formalism introduced by Glauber (8) to describe the stochastic updating of networks of binary elements. This formalism often been used in neuroscience applications (9, 10), including the study of correlations in recurrent networks (2) and the analysis of balanced recurrent networks (3). In this framework, neurons are modeled as binary elements. We will denote the state at time $t$ of neuron $i$ from population $\alpha$ as $\sigma_{i}^{\alpha}(t) = \{0, 1\}$ (greek letters refer to populations and latin letters to specific neurons). All neurons update their state independently and stochastically. We will denote as $w(\sigma_{i}^{\alpha})$ the probability per unit time that neuron $i$ from population $\alpha$ changes its state from $\sigma_{i}^{\alpha}$ to $1 - \sigma_{i}^{\alpha}$, and by $P(\bar{\sigma}, t)$ the probability that the state of the whole network is $\bar{\sigma} = \{\sigma_{i}\}$ ($i = 1, \ldots, 3N$) at time $t$. As described in (8), one can write an equation for the rate of change of $P(\bar{\sigma}, t)$ (the master equation) by noting that if neurons update independently, in an interval of length $dt$, at most one neuron can change its state. If follows
that
\[
\frac{d}{dt} P(\vec{\sigma}, t) = -P(\vec{\sigma}, t) \sum_{i} w(\sigma_i) + \sum_{i} P(\vec{\sigma}(\sigma_i), t) w(1 - \sigma_i)
\]  
(2)

where \( N' \equiv 3N \) and \( \vec{\sigma}(\sigma_i) = \{\sigma_1, \ldots, 1 - \sigma_i, \ldots, \sigma_{N'}\} \). The equation should be solved with the initial condition \( \{\vec{\sigma}, 0\} \). Using this equation, one can write up an equation for the temporal evolution of any arbitrary product of neuronal variables. For instance, the temporal evolution of the average activity of neuron \( i \) with respect to \( P(\vec{\sigma}) \) is given by

\[
\frac{d}{dt} \langle \sigma_i \rangle(t) \equiv \frac{d}{dt} \left( \sum_{\vec{\sigma}} P(\vec{\sigma}, t) \sigma_i \right) = \sum_{\vec{\sigma}} \left( \frac{d}{dt} P(\vec{\sigma}, t) \right) \sigma_i
\]

Substituting equation (2) into the previous equation, one obtains

\[
\frac{d}{dt} \langle \sigma_i \rangle(t) = \sum_{\vec{\sigma}} \left[ \sum_{j} P(\vec{\sigma}(\sigma_j), t) w(1 - \sigma_j) \sigma_i - P(\vec{\sigma}, t) \sum_{j} w(\sigma_j) \sigma_i \right]
\]

Since we are summing over all configurations \( \vec{\sigma} \), for each term with \( \sigma_j = 1 \) there is a corresponding term with all other neurons in the same state but \( \sigma_j = 0 \) and vice-versa, so that this expression can be re-written as

\[
\frac{d}{dt} \langle \sigma_i \rangle(t) = \sum_{\vec{\sigma}} P(\vec{\sigma}, t) [w(\sigma_i)(1 - 2\sigma_i)]
\]  
(3)

Using similar arguments it is straightforward to find the expression for the joint probability that two neurons are active at the same time

\[
\frac{d}{dt} \langle \sigma_i \sigma_j \rangle(t) = \sum_{\vec{\sigma}} P(\vec{\sigma}, t) [w(\sigma_i)(1 - 2\sigma_i) \sigma_j + w(\sigma_j)(1 - 2\sigma_j) \sigma_i]
\]  
(4)

One can also compute joint probabilities that different neurons will be active at different times. Let us define

\[
\langle \sigma_i(t) \sigma_j'(t + \tau) \rangle = \sum_{\vec{\sigma} \vec{\sigma}'} P(\vec{\sigma}', t + \tau ; \vec{\sigma}, t) \sigma_i \sigma_j' = \sum_{\vec{\sigma}} P(\vec{\sigma}, t) \sigma_i \sum_{\vec{\sigma}'} P(\vec{\sigma}', t + \tau | \vec{\sigma}, t) \sigma_j'
\]

It follows that

\[
\frac{d}{d\tau} \langle \sigma_i(t) \sigma_j'(t + \tau) \rangle = \sum_{\vec{\sigma}} P(\vec{\sigma}, t) \sigma_i \sum_{\vec{\sigma}'} \frac{d}{d\tau} P(\vec{\sigma}', t + \tau | \vec{\sigma}, t) \sigma_j'
\]

The equation for the rate of change of the conditional probability is the master equation where the state we are conditioning on \( \{\vec{\sigma}, t\} \) is to be interpreted as the initial condition. We thus obtain

\[
\frac{d}{d\tau} \langle \sigma_i(t) \sigma_j'(t + \tau) \rangle = \sum_{\vec{\sigma} \vec{\sigma}'} P(\vec{\sigma}', t + \tau ; \vec{\sigma}, t) \sigma_i w(\sigma_j')(1 - 2\sigma'_j)
\]  
(5)
The dynamics of rates and correlations (of any order) is therefore completely determined by the transition probabilities \( w(\ldots) \). In our case they take the form

\[
\begin{align*}
    w(\sigma^\alpha_i) &= \frac{1}{\tau_\alpha} \left[ \sigma^\alpha_i - \Theta(h^\alpha_i) \right]^2 \\
    w(\sigma^X_i) &= \frac{1}{2\tau_X} \left[ 1 - (2\sigma^X_i - 1)(2m^X_i - 1) \right]
\end{align*}
\]

(6) (7)

where \( \Theta(\ldots) \) is the Heaviside step function and \( h^\alpha_i \) is the net afferent current to this cell, given by

\[
    h^\alpha_i = \sum_{\beta} \sum_j E_{ij} J_{ij}^{\alpha\beta} \sigma^{\beta}_j - \theta^\alpha_i
\]

(8)

For notational simplicity we have included the threshold \( \theta^\alpha_i \) of each neuron as a constant negative term in its input current. A neuron’s output does not contribute to its input, so the summation in the definition of \( h^\alpha_i \) does not include the term proportional to \( \sigma^\alpha_i \). At the time of its update, therefore, a cell from the recurrent network becomes active (inactive) if the afferent input from all other neurons, including the external ones is greater (smaller) than its threshold. The state to which external cells are updated to, on the other hand, does not depend on the state of the rest of the network. Because of this, it will follow that for any given pair of external neurons, \( P(\sigma^X_i; \sigma^X_j) = P(\sigma^X_i)P(\sigma^X_j) \). Given the form of the transition probabilities, the symbol \( \langle \ldots \rangle \), which stands for an average over the sources of stochasticity in the dynamics, will stand for an average over the distribution of update times of all neurons, and over the probability that an external neuron will become activated when its turn to update its state comes.

1.2 Analytical Results

In this section, we describe how to calculate the leading order of firing rates and correlations in the network during steady states where the statistical properties of the neurons are constant.

Let us define the average activity of cell \( i \) from population \( \alpha \) at time \( t \) as \( m^\alpha_i(t) = \langle \sigma^\alpha_i \rangle(t) \). Using the transition probabilities (equations (6-7)), equations (3) for the temporal evolution of the average activities become

\[
\begin{align*}
    \tau_\alpha \frac{d}{dt} m^\alpha_i(t) &= -m^\alpha_i(t) + \langle \Theta(h^\alpha_i(t)) \rangle \\
    \tau_X \frac{d}{dt} m^X_i(t) &= -m^X_i(t) + \overline{m}^X
\end{align*}
\]

Similarly, we define the instantaneous correlation (strictly speaking this is the instantaneous covariance, but we will use the term correlation throughout the description of the theory) at
time $t$ between units $\alpha_i$ and $\beta_j$ as

$$r_{ij}^{\alpha\beta}(t) \equiv \langle \delta \sigma_i^\alpha(t) \delta \sigma_j^\beta(t) \rangle \quad \alpha_i \neq \beta_j$$

where $\delta x \equiv x - \langle x \rangle$ and $\alpha, \beta = E, I, X$. Substituting the transition probabilities in equations (6-7) into equations (3-4) one obtains the following equations for the temporal evolution of the pair-wise correlations

$$\tau_{\alpha\beta} \frac{d}{dt} r_{ij}^{\alpha\beta}(t) = -r_{ij}^{\alpha\beta}(t) + \frac{\tau_\alpha}{\tau_\alpha + \tau_\beta} \left[ \langle \sigma_i^\alpha(t) \Theta(h_j^\beta(t)) \rangle - \langle \sigma_i^\alpha(t) \Theta(h_j^\beta(t)) \rangle \right]$$

$$+ \frac{\tau_\beta}{\tau_\alpha + \tau_\beta} \left[ \langle \Theta(h_i^\alpha(t)) \sigma_j^\beta(t) \rangle - \langle \Theta(h_i^\alpha(t)) \sigma_j^\beta(t) \rangle m_j^\beta(t) \right]$$

$$\tau_{\alpha X} \frac{d}{dt} r_{ij}^{\alpha X}(t) = -r_{ij}^{\alpha X}(t) + \frac{\tau_X}{\tau_\alpha + \tau_X} \left[ \langle \Theta(h_i^\alpha(t)) \sigma_j^X(t) \rangle - \langle \Theta(h_i^\alpha(t)) \sigma_j^X(t) \rangle m_j^X(t) \right]$$

where $\tau_{\alpha\beta} \equiv (\tau_\alpha \tau_\beta) / (\tau_\alpha + \tau_\beta)$. We will be interested in the value of the firing rates and pair-wise correlations in a stationary situation (which we will also refer to as equilibrium) where the memory of the initial conditions has been lost and the statistical properties of the network activity are no longer changing. This is equivalent to taking the $t \to \infty$ limit of the previous equations, which results in

$$m_i^\alpha = \langle \Theta(h_i^\alpha) \rangle \quad (9)$$

$$m_i^X = \overline{m_i^X} \quad (10)$$

$$(\tau_\alpha + \tau_\beta) r_{ij}^{\alpha\beta} = \tau_\alpha \langle \delta \sigma_i^\alpha \delta \Theta(h_j^\beta) \rangle + \langle \delta \Theta(h_i^\alpha) \delta \sigma_j^\beta \rangle \tau_\beta \quad (11)$$

$$(\tau_\alpha + \tau_X) r_{ij}^{\alpha X} = \langle \delta \Theta(h_i^\alpha) \delta \sigma_j^X \rangle \tau_X \quad (12)$$

The reason the external-recurrent correlations only contain one term is that neurons from the recurrent network are disconnected from, and therefore have no influence on, the external neurons.

The difficulty in evaluating this set of coupled non-linear equations lies in the fact that arbitrary dependencies between the activities of different neurons preclude, in principle, a closed form for the probability distribution of the synaptic currents $h_i^\alpha$. Since the $h_i^\alpha$ are the sum of a large number of stochastic variables, the central limit theorem ensures that, if these variables were independent, the probability distribution of $h_i^\alpha$ would be well approximated by a Gaussian distribution for large networks. However, the existence of shared inputs introduces correlations in the activities of the cells. The central limit theorem, however, can still be used if these correlations are sufficiently weak. In fact, if the population-averaged correlations are inversely
proportional to the network size $N$ (and higher order cumulants decay fast enough), the distribution of $h^\alpha_i$ can still be well approximated by a Gaussian for large $N$ (11). Network states in which the population averaged correlations scale as $\sim O(1/N)$ are called asynchronous (2). In an asynchronous state, neurons are effectively independent (see section 3.1 of the Supplementary Information), in the sense that the correlations do not significantly impair how well the average firing rate in the network can be estimated.

Our strategy will therefore be to first assume that the network is asynchronous in the steady states. With this assumption, we will develop equations (9-12) to obtain expressions for the population averaged firing rates and pair-wise correlations, in the network. After this, we will show that there are solutions to these equations in which the network is indeed asynchronous.

We will do this in two steps. First, we will develop the set of equations (9-12) without using the fact that the synaptic connections $J^{\alpha\beta}_{ij}$ are stochastic, but using the central limit theorem to invoke a Gaussian distribution for the synaptic currents $h^\alpha_i$. This leads to a set of coupled equations for the firing rates and pair-wise correlations of each neuron and neuronal pair in the network, which we refer to as the microscopic equations. Second, we will average over the distribution of the synaptic connectivity in order to obtain macroscopic equations for the population averaged firing rates and correlations in the network.

1.2.1 Firing Rates

We assume that the distribution of the afferent current $h^\alpha_i$ to cell $\alpha_i$ is well approximated by a Gaussian. Let us denote the mean and variance of the the Gaussian distribution of the current to cell $\alpha_i$ at equilibrium by

$$\mu^\alpha_i \equiv \lim_{t \to \infty} \langle h^\alpha_i(t) \rangle$$

$$\left(s^\alpha_i\right)^2 \equiv \lim_{t \to \infty} \langle (\delta h^\alpha_i(t))^2 \rangle$$

In terms of these quantities, and following the notation in (12), equation (9) for the equilibrium firing rate of cell $\alpha_i$ becomes

$$m^\alpha_i = H(\psi^\alpha_i)$$

where $\psi^\alpha_i \equiv -\mu^\alpha_i / \sqrt{\left(s^\alpha_i\right)^2}$ and

$$H(z) \equiv \frac{1}{\sqrt{2\pi}} \int_z^{\infty} dx \exp(-x^2/2)$$

Equation (14) gives the firing rate of every individual neuron in the network in terms of the activity of all other neurons and the properties of the connectivity. We now would like to obtain
a statistical description of activity in the network, specifying, for instance, the average firing rate in a given sub-population \( m_i^\alpha \equiv 1/N \sum \alpha m_i^\alpha \). In order to do this, one takes advantage of the fact that the network connectivity is stochastic. Because of this, population averages can be thought of as sample averages which, if the network is large, will provide accurate estimates of the distribution averages induced by the probabilistic connectivity. Let us denote the probability distribution of a given connectivity matrix as \( P(J) \). To compute averages over \( P(J) \), we note that both the mean \( \mu_i^\alpha \) and the variance \((s_i^\alpha)^2\) of the current are linear combinations of a large number of uncorrelated random variables (the synaptic variables \( J_{ij}^{\alpha \beta} \)). Thus, \( P(J) \) induces a probability distribution in \( \mu_i^\alpha \) and \((s_i^\alpha)^2\) which will be well approximated by a Gaussian for large networks. We denote this by

\[
\mu_i^\alpha = \mu_\alpha + x_\mu_\alpha \Delta \mu_\alpha \\
(s_i^\alpha)^2 = s_\alpha^2 + x_{s_\alpha^2} \Delta s_\alpha^2
\]

where the \( x \)'s are zero-mean, unit-variance Gaussian random variables, and where we have defined \((\Delta a)^2 \equiv [(a - [a])^2]\). We use the notation \([...]\) to denote averages over the distribution of heterogeneity \( P(J) \). Although the variables \( x_\mu_\alpha \) and \( x_{s_\alpha^2} \) are in principle correlated, it can be shown that the cell-to-cell variability in the magnitude of the temporal fluctuations in synaptic current \( \Delta s_\alpha^2 \) decays with the network size, whereas \( \mu_\alpha, \Delta \mu_\alpha \) and \( s_\alpha^2 \) do not. Thus, for large networks, one only needs to consider

\[
\begin{align*}
\mu_\alpha &= \frac{1}{\epsilon} \sum_\beta J_{i\beta} m_\beta - \theta_\alpha \\
(\Delta \mu_\alpha)^2 &= \sum_\beta J_{i\beta}^{(2)} q_\beta + \sum_\beta J_{i\beta}^{(2)} (q_\beta - m_\beta^2) \\
s_\alpha^2 &= \sum_\beta J_{i\beta}^{(2)} (m_\beta - q_\beta) + c_{\alpha \beta}
\end{align*}
\]

where we have made the following definitions: \( \epsilon \equiv 1/\sqrt{N} \). \( J_{i\beta} \equiv [J_{ij}^{\alpha \beta}] = j_{i\beta} p_{\alpha \beta} \) and \( J_{i\beta}^{(2)} = [(J_{ij}^{\alpha \beta} - [J_{ij}^{\alpha \beta}]^2) = j_{i\beta}^2 p_{\alpha \beta} (1 - p_{\alpha \beta}) \) are, respectively, the average and variance of the distribution of synaptic efficacies between pre-synaptic neurons from population \( \beta \) and post-synaptic neurons from population \( \alpha \). Finally, \( q_\alpha \equiv 1/N \sum_i (m_i^\alpha)^2 \) is the second moment of the spatial distribution of firing rates, and \( c_{\alpha \beta} = 1/N^2 \sum_{ij} \langle \delta h_i^\alpha \delta h_j^\beta \rangle \) is the average correlation between the synaptic currents to neurons in populations \( \alpha \) and \( \beta \). We show below that the population-averaged current correlation decreases with the network size, \( c_{\alpha \beta} \sim O(\epsilon) \), so it can also be neglected in the previous equations. In terms of these quantities, the population-
averaged firing rate and the second moment of the rate distribution can therefore be, for large networks, approximated by

\[ m_{\alpha} = \int Dx \ H \left( -\frac{\mu_{\alpha} + \Delta \mu_{\alpha}}{\sqrt{s_{\alpha}^2 + (\Delta \mu_{\alpha})^2}} \right) \]

\[ q_{\alpha} = \int Dx \left[ H \left( -\frac{\mu_{\alpha} + \Delta \mu_{\alpha}}{\sqrt{s_{\alpha}^2}} \right) \right]^2 \]

where \( Dx \) is a Gaussian measure of zero-mean and unit-variance.

As shown in (3), one does not actually have to solve equation (16) in order to obtain the firing rates in the network. Because each neuron receives \( \sim O(N) \) synaptic inputs, but only \( \sim O(\sqrt{N}) \) are enough to make it fire, the net magnitude of the total excitation and inhibition felt by the neurons is very large compared to the firing threshold (factor 1/\( \epsilon \) in the r.h.s. of equation (15)) In order for the firing rates not to be at either zero or at saturation, these large excitatory and inhibitory drives have to cancel, but this cancellation can only happen if the firing rates take on precise values. Thus, for large networks, imposing the cancellation, determines the rates. Although this has already been shown in (3, 12), we briefly now outline the formal derivation of this idea for completeness and because an essentially identical rationale determines the average correlations: In order for the net synaptic input in equation (15)) to be of order unity (to avoid complete quiescence or saturation), it has to be true that

\[ \sum_{\beta} J_{\alpha\beta} m_{\beta} = \sum_{\beta = E,I} J_{\alpha\beta} m_{\beta} + J_{\alpha X} m_{X} \sim O(\epsilon) \]

Asymptotically, this is a linear equation that determines the firing rates at equilibrium

\[ \sum_{\beta = E,I} J_{\alpha\beta} m_{\beta} = -J_{\alpha X} m_{X} \]

so that

\[ m_{\alpha} = -\sum_{\beta = E,I} J_{\alpha\beta}^{-1} J_{\beta X} m_{X} \equiv A_{\alpha} m_{X} \]  

Thus, asymptotically, the population averaged firing rate of each population is proportional to the population averaged rate of the external neurons. The conditions for this solution to be realized have been described in (12).

1.2.2 Instantaneous Pair-wise correlations

In order to obtain an expression for the instantaneous pair-wise correlations in equations (11-12) one needs to evaluate terms of the type \( \langle \Theta(h_{i}^{\alpha}) \sigma_{j}^{\beta} \rangle \). Let us first rewrite them in terms of the
conditional probability that neuron $\alpha_i$ is active given that neuron $\beta_i$ is active at the same time. To do this, we note that

$$\langle \Theta(h^\alpha_i \sigma^\beta_j) \rangle = \sum_\sigma P(\bar{\sigma}) \sigma^\beta_j \Theta(h^\alpha_i) = \sum_\sigma P(\bar{\sigma}(\sigma^\beta_j)) P(\sigma^\beta_j) \sigma^\beta_j \Theta(h^\alpha_i)$$

$$= m^\beta_j \sum_\sigma P(\bar{\sigma}(\sigma^\beta_j)) \Theta(h^\alpha_i(\sigma^\beta_j) + J^\alpha\beta_{ij}) = m^\beta_j \langle \Theta(h^\alpha_i(\sigma^\beta_j) + J^\alpha\beta_{ij}) | \sigma^\beta_j = 1 \rangle$$

where $\langle \ldots | \sigma_i = 1 \rangle = \sum_\sigma P(\bar{\sigma}(\sigma_i)) | \sigma_i = 1 \rangle$ is an average over the conditional distribution of the network activity $\bar{\sigma}$ given that neuron $\sigma_i$ is active, and $\bar{\sigma}(\sigma_i)$ means that neuron $\sigma_i$ is excluded from all those included in $\bar{\sigma}$ (and similarly for $h^\alpha_i(\sigma^\beta_j)$). The average over the conditional distribution is equivalent to an average over a Gaussian random variable

$$z^\alpha_i(\sigma^\beta_j) = h^\alpha_i(\sigma^\beta_j) + J^\alpha\beta_{ij}$$

with mean and variance given by

$$\mu^\alpha_i \equiv \langle z^\alpha_i(\sigma^\beta_j) | \sigma^\beta_j = 1 \rangle$$

$$(\sigma^\alpha_i)^2 \equiv \langle (z^\alpha_i(\sigma^\beta_j))^2 | \sigma^\beta_j = 1 \rangle - \langle \mu^\alpha_i \rangle^2$$

so that

$$\langle \Theta(h^\alpha_i \sigma^\beta_j) \rangle = H(-\mu^\alpha_i / \sqrt{(\sigma^\alpha_i)^2}) m^\beta_j$$

(19)

We develop the previous expression in two steps. First, we relate averages over the conditional distribution to averages over the equilibrium distribution by noting that

$$\langle \sigma^\alpha_i | \sigma^\beta_j = 1 \rangle = \langle \sigma^\alpha_i (1 + \delta \sigma^\beta_j / m^\beta_j) \rangle$$

$$\langle \sigma^\alpha_i \sigma^\gamma_k | \sigma^\beta_j = 1 \rangle = \langle \sigma^\alpha_i \sigma^\gamma_k (1 + \delta \sigma^\beta_j / m^\beta_j) \rangle$$

Second, we relate properties of $h^\alpha_i(\sigma^\beta_j)$ to properties of $h^\alpha_i$ by recalling that

$$h^\alpha_i(\sigma^\beta_j) = h^\alpha_i - J^\alpha\beta_{ij} \sigma^\beta_j$$

$$(h^\alpha_i(\sigma^\beta_j))^2 = (h^\alpha_i)^2 + (J^\alpha\beta_{ij})^2 - 2 J^\alpha\beta_{ij} h^\alpha_i \sigma^\beta_j$$

which leads to

$$\langle z^\alpha_i(\sigma^\beta_j) | \sigma^\beta_j = 1 \rangle = \langle h^\alpha_i (1 + \delta \sigma^\beta_j / m^\beta_j) \rangle$$

$$\langle (z^\alpha_i(\sigma^\beta_j))^2 | \sigma^\beta_j = 1 \rangle = \langle (h^\alpha_i)^2 (1 + \delta \sigma^\beta_j / m^\beta_j) \rangle$$
Using these equations, one can express the conditional rate in terms of the mean $\mu_i^\alpha$ and variance $(s_i^\alpha)^2$ of the current over the (unconditional) equilibrium distribution. This is done by noting that

$$\langle (h_i^\alpha)^2 \delta \sigma_j^\beta \rangle = \langle (\delta h_i^\alpha)^2 \delta \sigma_j^\beta \rangle + 2\mu_i^\alpha \langle \delta h_i^\alpha \delta \sigma_j^\beta \rangle$$

and making the definitions

$$A_{ij}^{\alpha\beta} \equiv \langle \delta h_i^\alpha \delta \sigma_j^\beta \rangle \quad B_{ij}^{\alpha\beta} \equiv \langle (\delta h_i^\alpha)^2 \delta \sigma_j^\beta \rangle$$

one obtains

$$\mu_i^\alpha = \mu_i^\alpha + \left( \frac{A_{ij}^{\alpha\beta}}{m_j^\beta} \right) (s_i^\alpha)^2 = (s_i^\alpha)^2 + \left( \frac{B_{ij}^{\alpha\beta}}{m_j^\beta} \right) - \left( \frac{A_{ij}^{\alpha\beta}}{m_j^\beta} \right)^2$$

Equation (19) therefore becomes

$$\langle \Theta(h_i^\alpha)\sigma_j^\beta \rangle = H \left( \frac{-\mu_i^\alpha - \left( \frac{A_{ij}^{\alpha\beta}}{m_j^\beta} \right)}{\sqrt{(s_i^\alpha)^2 + \left( \frac{B_{ij}^{\alpha\beta}}{m_j^\beta} \right) - \left( \frac{A_{ij}^{\alpha\beta}}{m_j^\beta} \right)^2}} \right) m_j^\beta$$ (20)

If an asynchronous state exists in this network, the population average of the quantities $A_{ij}^{\alpha\beta}/m_j^\beta$ and $(B_{ij}^{\alpha\beta}/m_j^\beta) - (A_{ij}^{\alpha\beta}/m_j^\beta)^2$, which quantify the difference between the conditional and unconditional means and variances to neuron $\alpha_i$ respectively, must be of order $\sim O(1/N)$ at most. Imposing these conditions results in a series of equations that set the value, not only of the population-averaged correlations, but also of a number of other properties of the activity in the network such as the degree to which cells with a higher firing rate tend to have a higher correlation with all other neurons in the network. Here, however, we will only describe how to calculate the population-averaged correlations and firing rates in the network, for which we show below it is sufficient to keep track of terms linear in $A_{ij}^{\alpha\beta}/m_j^\beta$ (13). Developing equation (20), thus, up to first order in $A_{ij}^{\alpha\beta}/m_j^\beta$, one obtains

$$\langle \Theta(h_i^\alpha)\sigma_j^\beta \rangle = m_i^\alpha m_j^\beta + \dot{m}_i^\alpha A_{ij}^{\alpha\beta} + O((A_{ij}^{\alpha\beta})^2) + O(B_{ij}^{\alpha\beta})$$

where

$$\dot{m}_i^\alpha \equiv \partial m_i^\alpha / \partial \mu_i^\alpha = \partial H(-\mu_i^\alpha / \sqrt{(s_i^\alpha)^2}) / \partial \mu_i^\alpha$$

is the slope of the input-output relationship of the neuron evaluated at the value that the mean current takes in equilibrium. This allows us to write the following expression for the (microscopic) instantaneous correlations at equilibrium

$$\langle \tau_{\alpha} + \tau_{\beta} \rangle r_{ij}^{\alpha\beta} = \dot{m}_i^\alpha A_{ij}^{\alpha\beta} \tau_{\beta} + \dot{m}_j^\beta A_{ji}^{\beta\alpha} \tau_{\alpha}$$ (21)

$$\langle \tau_{\alpha} + \tau_{X} \rangle r_{ij}^{\alpha X} = \dot{m}_i^\alpha A_{ij}^{\alpha X} \tau_{X}$$ (22)
\[ A_{ij}^{\alpha\beta} = J_{ij}^{\alpha\beta} m_j^\beta (1-m_j^\beta) + \sum_{\gamma_k \neq \beta_j} J_{ik}^{\alpha\gamma} r_{kj}^{\gamma\beta} \]  

(23)

The quantity \( A_{ij}^{\alpha\beta} \) measures the influence of pre-synaptic cell \( \beta_j \) on the firing of post-synaptic cell \( \alpha_i \). The first term in \( A_{ij}^{\alpha\beta} \) contains the contribution of a direct connection from cell \( \beta_j \) to cell \( \alpha_i \) to their pair-wise correlation. This effect is also proportional to the temporal variance of the pre-synaptic cell \( m_j^\beta (1-m_j^\beta) \). The second term contains all the contributions of all those cells which project to the post-synaptic cell \( \alpha_i \) and with which the pre-synaptic cell \( \beta_j \) is correlated.

We would now like to obtain expressions for the population-averaged correlations \( r_{\alpha\beta} \equiv \frac{1}{N^2} \sum_{ij} r_{ij}^{\alpha\beta} \) (if \( \alpha = \beta \) in the previous expression, the pre-factor should be \( \frac{1}{N(N-1)} \)). As described above, we will do this by averaging over the distribution of randomly connected networks \( P(J) \). Let us start with the external-recurrent correlations in equation (22) first. Averaging over \( P(J) \) one gets

\[ (\tau_\alpha + \tau_X) r_{\alpha X} = \epsilon \bar{J}_{\alpha X} a_X + \frac{1}{\epsilon} \sum_{\gamma=E,I} \bar{J}_{\alpha\gamma} r_{\gamma X} \]  

(24)

where \( a_X \equiv m_X - q_X \) and \( \bar{J}_{\alpha\beta} \equiv \dot{m}_\alpha J_{\alpha\beta} \), with \( \dot{m}_\alpha \equiv [\dot{m}_\alpha^\mu] = \partial m_\alpha / \partial \mu_\alpha \). In the last section, we saw that due to the strong connectivity, there was a mismatch between the magnitude of the net input to the neurons and their activity unless there was a precise cancellation of net excitation and inhibition. A similar situation takes place here. Even if we assume that the network is indeed asynchronous, so that all population averaged correlations scale as \( r_{\alpha\beta} \sim O(\epsilon^2) \), the l.h.s. of the previous equation is \( \sim O(\epsilon^2) \) and the r.h.s is \( \sim O(\epsilon) \). Thus, the equation has no solution unless there is a precise cancellation between the different terms in the r.h.s. To reveal this explicitly, let us express \( r_{\gamma X} \) as a Taylor series in \( \epsilon \)

\[ r_{\gamma X} = \sum_{n=0}^{\infty} r_{\gamma X}^{(n)} \epsilon^n \]

substitute this expression in equation (24) and evaluate the equation at each order in \( \epsilon \) separately. Doing this shows that the first non-zero term in the series is \( r_{\gamma X}^{(2)} \), whose value is given by the solution of

\[ \sum_{\gamma=E,I} \bar{J}_{\alpha\gamma} r_{\gamma X}^{(2)} + \bar{J}_{\alpha X} a_X = 0 \quad \longrightarrow \quad r_{\gamma X}^{(2)} = -\sum_{\alpha=E,I} \bar{J}_{\gamma\alpha}^{-1} \bar{J}_{\alpha X} a_X = A_\gamma a_X \]  

(25)

The last equality follows from the fact that

\[ \sum_{\alpha=E,I} \bar{J}_{\gamma\alpha}^{-1} \bar{J}_{\alpha X} = \sum_{\alpha=E,I} \bar{J}_{\gamma\alpha}^{-1} J_{\alpha X} \equiv -A_\gamma \]
Thus, we have shown that

$$r_{\alpha X} = \epsilon^2 A_\alpha a_X + O(\epsilon^3)$$

Using similar arguments, equation (21) can be written as

$$(\tau_\alpha + \tau_\beta)r_{\alpha\beta} = \epsilon \tilde{J}_{\alpha\beta} a_\beta \tau_\beta + \frac{1}{\epsilon} \left[ \sum_{\gamma=E,I} \tilde{J}_{\alpha\gamma} r_{\gamma\beta} + \tilde{J}_{\alpha X} r_{X\beta} \right] \tau_\beta +$$

$$\epsilon \tilde{J}_{\beta\alpha} a_\alpha \tau_\alpha + \frac{1}{\epsilon} \left[ \sum_{\gamma=E,I} \tilde{J}_{\beta\gamma} r_{\gamma\alpha} + \tilde{J}_{\beta X} r_{X\alpha} \right] \tau_\alpha$$

(26)

Again, expanding the $r_{\alpha\beta}$ and $a_\alpha$ in powers of $\epsilon$ and evaluating the previous equation at each order, the term $\sim O(\epsilon)$ results in the following equation

$$\tilde{J}_{\alpha\beta} a_\beta^{(0)} \tau_\beta + \left[ \sum_{\gamma=E,I} \tilde{J}_{\alpha\gamma} r_{\gamma\beta}^{(2)} + \tilde{J}_{\alpha X} r_{X\beta}^{(2)} \right] \tau_\beta + \tilde{J}_{\beta\alpha} a_\alpha^{(0)} \tau_\alpha + \left[ \sum_{\gamma=E,I} \tilde{J}_{\beta\gamma} r_{\gamma\alpha}^{(2)} + \tilde{J}_{\beta X} r_{X\alpha}^{(2)} \right] \tau_\alpha = 0$$

where $a_\alpha^{(0)} = m_\alpha^{(0)} - q_\alpha^{(0)}$ is the leading-order population-averaged temporal variance of the activity of cells in population $\alpha$. In the general case, the solution to the previous equation is that the first three and last three terms in the last equation (which are identical if we exchange the values of $\alpha$ and $\beta$) are both equal to zero, i.e., $r_{\alpha\beta}^{(2)}$ is the solution of

$$\sum_{\gamma=E,I} \tilde{J}_{\beta\gamma} r_{\gamma\alpha}^{(2)} + \tilde{J}_{\beta X} r_{X\alpha}^{(2)} + \tilde{J}_{\beta\alpha} a_\alpha^{(0)} = 0$$

It is useful to define the correlation between the instantaneous activity of populations $\alpha$ and $\beta$ at equilibrium

$$v_{\alpha\beta} = \lim_{t \to \infty} \langle \sum_i (\delta \sigma_i^\alpha(t)/N) \sum_j (\delta \sigma_j^\beta(t)/N) \rangle = r_{\alpha\beta} + \epsilon^2 \delta_{\alpha\beta} a_\alpha$$

(27)

in terms of which the previous equation can be written as

$$\sum_{\gamma=E,I} \tilde{J}_{\beta\gamma} v_{\gamma\alpha}^{(2)} + \tilde{J}_{\beta X} r_{X\alpha}^{(2)} = 0 \quad \Rightarrow \quad v_{\gamma\alpha}^{(2)} = - \sum_{\beta=E,I} \tilde{J}_{\gamma\beta}^{-1} \tilde{J}_{\beta X} r_{X\alpha}^{(2)} = A_{\gamma} A_\alpha a_X$$

The solution for the population-averaged instantaneous pair-wise correlations in the steady states in our network is therefore

$$r_{EX} = \epsilon^2 A_E a_X + O(\epsilon^3)$$
$$r_{IX} = \epsilon^2 A_I a_X + O(\epsilon^3)$$
$$r_{EE} = \epsilon^2 (A_E^2 a_X - a_E^{(0)}) + O(\epsilon^3)$$
$$r_{II} = \epsilon^2 (A_I^2 a_X - a_I^{(0)}) + O(\epsilon^3)$$
$$r_{EI} = \epsilon^2 A_E A_I a_X + O(\epsilon^3)$$

(28)

(29)
1.2.3 Tracking of fluctuations in the asynchronous state

There is a simple way of expressing the leading order solution for the correlations in the network. Let us consider the difference between the normalized instantaneous activities of the excitatory and inhibitory populations

\[ m_\alpha(t) = \frac{\sum_i \sigma_\alpha^i(t)}{N} \]

and the instantaneous activity of the external population. They are given by

\[ \Delta_\alpha X(t) \equiv \frac{1}{A_\alpha m_X} \left( \sum_i \sigma_i^\alpha(t)/N \right) - \frac{1}{m_X} \left( \sum_i \sigma_i^X(t)/N \right) \]

We can measure the degree to which the activity in the recurrent network tracks the instantaneous activity in the external population by calculating the variance of \( \Delta_\alpha X(t) \) at equilibrium,

\[ \langle (\Delta_\alpha X(t) - \langle \Delta_\alpha X(t) \rangle)^2 \rangle = \frac{1}{Nm_X^2} \left( \frac{(a_\alpha + Nr_\alpha \alpha)}{A_\alpha^2} + a_X - 2Nr_\alpha X / A_\alpha \right) \]

Again replacing the expressions (28-29) into this formula we obtain that, to leading order, it vanishes. Similarly, it is simple to show in the same way that \( \Delta EI(t) \) also vanishes to leading order.

Thus, although the magnitude of the temporal fluctuations of the instantaneous firing rate of each population is \( \sim O(\epsilon) \), the magnitude of the temporal fluctuations of the instantaneous difference in firing rates is \( \sim O(\epsilon^{3/2}) \). This implies that as the network gets larger, the instantaneous firing rate in the three populations track each other more faithfully, and that, asymptotically, the tracking is perfect, i.e., as \( N \to \infty \)

\[ m_E(t) = A_E m_X(t) \]

\[ m_I(t) = A_I m_X(t) \]

This result captures the essential difference between the sparse balanced network and the densely-connected one. In the sparse balanced network, the recurrent feedback results in linear propagation of the average firing rate. In the dense network, not only the average firing rate, but also the instantaneous fluctuations in activity are faithfully propagated. In these conditions, referring to the average firing rate as ‘signal’ and to the fast temporal fluctuations as ‘noise’ becomes questionable, since both are propagated with the same accuracy.

1.2.4 Balance of current correlations

The leading order solution for the average pair-wise correlations in the network leads to a cancellation between the different components of the average correlation between the currents to a
pair of neurons. To see this, one just needs to note that

\[ c_{ij}^{\alpha\beta} \equiv \langle \delta h_i^\alpha \delta h_j^\beta \rangle = \sum_{\gamma k} A_{ik}^{\alpha\gamma} (J_{kj}^{\beta})^t \]

Thus, the average correlation between the synaptic currents to cells in populations \( \alpha \) and \( \beta \) is equal to

\[ c_{\alpha\beta} = \sum_{\gamma} J_{\alpha\gamma} a_{\gamma} J_{\gamma\beta}^t + \frac{1}{\epsilon^2} \sum_{\gamma\lambda} J_{\alpha\lambda} r_{\lambda\gamma} J_{\gamma\beta}^t \]  

(32)

Terms proportional to \( a_{\gamma} \) in the previous sum are the contribution of common input to the average current correlation. The other terms measure the contribution of correlations between pre-synaptic inputs, to the average current correlation. Given that the leading order of the population-averaged correlations in firing activity is \( \sim O(\epsilon^2) \), the leading order of each term in the previous sum is of order unity. However, it is straightforward to check that if one substitutes the solution in equations (28-29) into equation (32), the positive and negative terms cancel out. Thus,

\[ c_{\alpha\beta} \sim O(\epsilon) \]

Just as linear propagation of average firing rates in the sparse network is extended to linear propagation of instantaneous firing rates in the dense network, the cancellation of the mean excitatory and inhibitory synaptic inputs in the sparse network is extended to a cancellation of the positive components of the population-averaged current correlation (arising from shared input and from network amplification of correlations between excitatory cells and between interneurons), and a negative term coming from network amplification of the correlations that tracking induces between the excitatory and inhibitory cells.

The structure of synaptic current correlations is very different in a sparsely connected network. We say that the connectivity of the network is sparse if the average number of pre-synaptic inputs is independent of the network size, i.e., if the probability of connection scales as \( \sim O(1/N) \). In a sparse network, such as \((3, 4)\), the fraction of shared inputs decreases with the network size and, consequently, so do each of the components of the current correlations in an asynchronous state. Thus, in a densely connected network the asynchronous state is a purely dynamical phenomenon, whereas in a sparsely connected network it is the result of a static feature of the network architecture.
1.2.5 Delayed Correlations

Although a detailed treatment of the form of the delayed correlations (cross-correlation functions) is beyond the scope of this Supplementary Material, there is one qualitatively important point that we would like to discuss. We have just shown that the instantaneous population-averaged current correlations decay as $\sim O(1/\sqrt{N})$. How is this compatible with the instantaneous population-averaged activity correlations decaying as $\sim O(1/N)$ (equations (28,29))? We will show that this is related to the fact that the time-scale of current correlations is much faster than the time-scale of activity correlations. To simplify the discussion, we will only consider delayed correlations between recurrent neurons.

We define the delayed correlation between cells $\alpha_i$ at time $t$ and $\beta_j$ at time $t + \tau$ as

$$r_{ij}^{\alpha\beta}(t, t + \tau) \equiv \langle \delta\sigma_i^\alpha(t)\delta\sigma_j^\beta(t + \tau) \rangle$$

where note that, when averaging quantities evaluated at different times, $\langle \ldots \rangle$ stands for an average over the joint probability distribution $P(\sigma', t + \tau ; \sigma, t)$. Thus, delayed correlations are defined for $\tau > 0$.

Inserting the transition probabilities into equation (5) one obtains

$$\tau_\beta \frac{d}{d\tau} r_{ij}^{\alpha\beta}(t, t + \tau) = -r_{ij}^{\alpha\beta}(t, t + \tau) + \langle \delta\sigma_i^\alpha(t)\delta\Theta(h_j^\beta(t + \tau)) \rangle$$

Instead of using the previous strategy for evaluating the terms $\langle \delta\sigma_i^\alpha(t)\delta\Theta(h_j^\beta(t + \tau)) \rangle$, we will now use a different approach, expressing the activity of cell $\alpha_i$ at time $t$ in terms of its afferent current at the time when it was last updated. Since there is a constant probability per unit time (equal to $1/\tau_\alpha$) of neuron $\alpha_i$ updating its state, the probability of the interval after the last update is exponential with time-constant $\tau_\alpha$. We can therefore write

$$\langle \sigma_i^\alpha(t)\Theta(h_j^\beta(t + \tau)) \rangle = \int_0^\infty \frac{d\tau'}{\tau_\alpha} \exp\left(-\tau'/\tau_\alpha\right) \langle \Theta(h_i^\alpha(t - \tau'))\Theta(h_j^\beta(t + \tau)) \rangle$$

We thus need to evaluate

$$\lim_{t\to\infty} \langle \Theta(h_i^\alpha(t - \tau'))\Theta(h_j^\beta(t + \tau)) \rangle \equiv \hat{r}_{ij}^{\alpha\beta}(\tau + \tau')$$

The quantity $\hat{r}_{ij}^{\alpha\beta}(\tau)$ measures the probability that the current to cell $\alpha_i$ and the current to cell $\beta_j$ $\tau$ seconds into the future are both above threshold in equilibrium. If the distribution of the currents can be approximated by a Gaussian, it can be expressed in terms of the cross-correlogram of the currents

$$c_{ij}^{\alpha\beta}(\tau) \equiv \lim_{t\to\infty} \langle \delta h_i^\alpha(t)\delta h_j^\beta(t + \tau) \rangle$$
by the following equation
\[ \hat{r}_{ij}^{\alpha\beta}(\tau) = \hat{H} (\psi_i^\alpha, \psi_j^\beta, \hat{\rho}_{ij}^{\alpha\beta}(\tau)) \]
where we have defined
\[ \hat{\rho}_{ij}^{\alpha\beta}(\tau) \equiv c_{ij}^{\alpha\beta}(\tau)/\langle s_i^\alpha s_j^\beta \rangle \]
and
\[ \hat{H}(a, b, \rho) \equiv \frac{1}{2\pi} \int_a^\infty dy \exp(-x^2/2) \int_{b-y}^{\infty} dx \exp(-y^2/2) \]
The quantity \( \hat{H}(a, b, \rho) \) represents the probability that two Gaussian variables with means and variances characterized by \( a, b \) and correlation coefficient \( \rho \) will be greater than zero at the same time. Since correlations are weak in the asynchronous state, it is convenient to consider the expansion of \( \hat{H}(a, b, \rho) \) near \( \rho \sim 0 \),
\[ \hat{H}(a, b, \rho) = H(a)H(b) + e^{-a^2/2} \rho e^{-b^2/2} + O(\rho^2) \]
As in previous sections, in order to characterize the leading-order value of the correlations, it is sufficient to keep the first term in this expansion. Using these expressions, we can write equation (33) in equilibrium as
\[ \tau_\beta \frac{d}{d\tau} r_{ij}^{\alpha\beta}(\tau) = -r_{ij}^{\alpha\beta}(\tau) + \int_0^\infty \frac{d\tau'}{\tau_\alpha} \exp(-\tau'/\tau_\alpha) \hat{m}_i^\alpha c_{ij}^{\alpha\beta}(\tau + \tau') \hat{m}_j^\beta \]
which is equivalent to
\[ \tau_\alpha \tau_\beta \frac{d^2}{d\tau^2} r_{ij}^{\alpha\beta}(\tau) + \left( \tau_\alpha - \tau_\beta \right) \frac{d}{d\tau} r_{ij}^{\alpha\beta}(\tau) - r_{ij}^{\alpha\beta}(\tau) + \hat{m}_i^\alpha c_{ij}^{\alpha\beta}(\tau) \hat{m}_j^\beta = 0 \]
The population-averaged version of the previous equation is
\[ \tau_\alpha \tau_\beta \frac{d^2}{d\tau^2} r_{\alpha\beta}(\tau) + \left( \tau_\alpha - \tau_\beta \right) \frac{d}{d\tau} r_{\alpha\beta}(\tau) - r_{\alpha\beta}(\tau) + \hat{m}_\alpha c_{\alpha\beta}(\tau) \hat{m}_{\beta} = 0 \] (35)
and the cross-correlogram of the population-averaged currents is given by
\[ c_{\alpha\beta}(\tau) = \sum_{\gamma=E,I,X} J_{\alpha\gamma} a_{\gamma}(\tau) \tilde{J}_{\gamma\beta} + \frac{1}{e^2} \sum_{\gamma\lambda=E,I,X} \tilde{J}_{\alpha\gamma} r_{\gamma\lambda}(\tau) \tilde{J}_{\lambda\beta} \]
where \( a_\alpha(\tau) = 1/N \sum_i a_i^\alpha(\tau) \) is the population-averaged auto-correlation function of neurons in population \( \alpha \). For each neuron it is defined as \( a_i^\alpha(\tau) = \lim_{t \to -\infty} \langle \delta \sigma_i^\alpha(t) \delta \sigma_i^\alpha(t + \tau) \rangle \) and can be evaluated with the same techniques we have outlined for the cross-correlation functions.
Equation (35) can be studied using singular perturbation techniques. For our present purposes, note that for $\tau$ of order unity, i.e., not very close to the origin ($\tau \sim 0$), the derivatives in the first two terms of the equation do not change the dependency of those terms with $\epsilon$. Thus, expanding $r_{\alpha\beta}(\tau)$ in powers of $\epsilon$ as in the previous sections one obtains that the leading order of the population-averaged delayed correlations at lags of order unity have to obey

$$\sum_{\gamma=E,I,X} \tilde{J}_{\alpha\gamma} a_{\gamma}(0) \tilde{J}_{\gamma\beta} + \sum_{\gamma\lambda=\gamma E,I,X} \tilde{J}_{\alpha\gamma} r_{\gamma\lambda}^{(2)}(\tau) \tilde{J}_{\lambda\beta} = 0$$

The solution of this equation is that, at lags of order unity, the leading order of the cross-correlation function of the instantaneous network activity in each population (the delayed version of equation (27)) is again $\sim O(\epsilon^2)$ and proportional to the external auto-correlation function, i.e.,

$$u_{\alpha\beta}(\tau) = \epsilon^2 A_{\alpha} A_{\beta} a_X(\tau) + O(\epsilon^3)$$

Thus, as expected, the population-averaged delayed correlations are $\sim O(\epsilon^2)$. But that means that the first three terms in equation (35) are also $\sim O(\epsilon^2)$, which implies that

$$c_{\alpha\beta}(0)(\tau) = c_{\alpha\beta}^{(1)}(\tau) = 0$$

This is what we wanted to show. Although the instantaneous current correlations are $c_{\alpha\beta} \sim O(\epsilon)$, at lags of order unity $c_{\alpha\beta}(\tau) \sim O(\epsilon^2)$. Thus, the time-scale of the current correlations is very fast. In fact, it can be shown that the time-scale of the population-averaged recurrent correlations is $\sim O(\epsilon)$. The biological interpretation of this is that time-scale of the process of tracking is of order $\sim O(\epsilon)$, leading to a situation where both the peak height and time-scale of the population-averaged current correlations are of that same order, implying that the area under the current cross-correlogram is $\sim O(\epsilon^2)$.

The network is therefore self-consistent, because the instantaneous correlations in activity are proportional to the area under the current cross-correlogram. This can be shown by employing the same approach we used in equation (34) to the instantaneous correlations in equation (11). Doing this, one can obtain an alternative expression for the instantaneous population-averaged correlations

$$(\tau_\alpha + \tau_\beta)r_{\alpha\beta} = \int_{-\infty}^{0} d\tau \exp(\tau/\tau_\beta) \dot{m}_\alpha c_{\alpha\beta}(\tau) \dot{m}_\beta + \int_{0}^{\infty} d\tau \exp(-\tau/\tau_\alpha) \dot{m}_\alpha c_{\alpha\beta}(\tau) \dot{m}_\beta$$

We have just shown that the integrands in this equation are $\sim O(\epsilon^2)$ except for a thin slice of order $\sim O(\epsilon)$ around $\tau = 0$, in which they are $\sim O(\epsilon)$. Thus, the whole integral is $\sim O(\epsilon^2)$ as it should when the state of the network is asynchronous.
1.2.6 Self-consistent propagation of asynchronous activity

We have assumed throughout that neurons from the external population were independent. We made this assumption in order to avoid having to define the correlation structure of the external network \textit{ad hoc}. Our results, however, are still valid if the external neurons are not independent, as long as the external network is itself asynchronous. Note that this does not qualitatively change the properties of the external input. Simply the existence of common input makes the average correlation between the external component of the synaptic input \( \sim O(1) \). Thus, as long as the population-averaged correlation between the external neurons is \( \sim O(1/N) \), this will only lead to quantitative changes in the correlation structure of the input from the external network. Hence, asynchronous activity can be robustly propagated between densely connected, strongly coupled neuronal circuits.

Asymptotic expressions for how rates and correlations propagate from one asynchronous network to another can be derived from the simple equations (30-31). Let’s consider two asynchronous networks, with network 2 receiving excitation from network 1. In the large \( N \) limit, it holds that

\[
\begin{align*}
m_{E_2}(t) &= A_{E_1 ightarrow 2} m_{E_1}(t) \\
m_{I_2}(t) &= A_{I_1 ightarrow 2} m_{E_1}(t)
\end{align*}
\]

Equations for the transformation of rates and correlations can be obtained by equating the temporal average, variance and covariance of the previous expressions

\[
\begin{align*}
m_{E_2} &= A_{E_1 ightarrow 2} m_{E_1} \\
m_{I_2} &= A_{I_1 ightarrow 2} m_{E_1} \\
r_{EE_2} &= \frac{1}{N} \left[ \left( A_{E_1 ightarrow 2} \right)^2 (a_{E_1} + N r_{EE_1}) - a_{E_2} \right] \\
r_{II_2} &= \frac{1}{N} \left[ \left( A_{I_1 ightarrow 2} \right)^2 (a_{E_1} + N r_{EE_1}) - a_{I_2} \right] \\
r_{EI_2} &= \frac{1}{N} \left[ A_{I_1 ightarrow 2} A_{E_1 ightarrow 2} (a_{E_1} + N r_{EE_1}) \right]
\end{align*}
\]

where we again used \( a_{\alpha} = m_{\alpha} - q_{\alpha} \). Note that changes in the structure of the temporal fluctuations in network 1, either by changing \( r_{EE_1} \) or \( q_{E_1} \), lead to changes in the correlation structure of network 2 without changing its average firing rate.
2 Methods

2.1 Numerical Methods

2.1.1 Binary Networks

The results in Fig. 2 in the main text were obtained by numerical simulation of binary networks evolving in time using an asynchronous updating rule (see, e.g., (9)). The architecture of the networks was identical to that studied analytically. The update rule was as follows: On each iteration, a neuron $i$ out of the $3N$ that compose the network was chosen at random. If this neuron belonged to the external population, a random number $x$ was generated and its activity was set to one if $x < \bar{m}_i^X$ and was set to zero otherwise. The parameter $\bar{m}_i^X$ thus determines the mean number of updates which result in the cell being activated, i.e., the cell’s mean activity level. In all our simulations, all external neurons had the same activity level, i.e., $\bar{m}_i^X = m_X$ for all $i$. If the neuron to be updated belonged to the recurrent network, the synaptic current to this neuron was calculated using the instantaneous activity of all other cells in the network to which projected to it. If the synaptic current was larger than a threshold $\theta$, the neuron was set to one, and otherwise it was set to zero. Note that, for all cells, the outcome of the updating process is independent of the neuron’s state at the time of update. Using this update rule, each neuron is updated every $3N$ iterations on average, which is defined to be equal to the neuronal time constant $\tau$. Thus, the resolution of the dynamics increases with the network size, i.e., $dt = \tau/3N$. Since neurons from all three populations update their state at this rate, the time constants of the three populations is the same, i.e., $\tau_E = \tau_I = \tau_X = \tau$. The biological interpretation of $\tau$ is as the effective time constant with which a neuron changes its firing activity, i.e., $\tau \sim 10$-25 ms. Each dot in each curve in Fig. 2C of the main text is the average over 50 simulations in which the same parameters were used except for the random seed that sets the connectivity matrix. Each simulation for each network lasted $T_{sim} = 200,000 \tau$. The cross-correlograms in Fig 2F of the main text are averages over 10 statistically identical simulations of the same duration $T_{sim}$. The parameters we used in all simulations were $p_{\alpha\beta} = p = 0.2$, $m_X = 0.1$, $\theta = 1$, $j_{EE} = 5/\sqrt{N}$, $j_{EI} = -10/\sqrt{N}$, $j_{IE} = 5/\sqrt{N}$, $j_{II} = -9/\sqrt{N}$, $j_{I\!X} = 4/\sqrt{N}$, $j_{EX} = 5/\sqrt{N}$. The synaptic parameters were chosen so that (apart from the scaling factors) the effective size of a synaptic input $p_j_{\alpha\beta}$ would be the same as those used in (3). Networks were simulated using custom written C, C++, and MATLAB software.
2.1.2 Integrate-and-fire networks

To generate the results in Fig. 1B-F of the main text, a simple feed-forward network of current-based integrate-and-fire neurons was used. The membrane potential of each post-synaptic neuron evolved according to

\[ \tau_m \frac{dV_m}{dt} = -V_m + I_E \sum_{i=1}^{N_E} s^E_i(t) - I_I \sum_{i=1}^{N_I} s^I_i(t) \]

where \( \tau_m = 10 \text{ ms} \) is the membrane time-constant and \( I_\alpha, \alpha = E, I \) are constants chosen to obtain EPSPs (IPSPs when inhibitory inputs were considered) of peak-amplitude 0.75 (2.5) mV. The PSCs were modeled as simple exponential decays,

\[ \frac{ds^\alpha_i}{dt} = -s^\alpha_i/\tau_s + \sum_{t^\alpha_i} \delta(t - t^\alpha_i) \]

where the PSC decay time \( \tau_s = 5 \text{ ms} \), and \( t^\alpha_i \) are the spike times from pre-synaptic neuron \( i \) of population \( \alpha = E, I \). The spiking threshold was set at 20 mV relative to resting potential, the reset potential at 10 mV, and the refractory period at 2 ms. In Fig. 1B and the black trace of Fig. 1C (main text), all pre-synaptic inputs where excitatory \( (N_E = 250 \text{ and } N_I = 0) \). In the gray curve in Fig. 1C of the main text, \( N_E = 250 \text{ and } N_I = 60 \).

Each neuron of the pair analyzed in Fig. 1B of the main text shared exactly 250 \( \rho \) inputs, where \( \rho \) is the shared input fraction in the x-axis of the plot. All pre-synaptic inputs were independent and had Poisson statistics with a constant rate of 5 Hz. The output rate was also \( \sim 5 \text{ Hz} \). Each dot in the curve corresponds to 10,000 s of simulated time.

Each neuron in the pair analyzed in the black curve of Fig. 1C shared exactly 50 excitatory and 12 inhibitory inputs \( (\rho = 0.2) \), all having a rate \( \nu_{in} = 5 \text{ Hz} \). Their correlation \( \rho_{in} \) (spike count measured in windows of 50 ms) was varied along the x-axis. Correlations were generated by thinning of a mother Poisson spike train of rate \( \nu_{in}/\rho_{in} \). Each pre-synaptic train was produced by randomly and independently keeping each spike of the mother train with probability \( \rho_{in} \), followed by jittering each spike by a random time drawn from a two-tailed exponential distribution of zero mean and SD = 5 ms. Thus, all pre-synaptic trains were marginally Poisson, but had (approximately) exponential cross-correlograms with width 10 ms, and an area equal to \( \rho_{in} \). For the gray curve, which includes inhibition, the statistical properties of the inputs were identical except for their firing rates, which were adjusted to \( \nu_{in} = 12 \text{ Hz} \) in order for the output rates in the presence of pre-synaptic inhibition to still be 5 Hz when \( \rho_{in} = 0 \).
The results in Fig. 3 of the main text were obtained by numerical simulation of spiking conductance-based integrate-and-fire networks. Except for the sizes of each population, the architecture of the spiking and binary networks was identical. The spiking network was composed of $N_E = 4100$, $N_I = 1100$ and $N_X = 4000$ neurons. The membrane potential of each neuron $i = 1, \ldots, N_\alpha$ from population $\alpha = E, I$ of the recurrent network evolves according to

$$C_m \frac{dV_i^\alpha}{dt} = -g_L(V_i^\alpha - V_L) + I_{iE} + I_{iI} + I_{iX} + I_{app}$$  (36)

The total synaptic currents to this neuron $I_{i\beta}$, $\beta = E, I, X$ are given by

$$I_{i\beta} = -\left[ \sum_{j=1}^{N_\beta} c_{i\beta j} g_{i\beta j} s_{i\beta j}(t) \right] (V_i^\alpha - V_{rev}^\beta)$$  (37)

where $V_{rev}^\beta$ is the reversal potential of the corresponding conductance. We use $V_{rev}^E = V_{rev}^X = 0$ mV and $V_{rev}^I = -80$ mV. The variable $c_{i\beta j}$ is a binary random variable with probability $p = 0.2$ of being equal to one which determines if cell $\beta_j$ projects to cell $\alpha_i$. The variable $g_{i\beta j}$ measures the strength of the synaptic conductance between these two cells. All conductance strengths from cells in population $\beta$ to cells in population $\alpha$ are drawn from Gaussian distributions of means $\mu_{g_{EE}} = 2.4$ nS, $\mu_{g_{EI}} = 40$ nS, $\mu_{g_{IE}} = 4.8$, nS $\mu_{g_{II}} = 40$ nS, $\mu_{g_{IX}} = 5.4$ nS, $\mu_{g_{IX}} = 5.4$ nS; all distributions had a coefficient of variation (i.e. $\sigma_{g_{i\beta j}}/\mu_{g_{i\beta j}}$) equal to 0.5. The quantity $s_{i\beta j}(t)$ represents the instantaneous value of the synaptic gating variable describing the fraction of open channels of the synapse from cell $\beta_j$ to cell $\alpha_i$. We model unitary conductance changes in response to a pre-synaptic spike as a difference of exponentials, so that the gating variable evolves according to

$$\tau_d \frac{ds_{i\beta j}}{dt} = x_{i\beta j} - s_{i\beta j}$$  (38)

$$\tau_r \frac{dx_{i\beta j}}{dt} = \tilde{\tau} \sum_{t_{\beta j}} \delta(t - t_{\beta j} - d_{i\beta j}) - x_{i\beta j}$$  (39)

where $\delta(\ldots)$ is the Dirac delta function, $t_{\beta j}$ are the spike times of neuron $\beta_j$, $d_{i\beta j}$ is the conduction delay between the two cells, $\tau_r = 1$ ms and $\tau_d = 5$ ms are the rise and decay times of the unitary conductance change (equal for all synapses in the network), and the factor $\tilde{\tau} = 1$ ms ensures that the area under the unitary conductance is constant regardless of the rise and decay time-constants. Conduction delays from excitatory (inhibitory) cells were drawn from a uniform distribution $d_{iE_j} = [0.5 : 1.5]$ ms ($d_{iI_j} = [0.1 : 0.9]$ ms) independently for each synapse.
When the membrane potential of a cell reaches the firing threshold $V_{th} = -50$ mV, it fires a spike and is reset to the resting potential $V_L = -70$ mV during an absolute refractory period $\tau_{ref} = 2$ or 1 ms for pyramidal cells and inhibitory interneurons respectively. All neurons had a membrane capacitance $C_m = 0.25$ nF, and a leak conductance of $g_L = 16.7$ nS, resulting in resting membrane time constant of 15 ms. Neurons in the external network had Poisson statistics, and all fired at a constant rate of 2.5 Hz.

In Fig. 3 of the main text we simulated an intracellular recording where active and synaptic conductances are inactivated in order to measure the dynamics of the EPSPs and IPSPs. In order to achieve this, the spiking mechanism was inactivated in a number of neurons. To perturb the effective amounts of excitation and inhibition experienced by these cells, an amount $I_{app}$ of DC current was used (14, 15). In each simulation of Fig. 3E of the main text, ten groups of ten neurons each were held at average membrane potentials spanning the range between the reversal potentials of inhibition and excitation. For one group $I_{app} = 0$ nA, two groups where hyperpolarized $I_{app} = -0.65, -1.3$ nA, and 5 groups were depolarized $I_{app} = n0.74$ nA ($n = 1, \ldots, 5$). The results in this panel were averaged over ten different simulations (50 s of simulated time) with identical parameters differing only in the particular instantiation of their random connectivity.

Numerical integration of the differential equations in the simulations was performed using the second-order Runge-Kutta algorithm with an iteration time-step of 0.05 ms, using custom software written in C and C++.

### 2.2 Experimental Methods

Detailed descriptions of surgery and recording procedures have been published previously (16–18). Briefly, nine rats (Sprague-Dawley; 400 - 900 g) were anesthetized with urethane (1.2 - 1.5 g/kg body weight) plus additional injections of ketamine (20 mg/kg) and urethane (0.2 g/kg) as needed, and body temperature was retained with a heating pad. Rats were placed in a stereotaxic frame or naso-orbital restraint, and a window in the scalp was prepared over the somatosensory or auditory cortex. A silicon microelectrode (Neuronexus technologies, Ann Arbor MI) was attached to a micromanipulator and moved gradually to its desired depth position. Probes consisted of eight shanks (200 mm separation) each with eight staggered recording sites (20 mm vertical separation). Extracellular signals were high-pass filtered (1 Hz) and amplified (1,000 gain) by using a 64-channel amplifier (Sensorium, Charlotte, VT), and digitized at 25 kHz (DataMax System; RC Electronics, Santa Barbara, CA) or 20 kHz (United Electronic
Industries, Inc., Canton, MA). The location of the recording sites was estimated to be layer V by histological reconstruction of the electrode tracks, electrode depth, and firing patterns (16). As we observed no significant differences between the auditory and somatosensory data, these were pooled together in the analysis presented in the main text. Data from several of these animals were used in previous studies (16, 17). All experiments were carried out in accordance with protocols approved by the Rutgers University Animal Care and Use Committee.

2.3 Analysis Methods

2.3.1 Single-Unit Isolation

Units were isolated by a semiautomatic algorithm (http://klustakwik.sourceforge.net) followed by manual clustering (19) (http://klusters.sourceforge.net). Single units selected for further analysis had less than 10% contamination in an absolute refractory period of 2 ms and fired more than 75 action potentials in the recording session. Across the 18 recording sessions in 9 rats that we analyzed, an average of 69 (range [16:116], interquartile range [44:93]) simultaneously recorded single units met these conditions.

2.3.2 Classification cortical state

Under urethane anesthesia, the pattern of cortical background activity spontaneously undergoes transitions between periods of inactivation, characterized by global fluctuations in network excitability (up and downstates) similar to those seen in slow-wave sleep, and periods of activation, characterized by tonic activity more similar to REM sleep (20, 21). Periods of cortical activation were detected off-line, using the magnitude of the temporal fluctuations in multi-unit activity (summed spike trains of all well-isolated single units). Each recording session was divided into contiguous non-overlapping 10 s periods. In each period we computed the coefficient of variation (CV) of the number of events in the multi-unit spike train in 200 non-overlapping windows of 50 ms, thus obtaining a sequence of CVs at 10 s intervals. Periods of cortical activation were indicated by significantly lower CVs than periods dominated by Up-Down state transitions. The activated and inactivated states are not truly discrete, but two extremes of a continuum (21). For simplicity of analysis, however, we selected only periods at the extremes of the activation-inactivation continuum in each experiment. Although the CV values used as threshold varied between experiments, all activated periods used had an average CV of less than 0.5, and there was essentially no overlap between the distribution of CVs in the activated
and inactivated periods across all experiments. For each experiment, data from several periods corresponding to each state (all > 90s in length) were pooled. The mean duration of cortical activation (inactivation) analyzed per recording session was 610s (438s). While sensory stimuli were presented in some experiments, only unstimulated periods were used for the current analyses.

2.3.3 Down-state detection and exclusion

We used the following procedure to isolate periods of silence during the slow oscillation (Down-states). First, we constructed a multi-unit spike train (MUST) by merging together all well isolated single units. We then identified inter-spike intervals (ISIs) in the MUST longer than 50 ms. We also constructed an instantaneous firing rate corresponding to the MUST by convolution with a Gaussian density of width 10 ms. For each ISI > 50 ms, the associated a Down-state was said to begin at the first point in time left of the center of that ISI where the instantaneous rate dropped below 20% of its maximum for the whole recording session, and it was said to end at the first point in time to the right of the center of the ISI where the instantaneous rate went above the same (20%) threshold. Every period in between two Down-states was a defined as an Up-state unless the Up-state was shorter than 50 ms, in which case the two surrounding Down-states were merged together. In order to re-calculate correlations after Down-state removal (Fig. 4D-F of the main text), time-intervals classified as Down-states were removed from all spike trains of well isolated cells, and the correlations between the resulting spike trains were calculated identically as during periods of activation (see next section). Note that, beyond the requirement of a minimum duration longer than 50 ms, we did not impose any condition of stationarity on Up-states (e.g., the third Up-state in Fig. 4C of the main text is clearly non-stationary). Doing so would probably further reduce the average correlation during Up-states.

2.3.4 Quantifying Spiking Correlations

When assessing correlations over long periods of time, electrode drift or slow coordinated changes in excitability of the local network may induce spurious covariations in the activity of the recorded cells. When analyzing sensory responses, such artefactual correlations are typically removed with the shift predictor (22). To remove these during long periods of spontaneous activity, we used jitter methods (23, 24). In this approach correlations are computed relative to a distribution of surrogates generated by jittering the spike times of the original spike trains by a certain amount \( T_{jitt} \). Relationships between spike trains on time-scales shorter than \( T_{jitt} \)
are absent from the surrogates, but the temporal structure of all the surrogate spike trains is identical to that of the original data on time scales significantly longer than $T_{jitt}$. Thus, if the time-scale of the correlations generated by the artefactual sources is significantly longer than $T_{jitt}$, then these correlations will be present in both the original data and its surrogates, and the difference in correlation between the real and surrogate data will only reflect network-generated coordination on time-scales shorter than $T_{jitt}$.

Correlations in spike trains at a time-scale $T_{\text{win}}$ are usually assessed by looking at the correlation between sequences of spike counts, where each spike count is the number of spikes in each spike train in a window of length $T_{\text{win}}$. Let us consider two spike trains

$$s_i(t) = \sum_{t_i^{spk}} \delta(t - t_i^{spk}) \quad i = 1, 2$$

The covariance between the spike count sequences associated with these two spike trains can be expressed as

$$c_{12}(T_{\text{win}}) = \frac{1}{N} \sum_{j=1}^{N} \left[ \left( s_1^{SC(T_{\text{win}})}(t_j) - \langle s_1^{SC(T_{\text{win}})} \rangle \right) \left( s_2^{SC(T_{\text{win}})}(t_j) - \langle s_2^{SC(T_{\text{win}})} \rangle \right) \right]$$

in terms of the quantities

$$s_i^{SC(T_{\text{win}})}(t_j) = \int_{t_j-T_{\text{win}}/2}^{t_j+T_{\text{win}}/2} dt' s_i(t')$$

representing the spike count of each of the spike trains in windows of length $T_{\text{win}}$ centered at times $\{t_j\}$. This set of times can be chosen so that the windows are non-overlapping, but we will in general consider them to be more closely spaced, to increase the sample size $N$. $s_i^{SC(T_{\text{win}})}(t)$ is the convolution of the spike train with a square kernel centered at $t$. The quantities

$$\langle s_i^{SC(T_{\text{win}})} \rangle = \frac{1}{N} \sum_{j=1}^{N} s_i^{SC(T_{\text{win}})}(t_j)$$

are the mean spike counts of each spike train. A normalized measure of correlation, the correlation coefficient of the spike count, can be obtained by dividing the covariance by the product of the standard deviations

$$\rho_{12}(T_{\text{win}}) = \frac{c_{12}(T_{\text{win}})}{\sqrt{c_{11}(T_{\text{win}})c_{22}(T_{\text{win}})}}$$

Note that $c_{12}(T_{\text{win}})$ gives the amount of covariation in the spike counts $\langle s_1^{SC(T_{\text{win}})} s_2^{SC(T_{\text{win}})} \rangle$ relative to their expected amount if the two trains were independent on all time-scales, i.e.,
\[ \langle s_1^{SC(T_{\text{win}})} \rangle \langle s_2^{SC(T_{\text{win}})} \rangle \] (or at least on all time-scales lower than something much larger than the duration of the experiment).

We modified this procedure in two ways: First, in order to avoid discontinuities, we replaced the square kernel use in the computation of the spike count by a normalized Gaussian kernel of width \( T_{\text{win}} \). The fact that the kernel is normalized changes the covariance, but not the correlation coefficient. The convolution of the spike train with the normalized Gaussian kernel \( s_i^{G(T_{\text{win}})}(t_j) \) can be considered as an estimate of the instantaneous firing rate of the spike train at time \( t_j \), and its average across the experiment \( \langle s_i^{G(T_{\text{win}})} \rangle = \nu_i \) is equal to the average firing rate of spike train \( i \). Second, we measure covariations relative to their expected amount if the spike trains were only independent on a given time scale \( \ll T_{\text{jitt}} \). We do this by replacing the average firing rate across the experiment \( \langle s_i^{G(T_{\text{win}})} \rangle = \nu_i \), by its average \( \langle s_i^{G(T_{\text{win}})}(t_j) \rangle_{\text{jitt}} \) across a family of jittered surrogates, where each jittered surrogate is obtained by adding a random Gaussian variable of zero mean and SD = \( T_{\text{jitt}} \) to each spike time of the original spike train. Since both the counting kernel and the jitter distribution are Gaussian, \( \langle s_i^{G(T_{\text{win}})}(t_j) \rangle_{\text{jitt}} \) is a convolution of the original spike train with a Gaussian kernel of variance \( T_{\text{jitt}}^2 + T_{\text{win}}^2 \).

Thus, the covariation of the two spike trains on a time-scale \( T_{\text{win}} \) relative to what can be expected if the two spike trains were independent on time-scales \( \ll T_{\text{jitt}} \) is given by

\[
\tilde{c}_{12}(T_{\text{win}}, T_{\text{jitt}}) = \frac{1}{N} \sum_{j=1}^{N} \Delta s_1^{G(T_{\text{win}}, T_{\text{jitt}})}(t_j) \Delta s_2^{G(T_{\text{win}}, T_{\text{jitt}})}(t_j)
\] (40)

where

\[
\Delta s_i^{G(T_{\text{win}}, T_{\text{jitt}})}(t_j) = s_i^{G(T_{\text{win}})}(t_j) - \langle s_i^{G(T_{\text{win}})}(t_j) \rangle_{\text{jitt}}
\]

The quantity \( \Delta s_i^{G(T_{\text{win}}, T_{\text{jitt}})}(t_j) \) is the convolution of the spike train \( s_i(t) \) with a mexican-hat type of kernel (of zero area) given by the difference of a Gaussian of SD = \( T_{\text{win}} \) minus another Gaussian of SD = \( \sqrt{T_{\text{jitt}}^2 + T_{\text{win}}^2} \). Thus, algorithmically, the calculation of the covariance in equation (5) simply amounts to the dot-product of two time series obtained by a convolution of the original pair of spike trains by the mexican-hat kernel evaluated in the grid \( \{t_j\}, j = 1, \ldots, N \), divided by \( N \). The correlation coefficient obtained with this method is given by

\[
\tilde{\rho}_{12}(T_{\text{win}}, T_{\text{jitt}}) = \frac{\tilde{c}_{12}(T_{\text{win}}, T_{\text{jitt}})}{\sqrt{\tilde{c}_{11}(T_{\text{win}}, T_{\text{jitt}}) \tilde{c}_{22}(T_{\text{win}}, T_{\text{jitt}})}}
\] (41)

Since jittering by a Gaussian kernel of width \( T_{\text{jitt}} \) only destroys correlations of a time-scale \( \ll T_{\text{jitt}} \), we used counting kernels with a width \( T_{\text{win}} = T_{\text{jitt}}/4 \). In the main text, we used
$T_{\text{win}} = 50$ ms. The effect of using different values for $T_{\text{win}}$ is described in the Supplementary Figure COMPLETE!. Given $T_{\text{jitt}}$ and $T_{\text{win}}$, we used a grid spacing $\Delta t = t_{j+1} - t_j = 0.2 \text{ min}(T_{\text{jitt}}, T_{\text{win}})$.

### 2.3.5 Assessing significance of correlations

For each pair of spike trains (say 1 and 2) we calculated $\tilde{\rho}_{12}(T_{\text{win}}, T_{\text{jitt}})$ as described in the previous section. We also calculated $\tilde{\rho}_{12}(T_{\text{win}}, T_{\text{jitt}})_J (J = 1, \ldots, N_{\text{jitt}})$ for each of $N_{\text{jitt}} = 1000$ jittered surrogates of each spike train pair. Surrogates were again created by adding a Gaussian random variable of zero mean and SD = $T_{\text{jitt}}$ to each spike time of each train. We calculated a p-value for each $\tilde{\rho}_{12}(T_{\text{win}}, T_{\text{jitt}})$ as

$$p = \frac{N_{\text{pos}} + N_{\text{neg}}}{N_{\text{jitt}}}$$

where

- $N_{\text{pos}} = \text{number of } \tilde{\rho}_{12}(T_{\text{win}}, T_{\text{jitt}})_J > |\tilde{\rho}_{12}(T_{\text{win}}, T_{\text{jitt}})|$
- $N_{\text{neg}} = \text{number of } \tilde{\rho}_{12}(T_{\text{win}}, T_{\text{jitt}})_J < -|\tilde{\rho}_{12}(T_{\text{win}}, T_{\text{jitt}})|$

In Fig. 4 of the main text, the correlation coefficient of a pair of spike trains was deemed significant if $p < 0.01$.

### 2.3.6 Cross-correlograms

The insets of Fig. 4B in the main text shows average raw cross-correlograms. The value of the raw cross-correlogram between two spike trains was calculated by realigning one of the spike trains to each spike in the other spike train. For a given time-bing $t_b$, the value of the cross-correlogram at lag $nt_b$ ($n = \ldots, -2, -1, 0, 1, 2, \ldots$) is given by the number of times that there was a spike in the realigned spike train between $nt_b - t_b/2$ and $nt_b + t_b/2$, divided by the product of the average spike counts of the two trains in a window of length $t_b$. With this normalization, if the spike trains were independent, the value of the cross-correlogram would be equal to one at all lags (except for finite sample fluctuations). In Fig. 4B, we used $t_b = 5$ ms.

### 2.3.7 Distance-dependence of correlations

We assessed the distance dependence of the mean $\bar{\rho}$ and standard deviation $\sigma_r$ of the histogram of correlations during periods of activation (Fig. S3). To do this, each pair of spike trains was
assigned a distance $d$ label, from 0 to 7, corresponding to the number of intervening shanks between the two shanks where the two cells in the pair were recorded. Pairs of cells recorded in the same shank were assigned a distance label equal to zero. We then recomputed 7 spiking correlation histograms for each recording session, each of them composed of all pairs assigned with the same distance $d$.

We calculated by a simple linear regression how the particular statistic ($\bar{r}$ or $\sigma_r$) depended on the distance between shanks across recording sessions. In order to know whether the slope $m_{\text{data}}$ of the regression was significantly different from zero we used a non-parametric shuffle test. For each condition, each point was given by a pair (distance-correlation), corresponding, for instance, to the mean correlation of all pairs recorded in the same shank in a given experiment. We created 5000 surrogate data sets by randomly shuffling the distance labels of each point, and calculated the slope of the regression for each surrogate. The p-value reported in the text is the fraction of the surrogates with a slope greater than the absolute value of $m_{\text{data}}$ or smaller than minus the absolute value of $m_{\text{data}}$. 
3 Supplementary Results

3.1 Relationship between instantaneous firing rate fluctuations and population-averaged correlations

An intuitive way of quantifying the degree of correlations in a neuronal population could be the average across pairs $\bar{r}$ of the correlation coefficient of each pair in the population. For instance, if $\bar{r} \sim 0.05$ the population would seem to be weakly correlated, whereas if $\bar{r} \sim 0.5$ correlations would seem to be relatively strong. However, there is something unsatisfactory about this way of quantifying correlations, as the numerical value of $\bar{r}$ can take any value along a continuum. For instance, would correlations be strong if $\bar{r} \sim 0.1$? what about $\bar{r} \sim 0.2$?

Although in an experimental situation it is difficult to get around this problem, when analyzing a network theoretically there is an unambiguous way of differentiating networks where correlations are strong or weak. This idea was first introduced in a rigorous way in (2). Here we simply illustrate it graphically.

Consider the top row of the left two columns in Fig. S1A. They show a raster plot of 50 Poisson neurons, independent on the left, and with a correlation coefficient of $\bar{r} = 0.1$ on the middle (throughout this figure, correlations were generated exactly as in Fig. 1C in the main text (see Supplementary Methods above)). The difference between these two situations does not seem striking. It becomes more obvious, however, when the number of simulated neurons is increased (second and third rows). Although the correlation between the neurons is identical in all rows of the first and second columns, the plots seem to be more different when there are more cells. The reason is that what the eye is picking up from the raster is the magnitude of the temporal fluctuations in the average activity of all neurons, not the correlation of each pair. The average activity, or instantaneous firing rate, of the population is shown in the fourth row of the figure, in gold, magenta and black for the populations of $N = 50, 200, \text{and } 1000$ neurons respectively. As is apparent in these plots, when neurons are independent, the temporal fluctuations in the instantaneous rate become smaller the larger the population. When the correlations are equal to $\bar{r} = 0.1$, however, the magnitude of these fluctuations initially decreases but then saturates to a constant value.
It is easy to show this effect quantitatively by considering a set \( \{ \sigma_i \} \) \((i = 1, \ldots, N)\) of \( N \) binary variables, representing for instance the presence or absence of a spike in a given time-bin. Let us assume that their variance is \( v \) and their covariance is \( \text{cov} \). The instantaneous average activity is \( m = \sum_i \sigma_i/N \). The variance of \( m \) is equal to \( V(m) = \frac{1}{N}(v + (N - 1)\text{cov}) \). The variance of the average \( V \) normalized by the individual variance \( v \) is therefore

\[
\frac{V}{v} = \frac{1}{N}(1 + (N - 1)r)
\]

(42)

where \( r \) is the correlation coefficient of the \( \sigma_i \). Thus, as shown in the figure, if neurons are independent \((r = 0)\), the magnitude of the temporal fluctuations in \( m \) (the ‘error’ of the mean) decays as \( \sim O(1/\sqrt{N}) \), whereas if their correlation is \( r \), the error in the mean saturates to the value \( \sqrt{r} \). Importantly, this qualitative difference between the independent scenario, and
one with a correlation \( r \) is always there regardless of the numerical value of \( r \). For smaller \( r \)'s, the saturation happens at larger \( N \)'s, but it always happens nevertheless. This observation suggests quantifying the level of correlation, not by the value of \( r \), but by the dependency of the magnitude of the temporal fluctuations in the instantaneous rate (the error in \( m \)) with \( N \). In (2) an asynchronous network was defined as one in which the error in \( m \) scales as \( \sim O(1/\sqrt{N}) \).

Although a network of independent neurons is asynchronous (left column of Fig. S1A), equation (42) shows that the asynchronous property does not require independence. In fact, a network of correlated neurons can be asynchronous as long as the average correlation between neurons scales as \( \sim O(1/N) \). This is illustrated in the third column of Fig. S1A. For each \( N \), we used \( r = 5/N \), which leads to smaller temporal fluctuations in the rate of the population for larger networks (fourth row).

These results are summarized in Fig. S1B, in a similar format to the one used in previous discussions of this issue (25, 26) (we varied the network size \( N \) along the x-axis instead of the size of the neuronal pool being used to estimate the rate). This plot shows equation (42) for the three different cases we have just described. The error in \( m \) can be interpreted as the error in the estimation of the firing rate of our population that a downstream network would make by simple averaging. Although any given network has a fixed size, if the network is capable of being in an asynchronous state, the correlations generated by the architecture and the dynamics will not pose a fundamental limit to how well the firing rate of the population can be estimated.

### 3.2 Time-scale dependence of correlations in the rat cortex in vivo

We repeated the analysis of the experimental data using different counting windows \( T_{\text{win}} \). We calculated correlation coefficients as described in Section 2.3.4, keeping the jitter time-scale fixed to four times the counting window, i.e., \( T_{\text{jitt}} = 4T_{\text{win}} \). In Fig. S2 we show the average across experiments of the mean \( \bar{r} \) of the correlation histogram (empty dots) and the histogram width (filled dots) \( \sigma_r \) for counting windows ranging from 10 ms to 500 ms during the ACT state.

We did not see qualitative differences from the results in Fig. 4 of the main text (in which the counting window was \( T_{\text{win}} = 50 \) ms) when we considered different counting windows. The mean correlation is very small (less than 0.02) for all counting windows up to \( T_{\text{win}} = 500 \) ms, although it shows a slight increasing tendency. Correlations on time-scales of the order of several seconds, however, are expected to reflect processes other than synaptic transmission and integration, which are, in general one to two orders of magnitude faster. As expected, the width of the histogram goes to zero with decreasing \( T_{\text{win}} \), since spike count correlations become linear.
in the counting window as $T_{\text{win}} \to 0$ (27).

![Figure S2: Effect of the counting window on the distribution of correlations.](image)

**Figure S2: Effect of the counting window on the distribution of correlations.** Empty and filled dots correspond to the average (plus minus standard deviation) across recording sessions of the mean of the correlation histogram $\bar{r}$ and its width $\sigma_r$. The histogram is wide across a large range of counting windows.

### 3.3 Examples of CCGs of individual pairs

In order to ensure that the spiking correlations that we are estimating through the use of jitter methods during spontaneous activity are consistent with more conventional measures of correlation between spike trains, in Fig. S3 we show an example of one hundred cross-correlograms (CCGs) from the experiment illustrated in Fig. 4B of the main text, during the ACT period.
Figure S3: Examples of individual CCGs. One hundred raw CCGs (see section 2.3.6, bin size = 10 ms) from the experiment shown in Fig. 4 of the main text. CCGs were chosen to span the whole range of correlations observed for this experiment. Top, distribution of correlations $r$ for this experiment (identical to the one in Fig. 4B of the main text). The value of $r$ for each pair is shown as a color line in the histogram and as the background color of each CCG. The gray dashed line marks the value 1 which signals no correlation. The red line shows the average CCG across 1000 jittered surrogates (jitter time = 200 ms).

We selected the 100 pairs in an effort to illustrate the diversity of CCGs associated with the diverse correlation coefficient $r$ values that we measured. To do this, first, we chose a range of correlation coefficients (calculated as described in Section 2.3.4 of the Supplementary Information) from -0.18 to 0.2, which spans almost the whole range of $r$ in this experiment (Fig. 4B blue of the main text). Then, we divided this range into 100 equi-spaced correlation
values $R_n$ (where $R_1 = -0.18$ and $R_{100} = 0.2$), and for each value of the $R_n$ we selected the pair with the closest CC to $R_n$ (in order to avoid extremely sparse CCGs, we only considered pairs in which the geometric mean of the firing rates of both cells in the pair was above 1 Hz). Note that, because every value of correlation is equally represented in the figure, the sample of CCGs is not a random sample. Instead the sample is meant to illustrate the typical shapes of the CCGs associated with all the $r$ values that we observed in the experiment.

We labeled the $r$ of each selected pair by a color, with blue and red representing negatively or positively correlated pairs respectively. The range of selected $r$ values along with their color label is shown in the top panel of Fig. S3, underneath the $r$ histogram (identical to the one in Fig. 4B of the main text). The CCGs of the corresponding pairs are shown, as a matrix, in the bottom panel. The background color of the CCG represents the value of $r$ of this pair, and the pairs have been arranged so that the negative-to-positive range is spanned from the lower left corner to the upper right corner of the CCG matrix. On each plot we show the raw CCG (calculated as described in Section 2.3.6 of the Supplementary Information, with bin size = 10 ms) in white. The y-axis of each plot goes from zero to the maximum between two and 1.1 times the maximum of the CCG. The dashed light-gray line is at a value of one for all CCGs, and it represents the value that (except for finite-size fluctuations) the CCG would take, at all lags, if the two spike trains were stationary and independent. In red we show the average CCG across 1000 jittered surrogates for each pair of spike trains. Both the counting window (50 ms) and the jitter time (200 ms) were equal to those used in Fig. 4 of the main text.

Note that most negative $r$ values are associated with CCGs which have an approximately symmetric trough around zero. CCGs with a symmetric structure around zero have been interpreted as being the result of shared input. However, shared input can only possibly induce positive correlations, i.e., CCG peaks. Thus, all of the symmetric troughs and many of the symmetric peaks are likely to be caused by specific combinations of positively and negatively correlated inputs to the pairs in question, instead of by shared inputs.

### 3.4 Distance dependence of correlations

Since our silicon electrodes consist of 8 shanks separated by 200 $\mu$m each, the whole electrode array spans a considerable distance across the cortex (1.4 mm). In order to investigate whether the distance between two cells in a pair has some influence over the measured value of their spiking correlation, we recomputed correlation histograms with pairs recorded a given number of shanks away from each other (see Section 2.3.7 of the Supplementary Information) during
periods of cortical activation.

![Graph showing distance dependence of correlations]

**Figure S4: Distance dependence of correlations.** The two curves show the average across recording sessions (error bars indicate standard deviations) of the mean $\bar{r}$ of the correlation histogram (empty dots) and of the histogram width $\sigma_r$, as a function of the distance between the shanks where each of the neurons in the pair were recorded. Zero distance means both neurons were recorded in the same shank. The mean correlation $\bar{r}$ does not depend on the distance, but the correlation width $\sigma_r$ does (see text).

As shown in Fig. S4, only $\sigma_r$, but not $\bar{r}$, decreased with the distance ($\sigma_r$ slope=$-0.017$/mm, $p < 0.001$; $\bar{r}$ slope=$-0.002$/mm, $p=0.35$, p-values against a null hypothesis of no distance dependence, see Section 2.3.7). Thus, distant pairs tended to be more weakly correlated (for both signs of correlation), but there were similar numbers of positively and negatively correlated pairs at all distances. The distribution of correlations is wider (relative to its mean) for neurons recorded in the same shank.
References and Notes


13. By this we mean that keeping track of terms \( \sim O((A_{ij}^{\alpha \beta})^2) \) and \( \sim O(B_{ij}^{\alpha \beta}) \) does not change the leading order value of the population-averaged correlations that one obtains neglecting them.


