

A Distributed Neural Code in the Dentate Gyrus and in CA1

Highlights

- Position, direction of motion, and speed are encoded in CA1 and DG neurons
- Single-cell tuning only weakly predicts a cell's importance for position encoding
- Non-place cells contribute to position encoding
- Disrupting correlations between neurons leads to decreased decoding accuracy in CA1

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In Brief

Using high-resolution calcium imaging and machine learning techniques, Stefanini et al. studied how information about position, direction of motion, and speed is represented in the hippocampus. They show that neurons cooperate to encode this information, and that cells with easily interpretable responses are not necessarily the most important ones.



Article

A Distributed Neural Code in the Dentate Gyrus and in CA1

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SUMMARY

Neurons are often considered specialized functional units that encode a single variable. However, many neurons are observed to respond to a mix of disparate sensory, cognitive, and behavioral variables. For such representations, information is distributed across multiple neurons. Here we find this distributed code in the dentate gyrus and CA1 subregions of the hippocampus. Using calcium imaging in freely moving mice, we decoded an animal's position, direction of motion, and speed from the activity of hundreds of cells. The response properties of individual neurons were only partially predictive of their importance for encoding position. Non-place cells encoded position and contributed to position encoding when combined with other cells. Indeed, disrupting the correlations between neural activities decreased decoding performance, mostly in CA1. Our analysis indicates that population methods rather than classical analyses based on single-cell response properties may more accurately characterize the neural code in the hippocampus.

INTRODUCTION

The hippocampus has been studied extensively in experiments regarding navigation and spatial memory. The responses of some of its cells are easily interpretable because these tend to fire only when the animal is at one location in an environment (place cells). However, it is becoming clear that, in many brain areas, which include the hippocampus and entorhinal cortex, the neural responses are very diverse (Rigotti et al., 2013; Eichenbaum, 2018; Fusi et al., 2016; Hardcastle et al., 2017) and highly variable in time (Fenton and Muller, 1998; Ziv et al., 2013; van Dijk and Fenton, 2018). Place cells might respond at single or multiple locations in an orderly (grid cells) or disorderly way, and multiple passes through the same location typically elicit different responses. Part of the diversity can be explained by assuming that each neuron responds non-linearly to multiple

variables (mixed selectivity) (Rigotti et al., 2013; Kriegeskorte and Douglas, 2019; Saxena and Cunningham, 2019). Some of these variables may not be monitored in the experiment and, hence, contribute to what might appear as noise. A neural code based on mixed selectivity is highly distributed because some variables can be reliably decoded only by reading out the activity of a population of neurons. It has been shown recently that the mixed selectivity component of the neuronal responses is important in complex cognitive tasks (Rigotti et al., 2013; Fusi et al., 2016) because it is a signature of the high dimensionality of the neural representations. Place cell discharges are also highly variable (Fenton and Muller, 1998) to the extent that the variability, not the spatial tuning alone, can capture changes because of learning in a spatial memory task (Olypher et al., 2003; Kelemen and Fenton, 2010; van Dijk and Fenton, 2018). These recent studies naturally pose the question



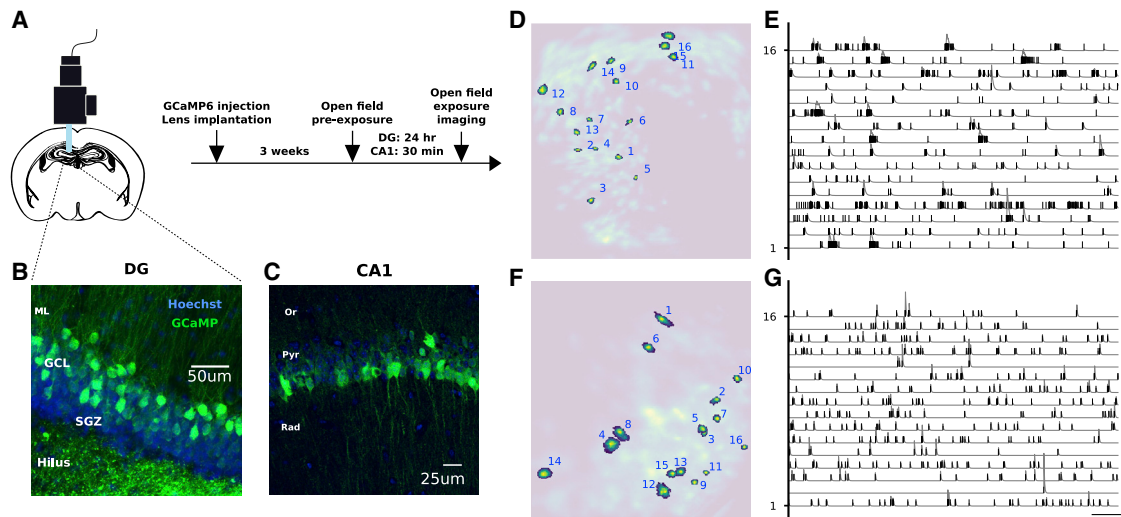


Figure 1. Calcium Image Recordings

(A) Experiment protocol. Mice were anesthetized with isoflurane and placed in a stereotactic apparatus. DG mice were then injected in the dorsal DG with a virus encoding GCaMP6m. CA1 mice were injected with GCaMP6f. Mice were then implanted with a GRIN lens, and a baseplate was attached to the skull at the optimal imaging places. Three weeks after surgery, they were checked for GCaMP expression with a miniaturized microscope (Inscopix, Palo Alto, CA) and procedures described previously (Resendez et al., 2016). The imaging plane was later assessed through histology (Figure S22).

(B) DG recording site. GCL, GC layer; SGZ, subgranular zone.

(C) CA1 recording site. Pyr: pyramidal layer; Or, stratum oriens; Rad, stratum radiatum.

(D–G) Automated signal extraction using CNMF-E (Zhou et al., 2018). The algorithm identifies the spatial (D, F) and temporal (E, G) components of the signal sources; i.e., putative cells. It uses a generative model of calcium traces and non-negative matrix factorization to separate actual signal sources from the background because of diffused neuropil fluorescence. The extracted spatial components are displayed in (D) (DG) and (F) (CA1), where a few representative ones are highlighted. The corresponding signals are shown in (E) (DG) and (G) (CA1), where vertical ticks correspond to the times of the inferred calcium events and gray lines to the temporal profiles (Figure S1). In line with electrophysiology studies, DG GCs are sparsely active but often in bursts (Pernia-Andrade and Jonas, 2014).

Scale bars, 1 min and 1 SD.

of how position is encoded within the population activity in the hippocampus. To answer this question, we used calcium imaging to record the activity of large populations of neurons in the dentate gyrus (DG), a region of the hippocampus in which the neural responses are highly sparse and diverse (Leutgeb et al., 2007; Danielson et al., 2016; van Dijk and Fenton, 2018), and in CA1, a region that has been studied extensively in relation to spatial navigation using electrophysiology (Moser et al., 2008; Harvey et al., 2009; Keinath et al., 2014; Agarwal et al., 2014) and imaging (Dombeck et al., 2010; Ziv et al., 2013).

We show that the position of a mouse freely exploring an environment can be decoded from the activity of a few tens of granule cells (GCs) of the DG with an accuracy comparable with that of CA1. Using machine learning techniques, we ranked neurons by their contribution to position encoding. We found that trial-averaged, single-neuron tuning properties are insufficient to predict a neuron's contribution to position encoding at the population level. Cells that were not spatially tuned according to a statistical test based on spatial information (non-place cells) also contributed to the population code, to the extent that position could be decoded from the ensemble of these untuned cells alone in both areas. We further found that neurons in the DG and CA1 reliably encoded other variables, such as the direction and speed of movement. These neurons were not distinct from the neurons that encoded position; i.e., the majority of neurons encoded multiple variables and contributed to all of them. We then found that destroying correlated activities among neurons

while maintaining their spatial tuning had an effect on decoding performance in CA1 but not in the DG. Taken together, these results show that the information encoded at the population level is far richer than at the single-cell level and allowed us to uncover the strong robustness of DG and CA1 spatial coding through the distributed nature of their neural representation.

RESULTS

We studied the neural code in the DG and in the CA1 area of the hippocampus of freely moving mice. We used miniaturized head-mounted microscopes to perform calcium imaging of GCs in the DG and of pyramidal cells in CA1. To image cell activity patterns, we injected a virus encoding the calcium indicator GCaMP6 and implanted a gradient index (GRIN) lens for chronic imaging (Figure 1A–1C). Four weeks after surgery, we imaged cellular activity while mice foraged for sucrose pellets in an open field arena. We then used a recently developed algorithm for reliably extracting the GCaMP signals from the raw videos, CNMF-E (Zhou et al., 2018; Figures 1D–1G). This algorithm separates local background signals resulting from changes in fluorescence in the neuropil from signals resulting from calcium concentration changes in individual cells. This was necessary to identify signal sources in our GC imaging data without introducing spurious distortions or correlations among cells because of artifacts. We identified a total of 1,109 DG cells across 3 animals, of which 352 (32%) were significantly tuned to position,

and a total of 863 CA1 cells across 3 animals, of which 38 (4%) were significantly tuned to position (STAR Methods; Figure S2).

The low fraction of place cells in CA1 seems to be in contrast with reports from previous studies in CA1 (Meshulam et al., 2017; Pfeiffer and Foster, 2013; Talbot et al., 2018; Ziv et al., 2013). However, modern tools for source extraction from calcium imaging can detect cells with very low activity, which are largely underestimated in electrophysiological recordings, as other recent studies have also suggested (Dipoppa et al., 2018; Tang et al., 2018). If one excludes these low firing rate cells from the analysis, the fraction of place cells becomes significantly higher (Figure S3; Table S1). Moreover, although calcium signal extraction may miss isolated spikes, this is likely less of an issue for DG GCs than pyramidal cells because the former are often active in burst, as electrophysiology studies have shown (Pernia-Andrade and Jonas, 2014) and as our data also show (Figure 1E). See Figure S3 and Table S1 for a brief review of the literature comparing firing rates in the DG and CA1 across studies.

The first step of our analysis was to assess whether the position of the animal is encoded in the recorded neural activity during mobility. We therefore removed all time bins in which the animal was slower than 2 cm/s for a period longer than 1 s after confirming by visual inspection that this procedure would exclude moments of immobility. To decode position, we discretized the x and y coordinates of the animal by dividing the arena into 64 regions (8 × 8 grid) (50-cm square arena for DG mice and 50 × 28 cm for CA1 mice). We then trained a battery of linear classifiers for each pair of discrete locations. Each session was divided into 10 1-min-long intervals, 9 of which were used to train the classifiers and the remaining ones to test them (10-fold cross validation). We used a majority rule (Bishop, 2006) to combine the outputs of the linear classifiers as an instantaneous estimate of the animal's location, using the center of the selected location as the decoded position.

In both areas, the median decoding error was comparable with the animal size, revealing for the first time that instantaneous position can be decoded from DG GC population activity (Figure 2). Our analysis of the CA1 data shows a comparable decoding accuracy in the DG and CA1 after correcting for the number of cells (Figure 2C; Figure S4). The accuracy was slightly higher than the one observed in previous studies in CA1 (Ziv et al., 2013). Different decoding strategies, such as decoding from raw calcium traces or events, produced similar results (Figure S6). The decoding error was found to weakly correlate to the speed of movement (Figure S7). To our knowledge, this is the first time that decoding of position from populations of DG cells has been reported.

We could also decode the direction of motion of the animal in both regions and its speed only in the DG. Speed was weakly correlated with the overall level of activity in the DG, and we could decode it in two animals of three using linear regression (Figures 2B and 2C). To decode the direction of motion, we divided the full range of possible directions into 8 angular bins and labeled time bins according to the instantaneous discrete direction of motion of the mouse (STAR Methods). To our knowledge, this is also the first time that decoding of direction and speed of motion from populations of the DG and CA1 cells has been reported, although direction tuning has been observed pre-

viously in CA1 pyramidal cells in rats (Acharya et al., 2016). We did not find differences in decoding performance for direction of motion between the DG and CA1 areas (Figure 2C).

To better characterize the neural code, we tried to determine which features of the response properties of individual neurons are important for encoding the variables we could decode. It is important to realize that these response properties could be dissociated from the contribution of a cell to the accuracy of a decoder that reads out a population of neurons. For example, there could be neurons that are only weakly selective to position and individually would not pass a statistical test for spatial tuning. However, when combined with other neurons, they can still contribute to position encoding. Alternatively, there are situations where the decoder might assign a large weight to neurons that are weakly selective or even not selective at all, but they are correlated to selective neurons. This situation can be illustrated with the intentionally extreme case shown in Figure 3, where we show how the responses of individual neurons can be dissociated from their importance for the decoder. A simulated animal visits two locations of the arena multiple times. The activity of two hypothetical neurons is represented in the activity space (Figure 3B), with the horizontal and vertical axes representing the activity of the first and the second neuron, respectively. At each pass through each location, the two neurons have different activity because of other variables that might also be encoded; e.g., the direction of movement, the speed of the animal, or other variables that are not under control in the experiment. Each point in the activity plot represents the activity of the neurons in a single pass. The responses of neuron 2 to the two different locations have the same distribution (Figures 3B). A cell with such response properties is untuned to space (a non-place cell), and, therefore, it is typically considered unimportant for encoding position. However, a linear decoder trained to decode the position of the animal can make use of the untuned neuron because of the correlations between the activities of the two neurons. Although the activity of neuron 1 is only partially predictive of the animal's location (the distributions partially overlap), by reading out neuron 2 together with neuron 1, it is possible to decode position with no errors using a linear decoder. In such a situation, the linear decoder would assign equal weights to the two neurons, as shown in Figure 3B.

In the real data, there might be a spectrum of different situations that are less extreme than the one illustrated in Figure 3, in which a decoder can take advantage of weakly tuned cells. Cells like the untuned one shown in Figure 3 or weakly tuned cells can “cooperate” with more tuned cells to more precisely encode a variable like position. This is a situation similar to the one shown in Figure 3, where the correlations between the activities of different neurons would be important. However, there might also be weakly tuned cells that are uncorrelated but, when combined, would contribute to the accuracy of a decoder. In both cases, the decoder can use the weakly tuned cells to improve its accuracy. Analogously, a downstream neuron can, in principle, harness the activity of weakly tuned neurons to read out the animal's position.

In our analysis, we took the perspective of such a readout neuron and analyzed the weights assigned to cells by our decoder to determine the importance of input neurons in a population for encoding position. The procedure we adopted was to

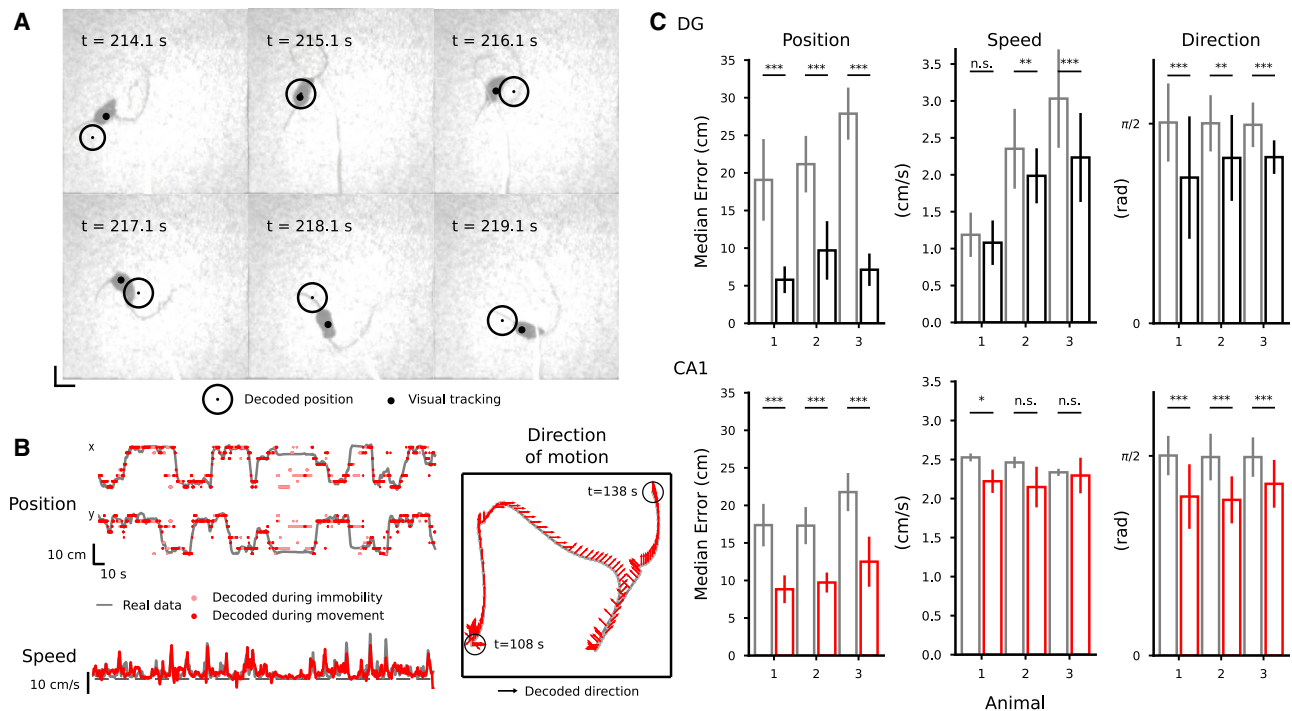


Figure 2. Decoding Position, Speed, and Direction of Motion

(A and B) Decoding results for a representative DG mouse. See also Videos S1 and S2.

(A) Selected frames of a video showing the arena and a DG animal from above. The black filled dot represents the mouse's actual position, and the black circle with the dot in the center is the decoded position, obtained with a probabilistic decoder that reads the activity of 317 DG cells (STAR Methods). Neural activity was pre-processed to identify putative calcium events, as explained in STAR Methods.

(B) Examples of decoding position, speed, and direction of motion (DG-representative mouse). Grey lines correspond to the real values of position and speed variables in the top left and bottom left panels, respectively, whereas the red dots correspond to their decoded values. The time bins marked in light red for position and direction of movement correspond to moments of immobility that were excluded from the training data. The gray line in the right panel corresponds to the position of the mouse, and the red arrows correspond to the decoded direction of motion in a 30-s time window.

(C) Decoding accuracy (top, DG; bottom, CA1). The decoding error for position and head direction is computed as the median of the distances computed between the decoded value in each time bin and the actual value of the decoded variable in the test data. For the direction of motion, the smallest angle between the decoded and the actual value is considered. The black and red vertical bars correspond to the mean over the 10-fold cross-validation (error bars correspond to SD). Gray, chance error obtained by decoding from shuffled data in a way that preserves the autocorrelations in the data (* $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, STAR Methods; Figure S5).

Number of cells: 483, 309, and 317 in DG mice; 371, 286, and 206 in CA1 mice.

See also Figures S4–S7 and S12.

first train the position decoder on each pair of locations and then to combine the resulting weights to obtain a single importance index (ω) for each cell (STAR Methods). Similar methods are used to assess the importance of individual features in a feature space (Haufe et al., 2014; Mladenović et al., 2004) and have been used recently to identify important synapses in learning models (Zenke et al., 2017). We then ranked the neurons according to this importance index and estimated the decoding accuracy for populations of 50 neurons (Figures 4A and S17) to assess the validity of our approach. The 50 neurons with the largest importance index indeed performed significantly better than the worst 50 neurons, although position could be decoded above chance level even from the worst neurons. The accuracy decreases progressively between the performance for the best and for the worst neurons, validating the method for ranking the neurons on the basis of the importance index. We also controlled that the ranking was stable within the session (Fig-

ure S8) and that it was not due to poor cell segmentation (Figure S24).

The observation that most neurons could contribute to decoding of position indicates that the neural code is highly distributed. Indeed, the importance index is rather similar for most of the cells. To quantify the distribution of importance across cells, we used the Gini coefficient, a quantity that is often used to represent wealth inequality in a country. A high Gini coefficient indicates high inequality, as in a dedicated code where few neurons strongly encode a given variable, whereas low values correspond to an equal distribution of resources, as in a distributed code. We observed low values in the DG and CA1, indicating that different neurons tend to contribute equally to the encoding of position, a signature of a distributed code rather than a situation where only a few cells are important (Figure S13).

Not too surprisingly, one important feature of an individual neuron is its average activity, which is strongly correlated with

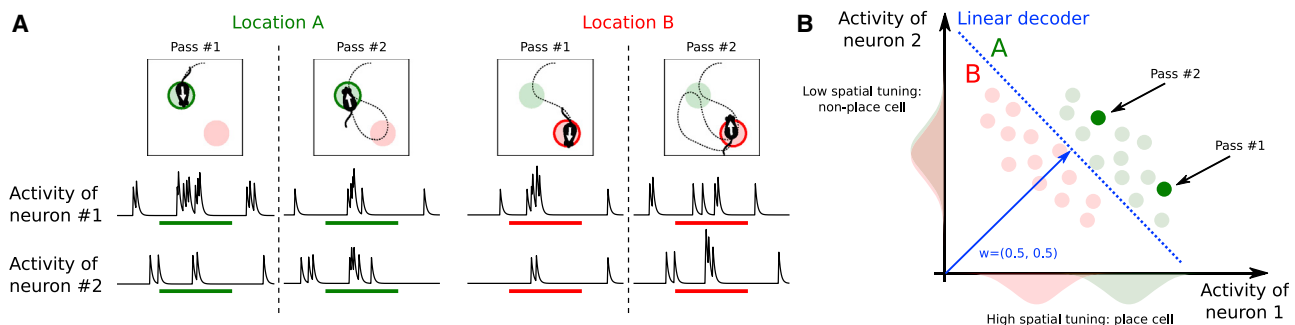


Figure 3. The Contribution of Untuned Cells for Encoding Position

We show an extreme situation where one simulated neuron has the same activity distribution when the animal is in two different locations of the arena. Hence, the neuron is not selective to position. Nevertheless, for a decoder, this neuron can be as important as other selective neurons because of its contribution to the population coding.

(A) Activity of two simulated neurons as a function of time. Top: the simulated animal visits the same discrete location twice (location A in green, location B in red). Bottom: simulated traces around the time of pass through each location. Different responses for the two neurons are elicited by different experiences; for example, because of the different direction of motion.

(B) Example of how place cells and non place-cells can be equally important for encoding the position of the animal. In the scatterplot, the x axis represents the average activity of the first neuron during one pass, and the y axis represents the activity of the second neuron. Each point in the space represents an average population response in a single pass. Their responses are typically highly variable and scattered around their mean values. The two neurons in the example have very different activity profiles; the first has a strong spatial tuning (place cell), whereas the second has only a weak tuning. The distributions of their activities in each location, reported along the axis, overlap only partially (neuron 1, place cells) or almost completely (neuron 2). Despite this variability in the single neuron responses, the neural representations at the population level are well separated, making it possible for a linear decoder (blue dashed line) to discriminate them with high accuracy. The resulting decoder's weight vector has two equal components corresponding to the importance of the two neurons in encoding position. In this example, both neurons are important for encoding position despite their very different tuning properties.

the importance index and, hence, to the overall ability to encode position (Figures 5A and 5B; Figures S9 and S19). However, inspection of the firing fields of Figure 4B indicated that there were no other obvious properties that predicted whether a neuron is important in the DG and CA1 neuron populations. We then identified which neurons were spatially tuned and called them place cells when the spatial information contained in their activity was statistically significant (see STAR Methods for details). The difference between the spatial information for the recorded activity and the spatial information obtained for shuffled data, properly normalized, is what we defined as significance of spatial information (SSI). It is indeed a measure used to assess whether a cell is a place cell relative to a null distribution (Allegra et al., 2019; Danielson et al., 2017; Meshulam et al., 2017; Panzeri et al., 2007; Skaggs et al., 1992).

From Figure 4B, it is clear that, in our data, there are non-place cells that have a large importance index. The animal's position could be decoded from these cells alone in the DG and CA1 (Figures 4C and S17). This indicates that the activity of the non-place cells contains some spatial information. However, because of noise and limited data, the activity of these cells did not pass the statistical test we adopted to characterize place cells.

Although the SSI is a property of a single cell, the importance index depends on the contribution of a cell to the population code. We thus analyzed the relation between each cell's SSI and its importance index. Although we did not find a one-to-one correspondence between SSI and importance index, the two quantities were correlated (Figures 5A–5C; Figure S19), indicating that some individual response properties are at least partially informative about the importance of a cell in encoding position. To compute the SSI, one has to compute the spatial in-

formation and subtract a baseline obtained by shuffling the activity. The spatial information without the baseline subtraction, which is sometimes used as a measure of the tuning of the cells, was actually negatively correlated with the importance index (Figure S9A; Kelemen and Fenton, 2010). However, the baseline was also negatively correlated with the importance index (Figure S9B). The net effect is that the correlations between SSI and importance index were positive. The negative correlations are a reflection of the sampling bias problem that affects cells with low activity (Panzeri et al., 2007). Low-activity cells tend to be more selective because the fluctuations of the activity are relatively large. However, these cells are typically unreliable (e.g., they fire at a particular location only during one pass); hence, their importance index is low.

We performed a similar analysis of importance for the direction of movement. In Figure 6 (see also Figure S18), we show that we could rank the cells according to their contribution to decoding (Figure 6A; Figure S18) and that the important cells were highly heterogeneous in their direction tuning (Figure 6B). Considering all recorded cells, we also found that a cell's activity correlated with the importance index for direction of movement in the DG and in CA1 (Figure 6C). We defined the significance of directional information (SDI) in a similar way as the SSI by comparing the mutual information between direction of motion and a cell's activity to a distribution obtained by shuffling the cell's calcium events in time. The importance index and this directional information were correlated in the DG and CA1 (Figure 6D; Figure S20).

All of these analyses indicate that single-neuron properties are only partially predictive of the importance of a cell for decoding. Moreover, the importance is not an intrinsic property of an

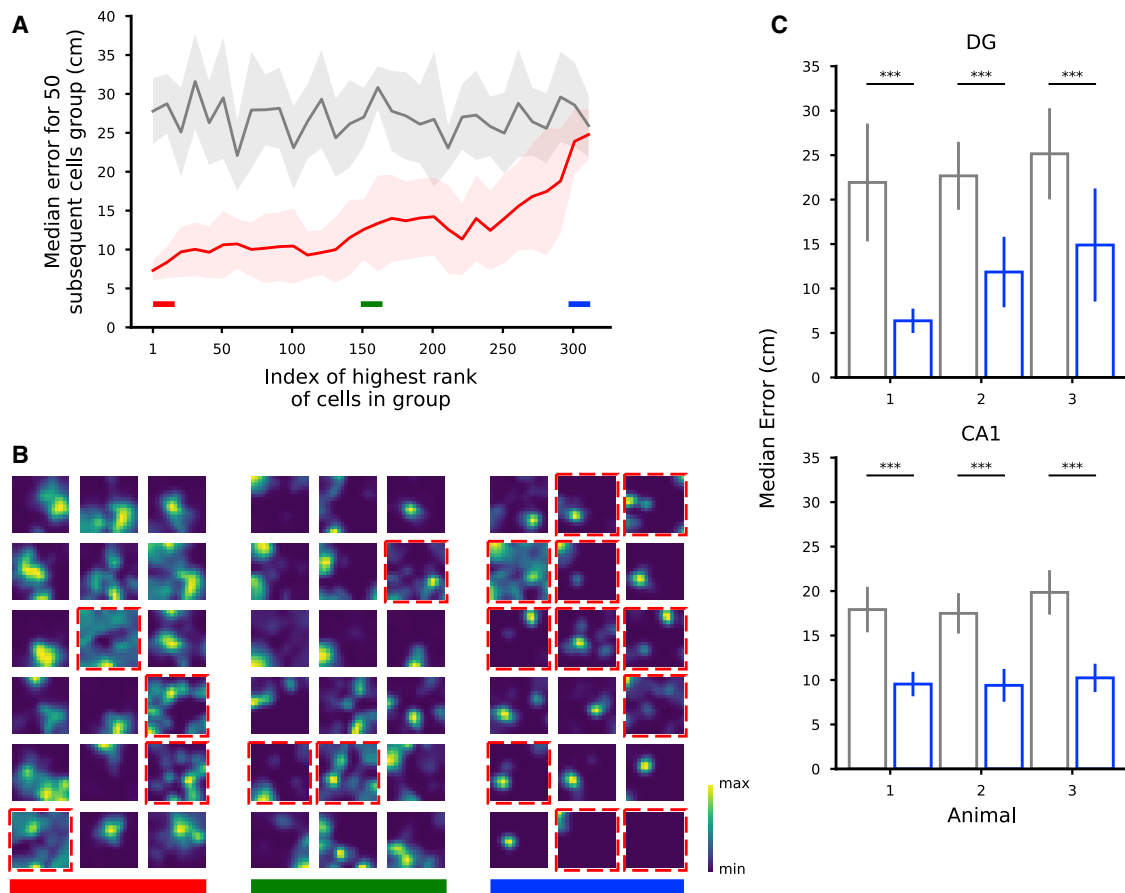


Figure 4. Ranking Neurons According to Their Contribution to the Decoding Accuracy for Position

(A) Validation of the importance index. We show the median error for various selections of 50 DG cells from a representative animal ranked by their importance index as obtained using the decoder's weight. Each point in the plot is aligned to the rank of the first cell in the selection (for example, the first dot corresponds to the selection of the first 50 cells from index 1 to index 50; the shaded region represents the SD for the 10-fold cross-validation). Gray: chance level and SD. As expected, the median error for the population of the 50 top-ranked (best) cells is much smaller than the median error for the last (worst) 50 ones.

(B) Spatial tuning maps for groups of 18 cells ordered by importance index (the same cells as in A). We ranked the cells using the importance index for position (STAR Methods). The three groups of best, mid, and worst cells are highlighted with the color bands in (A) for reference. The maps are normalized to the peak rate in each map. Dashed red borders indicate cells that do not pass the criteria for place cells using a commonly used statistical test for tuning (STAR Methods). Even among the most important cells, there appear some non-place cells (and vice versa). Similarly, some place cells appear in the group of cells with medium and low importance. The small fields in the group of low-importance cells are due to significantly lower activities (Figure 5).

(C) The position of DG and CA1 animals can be decoded from the activity of the non-place cells with a performance significantly higher than chance (vertical bars correspond to mean and SD, *** $p < 0.001$, STAR Methods).

Number of cells: 451, 208, and 98 in DG mice; 350, 277, and 198 in CA1 mice.

See also Figures S2, S3, S8, S10, and S24 and Table S1.

individual cell because it clearly changes depending on which other cells are part of the population of neurons that are used by the decoder. This is illustrated in Figure 3, where the untuned cell is important when combined with the cell represented on the horizontal axis, but it would be useless when combined with another untuned cell or with an uncorrelated tuned cell.

Because we could decode at least two variables from the neural activities, we wondered whether we could identify some form of specialization where segregated groups of neurons encoded different variables. In Figure 7, we report the importance index for the direction of movement versus the importance index for position (Figure 7A; Figure S21). The situation where different variables would be encoded by segregated populations of neu-

rons would predict a negative correlation between these two importance indices: cells with a large importance index for position should have a small importance for the direction of movement and vice versa. Instead, for both regions we analyzed, we found a positive correlation between the two quantities, with a higher correlation in CA1, suggesting that neurons that are important for encoding one variable are also important for encoding the other. This is partially explained by the fact that, for position and direction of movement, the most active cells tend to be the most important ones. However, when we regressed out the components explained by the activity, we still found a positive correlation between the importance indices of the two variables (Figure 7A). In addition, this could not be explained

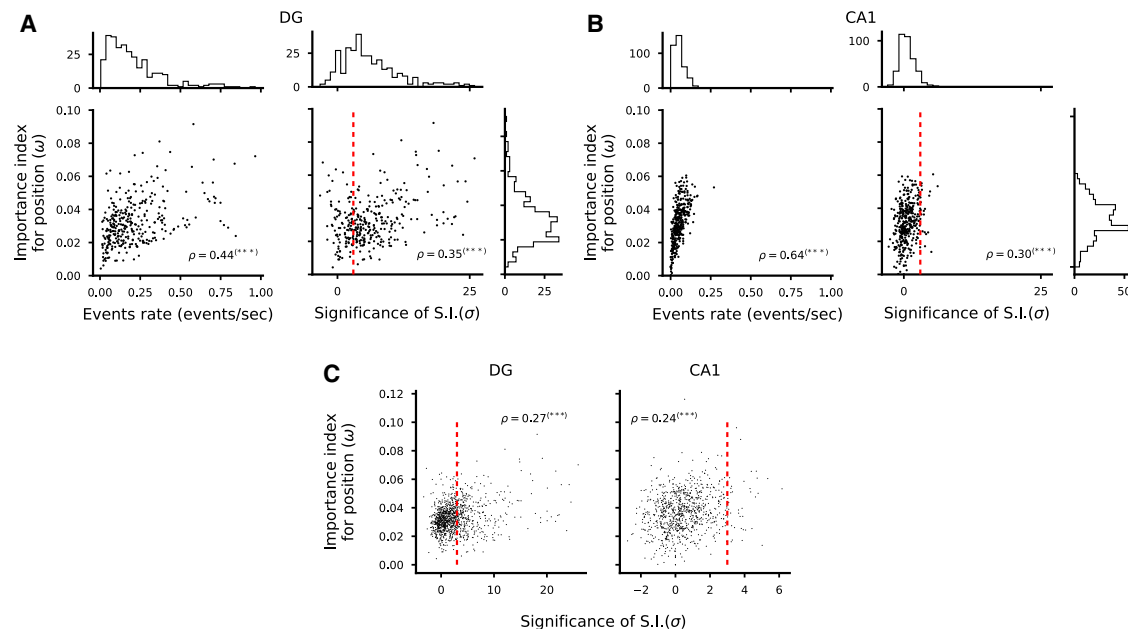


Figure 5. Correlation between Importance Index and Spatial Information

(A and B) Left: scatterplot of the importance index and overall cell activity for each cell in one representative animal. As expected, we found a strong correlation between these quantities because it is unlikely that a weakly active cell can contribute to decoding. Right: scatterplot of the importance index and statistical SSI with respect to independent random temporal shuffling of each cell's identified calcium events. DG cells are shown in (A) and CA1 cells in (B). Each dot corresponds to one cell in one representative animal. Pearson's correlation factor ρ between the plotted quantities are reported (Pearson's correlation significance, *** $p < 0.001$). Significant correlations are found between the analyzed quantities, but single-cell statistics only partially capture the information available at the population level. For each quantity, overall histograms are reported on the side of the plot. The dashed red line corresponds to a value of a threshold of 3 used to define place cells (STAR Methods).

(C) The same plots as in (A) and (B) but for all cells identified in all fields of view (FOVs) in DG (left) and CA1 (right) (Pearson's correlation significance, *** $p < 0.001$). See also Figures S9 and S13.

by a correlation between direction of movement and position (Figure S11).

We then focused on cells that had a high importance for one variable but not for the other as candidate specialized cells. However, we could decode position from the most important cells for encoding direction of motion and vice versa, showing that even the most important cells for one variable carry information about the other variable in both regions (Figure 7B). We conclude that, in CA1 and the DG, neurons have mixed selectivity to the variables we decoded, in line with recent studies in CA1 (Meshulam et al., 2017) and in the cortex (Rigotti et al., 2013; Fusi et al., 2016; Hardcastle et al., 2017; Lindsay et al., 2017; Discussion).

So far, we have shown that the code that is used to represent position is distributed; i.e., all active cells contribute to some extent to the population code. We therefore sought to see whether correlations between the activities of different neurons contribute to the decoding performance in a similar way as what we described in Figure 3. To understand the contribution of correlations to the encoding of position, it is important to distinguish different components, and in particular the correlations generated by the signal (i.e., the position of the animal) and those that can be considered noise (i.e., not related to encoding of position). The signal component is induced by the tuning properties of individual neurons. For example, two place cells

that have highly overlapping fields are going to be correlated because they tend to be co-active when the animal is at a particular location. Noise correlations represent the component that cannot be explained by the signal, and they are essentially due to the fact that every time the animal is at particular location, the neural response can be different. Noise correlations can be beneficial, detrimental, or irrelevant for the neural code (Abbott and Dayan, 1999; Schneidman et al., 2003; Brody, 1999). However, our initial hypothesis was that a large portion of the noise variance can be explained by the fact that neurons encode multiple variables besides position (Discussion). For example, the different points that encode the same position in Figure 3 might correspond to visitations where the head direction and/or the speed were different. In this case, destroying the correlations would result in a decrease or no change in decoding performance (Figure 8A).

We devised a procedure to shuffle the data in a way that destroys the noise correlations across neurons maintaining the spatial tuning of each cell (STAR Methods; Figure S14). We then studied the effect of this procedure on the decoding accuracy for position. At each pass through a location, we randomly picked the activity of a cell from the pool of recordings corresponding to that location and that cell (Figure 8B). We then corrected for the different time spent in each pass at the same location and repeated the procedure for all cells independently.

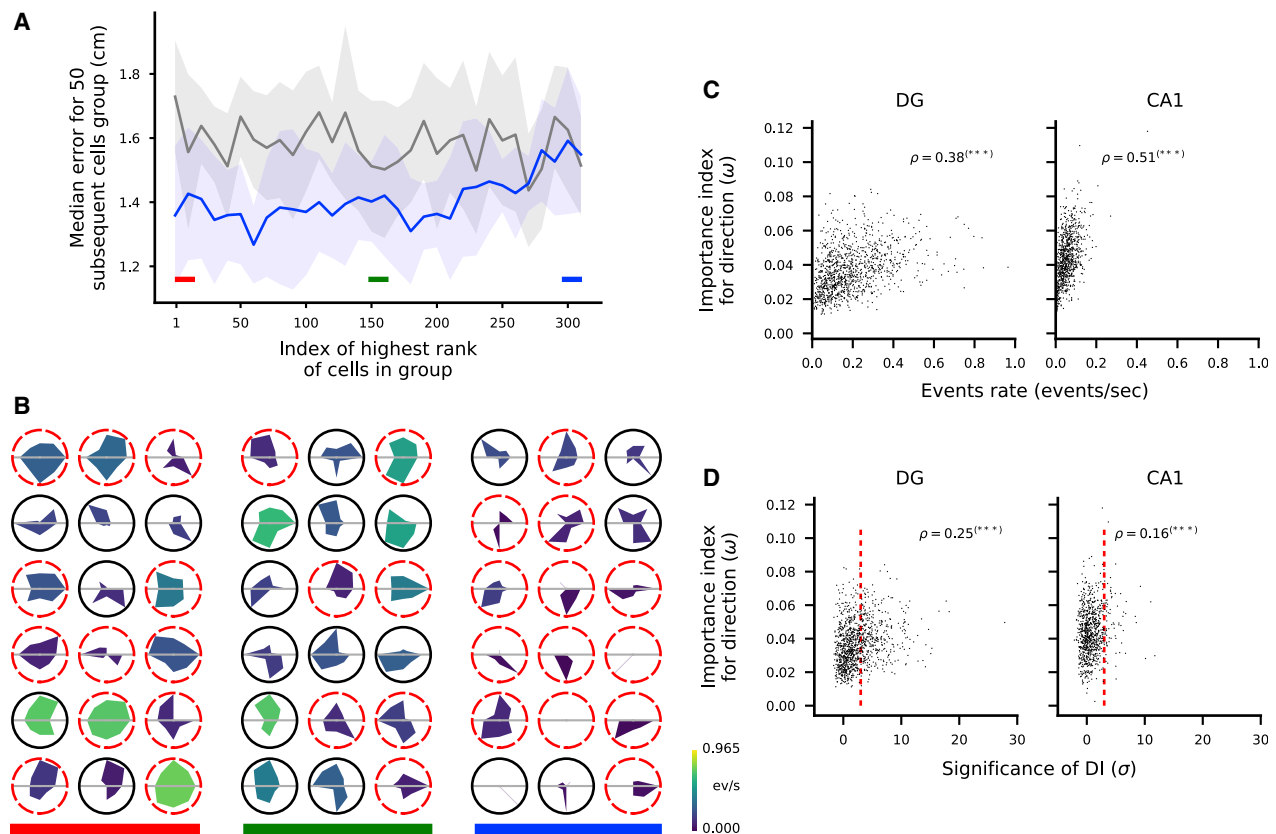


Figure 6. Ranking Neurons According to Their Contribution to the Decoding Accuracy for Head Direction

(A) Validation of the importance index as in Figure 4A, but we ranked the cells according to the importance index for decoding direction of motion (STAR Methods). (B) Tuning maps as in Figure 4B. Here we show the tuning for direction of motion of single cells as polar tuning maps for groups of 18 cells ordered by importance index. The area color represents the overall activity of the cell throughout the trial. Dashed red borders indicate cells that do not pass the criteria for significant direction tuning using a commonly used statistical test (STAR Methods). As in the case of position tuning, some untuned cells appear among the most important cells, and highly tuned cells appear among the least important.

(C) Scatterplots of cell activity and importance for position decoding for all identified cells combined from all FOVs in the DG (left) and CA1 (right). The Pearson correlation factor ρ between the plotted quantities is reported (Pearson's correlation, *** $p < 0.001$).

(D) Same as in (C) but for importance index for direction and significance of direction information.

By using this procedure, we effectively destroyed the noise correlations between neurons because, after this manipulation, each cell's activity was independent from the others. However, by restricting the manipulation to each discrete location, we did not alter the spatial tuning of the cells (Figure 8C) or the signal correlations among neurons induced by their tuning profiles. By comparing the performance of the decoder on the modified data with the one on the original data, we could then assess the contribution of the noise correlations to decoding. This is a direct test of the presence of a structure in the neural representations that is beneficial for representing information (Abbott and Dayan, 1999; Averbeck and Lee, 2006; Pillow et al., 2008; Eyherabide and Samengo, 2013). In 4 of the 6 analyzed animals, we found that the decoding error increased when correlations were destroyed through the shuffling procedure, revealing the importance of correlations (Figure 8D). The effect was very consistent in CA1 neurons, where performance was reduced by about 20%, whereas almost no effect was observed in the DG (Figure S14). Pairwise correlations were found to be lower in the DG than in

CA1 (Figure S16), and this may partially explain the main effect that disrupting correlations can lead to different changes in decoding accuracy in the two areas. However, it might only partially explain the effect because the correlations are not completely absent in the DG, and those we observed certainly changed after disrupting the noise correlations (for an analysis of how destroying correlations affects pairwise correlations and the importance index, see Figures S16 and S23).

DISCUSSION

Neurons in the DG and CA1 have rather diverse response properties, and often the responses are not easily interpretable (Danielson et al., 2016; Leutgeb et al., 2007). Despite this seemingly disorganized neural code, it is possible to decode, from the activity of a population of neurons, the position, speed, and direction of motion of the animal. Neurons respond to mixtures of the decoded variables, as observed in other highly cognitive brain areas (Rigotti et al., 2013; Fusi et al., 2016). The information

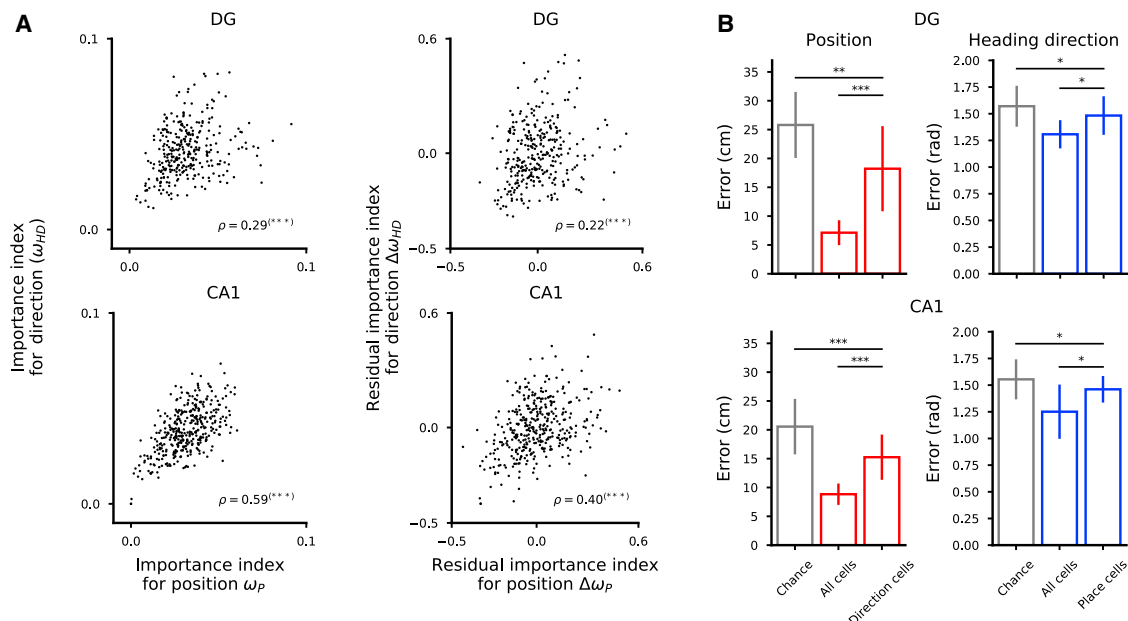


Figure 7. The Representations for Space and Direction of Motion Are Distributed in DG Cells and CA1 Cells

(A) Left: scatterplots of importance index for position and direction of motion (top, DG cells in one representative mouse; bottom, CA1 cells). Each dot corresponds to one cell for which we computed the importance index for the variables we decoded. Pearson's correlation values ρ are reported (Pearson's correlation, ***p<0.001). Right: same as left, but the component due to the correlation between importance index and cell activity was removed from the data. Residuals from linear regression are considered for both quantities. The residuals also show a positive correlation.

(B) Even the most important cells for encoding one variable carry information about the other variable. We show the decoding performance of position (left) and direction of motion (right) using the most important cells for direction and position (left and right plots, respectively). Vertical bars correspond to mean and SD (*p<0.05, **p<0.01, ***p<0.001, STAR Methods).

about these variables is highly distributed across neurons to the point where the responses of individual neurons are only weakly predictive of their contribution to the neural code. It is therefore crucial to consider neurons in one region of the brain as part of an ensemble to assess their importance for processing and transferring information about a particular variable.

One implication of such a distributed neural code is that it can be misleading to characterize the function of a brain region based only on the statistics of individual neuron properties. In the specific case of position encoding, for instance, it is not possible to conclude to what extent the position of the animal is encoded only by analyzing the tuning of individual cells to space. Indeed, populations of cells whose activities do not pass a selectivity criterion for space encoding (for example, through an information-theoretical approach), may still encode position via the ensemble activity patterns, as we showed by decoding position and direction of motion from untuned cells in the DG and CA1 regions of the hippocampus.

The population coding rescues the ability of these areas to encode position despite the sparsity of its activity and the variability of its representations. Here we show that, indeed, even a few tens of cells encode position with high precision in both analyzed areas. Furthermore, the decoding was accurate even when the model training and model test periods were separated by up to 18 min, indicating that, at the population level, the representations were stable despite the elevated variability of individual cells (Figure S12).

Our findings are in line with studies suggesting that session-averaged, single-cell statistics fall short in describing the activities of hippocampal cells. For example, although place fields are widely used to analyze DG activities in remapping studies (Leutgeb et al., 2007), it is only when sub-second network discharge correlations are taken into account in the analysis that memory discrimination signals can be revealed (van Dijk and Fenton, 2018). More importantly, we address one important question about the role of non-place cells in the CA1 and DG areas of the hippocampus. A recent work by Meshulam et al. (2017) used a maximum entropy model to describe the neural activity recorded in CA1. The model is constructed from the second-order statistics (the correlations between neurons), and it accurately predicts the activity of each neuron from the state of all other neurons in the network, regardless of how well that neuron codes for position. They conclude that correlation patterns in the CA1 hippocampus only partially arise from place encoding. Moreover, their results suggest that understanding the neural activity may require not only knowledge of the external variables modulating it (i.e., the position of the animal) but also of the internal network state. Our results indicate that the correlation patterns not due to position encoding can be partially explained by the encoding of other external variables (e.g., the direction of movement). However, it is likely that some components of the correlation patterns encode the internal state of the animal, as suggested by Meshulam et al. (2017). Our analysis also shows directly that non-place cells contribute to encoding of the position of the animal. This is partially due to the fact that some of the cells,

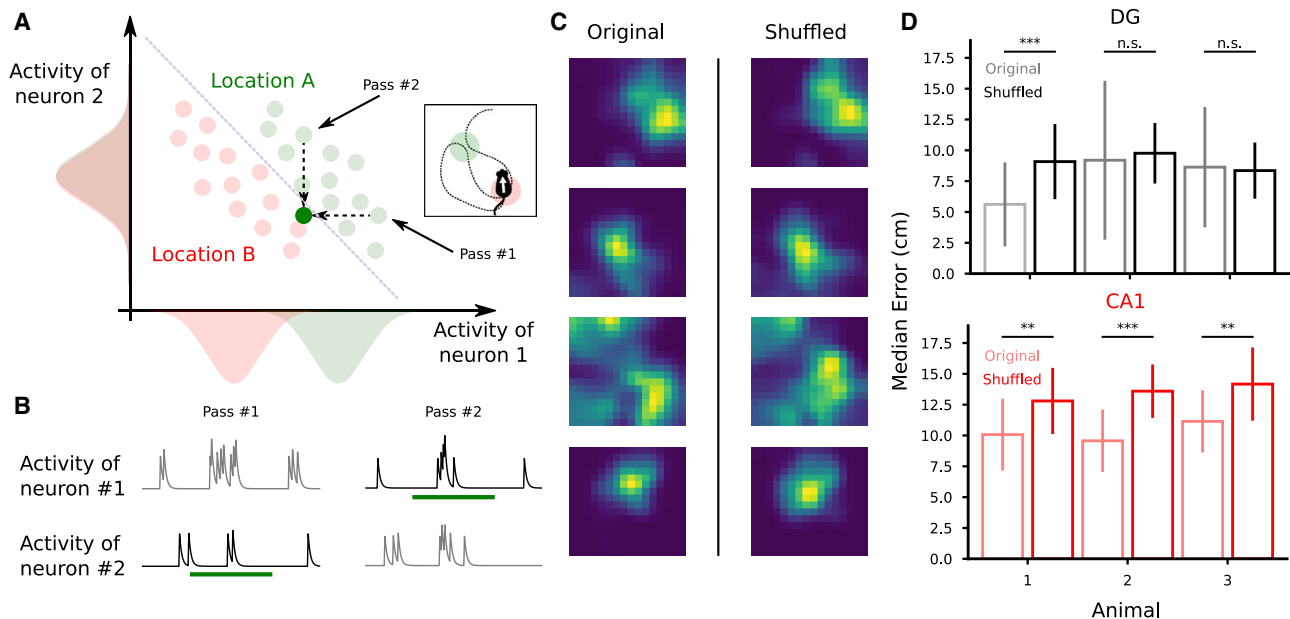


Figure 8. Destroying Correlations Affects Decoding Performance in CA1 but Not in the DG

For a Figure360 author presentation of this figure, see <https://doi.org/10.1016/j.neuron.2020.05.022>.

(A) Procedure to test the presence of correlations between cells. We recorded neural activity during multiple passes through location A (green). Then we generated a new recording by randomly choosing one of the activities recorded in that location for each cell independently. The green dot below the decoder's discrimination line in the activity plot corresponds to the newly generated activity. We repeated this procedure for all the passes through each location and for each cell independently, destroying the correlations between cells, if any. In the extreme case depicted in the cartoon, this procedure will introduce errors in decoding position because the generated activity will be classified as the wrong location.

(B) Cartoon activity traces for the two correlated neurons during the two passes through the same location. As described in (A), we destroyed correlations by choosing, for each neuron, the activity during one of the passes through that location and combined them to generate a new activity pattern corresponding to that location. In this example, we chose pass 2 for neuron 1 and pass 1 for neuron 2.

(C) Spatial tuning maps of four representative cells before (left) and after (right) applying the shuffling procedure to destroy correlations. The spatial tuning of the cells remain unaltered after the procedure.

(D) Decoding performance before (light colors) and after destroying correlations through shuffling (full colors). Top: DG animals. Bottom: CA1 animals. Vertical bars correspond to mean and SD (* $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, STAR Methods).

See also Figures S14, S15, and S24.

when taken individually, encode position only weakly and, hence, do not pass the statistical test for being categorized as place cells; the criterion used by Meshulam et al. (2017) to select place cells is similar to ours. However, non-place cells contribute to position encoding also because of their correlations with place cells. Indeed, when the noise correlations are destroyed, the decoding accuracy decreases in CA1. This is compatible with their observation that place and non-place cells belong to the same network when the patterns of correlations are considered, but it also goes beyond their analysis because it shows directly that correlations are important for encoding position. In conclusion, to study the neural code in one particular region of the brain, one has to consider all cells in a population because tuning properties that are based on single-cell statistics might not be sufficient to understand how task-relevant variables are encoded (Fusi et al., 2016; Kriegeskorte and Douglas, 2019; Saxena and Cunningham, 2019).

Poor Spatial Tuning and the Advantages of Mixed Selectivity

One of the important observations we discussed in the article is that there is a large proportion of cells that exhibit poor spatial tun-

ing. The computational advantage of poor spatial tuning can be understood only when one considers a situation where the neurons in a population encode not only the position of the animal but also several other variables (e.g., head direction, the velocity of the animal, and other unknown variables that are not under control in our experiment). This can be implemented in different ways. For instance, each variable could be encoded by a different group of highly specialized neurons. However, these representations are low-dimensional; hence, they greatly limit the number of combinations of input variables to which a linear readout or a downstream neuron can respond; see, for instance, Fusi et al. (2016). One simple example is a downstream neuron that must respond when the animal is looking at the center of the arena from two opposite corners. Such a simple situation is equivalent to the exclusive-or (XOR) problem in which the combinations of variables (position and head direction) that should activate the neuron (animal looking at the center of the arena) and those that should not (same positions, animal looking in the opposite directions) are not linearly separable. Instead, when head direction and position are mixed non-linearly, the neural representations can be high-dimensional, and a linear readout can separate any set of combinations of

inputs from the others. This is why, in most problems that involve at least two variables, mixing all relevant variables non-linearly is beneficial. Mixing position with other variables, like head direction, leads to relatively poor spatial tuning, but it also confers more flexibility to linear readouts, greatly increasing the computational ability of the network.

In our paper, we also showed that our data support the hypothesis for mixed selectivity, already entertained by previous research, in the specific case of spatial representations in the hippocampus. We verified this hypothesis by showing that neurons in the DG and CA1 encode multiple spatial variables, not only position, through decoding. In such a situation, it is possible, and very likely, to find that neurons that do not explicitly encode position; i.e., they do not have significant spatial tuning but are still important to discriminate between pairs of locations through correlations imposed by the geometry of the neural representations. In the cartoon in [Figure 3](#), for instance, we show how modulation of activity imposed by correlations can be used by a decoder to perfectly discriminate two locations (see also recent reviews in [Kriegeskorte and Douglas, 2019](#); [Saxena and Cunningham, 2019](#)). That modulation must therefore be intended as the result of the population response to combinations of variables that include position, speed, movement direction, and possibly other variables that were not under our control ([Allegra et al., 2019](#)). We modeled such a situation in [Figure S15](#) and found regimes in which correlations imposed by other variables help and situations where they do not have a significant effect on decoding performance, depending on the geometry of the neural representations. Taken together, our results show the advantages of a distributed code in that it can reliably represent multiple combinations of variables.

The Encoding Role of Correlations

Destroying correlations among neurons did not have a strong effect on decoding performance in DG neurons, but it consistently reduced decoding performance in CA1 data. Whether neural correlations are used in the population code is a long-standing question. In the data, it has been shown in the past that the pairwise correlations only accounted for about 10% of the information contained in neural activities ([Averbeck and Lee, 2006](#); [Latham and Nirenberg, 2005](#); [Schneidman et al., 2006](#)), whereas using models that exploit higher-order correlations can recover about 20% of information related to the stimulus in a population of retinal ganglion cells ([Pillow et al., 2008](#)). Here we showed that the disruption of correlations leads to a relatively modest but statistically significant decrease in decoding accuracy in CA1 but not in the DG.

These observations indicate that the correlations we are destroying should be considered signal correlations rather than noise correlations, at least in CA1. The variability across visitations can probably be explained by the fact that neurons encode multiple variables in a consistent way and may induce the observed neural correlations ([Wood et al., 1999](#); [Allegra et al., 2019](#)). This situation would be similar to the one discussed in [Figure 3](#) (e.g., passes 1 and 2 would correspond to two visitations of location A with a different direction of motion); i.e., the disruption of the correlations decreases the performance of the decoder. In [Figure S15](#), we show, in simulations, that this is indeed the case. We considered a model where the neural activity depends on

multiple variables; for instance, the position of the animal, the direction of motion, etc. Each variable can assume a discrete set of different values, and every set of values of the encoded variables defines one specific condition. We then constructed different neural representations by arranging the different conditions in the space of neural activities. In particular, we considered two scenarios, one with unstructured representations, where different conditions are represented by different random vectors in the activity space, and one with a kind of structured geometry that is beneficial for generalization across conditions ([Bernardi et al., 2018](#)). In both cases, the encoded variables are linearly separable; i.e., they can be decoded with a linear classifier. We then compared the linear decoder's performance before and after destroying the correlations, as we did in the real data, for different numbers of conditions in each scenario.

In most of the scenarios we simulated, the decoder performance is either disrupted, or it remains the same when the correlations are destroyed. The beneficial effect of the correlations is maximal when the representations are fairly unstructured. In the case of random representations, the effect is maximal for a certain number of conditions. This number depends on the number of encoded variables and on the number of values each variable can hold (i.e., the total number of conditions). Our experimental observations that show that the decoder's performance is disrupted more in CA1 than in the DG are compatible with a scenario in which the representations in CA1 are unstructured, similar to the simulated representations obtained with the random model. Our results also show that the representations in the DG are compatible with at least two scenarios: (1) they could be structured, as we described them in [Figures S15D–S15F](#), or (2) they could also be unstructured as in CA1 but with a different number of encoded variables, either very small or very large. It is important to stress that the scenarios studied in [Figure S15](#) are all plausible in the sense that they are based on representations that have already been observed in other studies ([Rigotti et al., 2013](#); [Bernardi et al., 2018](#)). However, the examples we report are certainly not exhaustive, and so we cannot exclude that other codes we did not consider may be more appropriate to describe DG and CA1 representations.

One alternative explanation for the difference between CA1 and the DG comes from the fact that the performance reduction that follows the disruption of correlations depends on the level of activity of the cells and that CA1 and the DG exhibit different levels of activity. However, in our data, this difference in activity levels could not fully account for the difference between CA1 and the DG in the effect of destroying correlations because we did not observe any performance reduction in the DG when the level of activity was matched to the one observed in CA1 ([Figure S14](#)).

Our simulations where multiple variables are encoded are compatible with recent models of the hippocampus that emphasize its role in memory compression ([Gluck and Myers, 1993](#); [Benna and Fusi, 2019](#)), and memory prediction ([Dayan, 1993](#); [Stachenfeld et al., 2014, 2017](#); [Gershman et al., 2012](#); [Recanatesi et al., 2018](#); [Whittington et al., 2019](#)). For all of these models, the neural representations in the hippocampus are constructed by learning the statistics of the sensory experiences to generate compressed representations of the memories to be stored or, when focused on temporal sequences, to generate a prediction

of the next memory (successor representation). Future theoretical work will establish more quantitatively whether this scenario is fully compatible with our observations and what the different roles of CA1 and DG could be in this compression process.

Average Activity in the DG Is Larger Than in CA1

One of the observations that requires some discussion is that the average activity in the DG is larger than that in CA1 in our data. This might sound surprising, but a careful review of the literature shows that our observations are compatible with other studies (Figure S3; Table S1). Indeed, the average firing rate that is reported varies from study to study, depending on the recording technique, the type of experiment, and whether rats or mice were employed. Our conclusion is that our results fall within the range of values reported in the existing literature. The review reported in the Table S1 is not exhaustive by any means, but we believe it is highly representative of the existing literature.

Conclusion

Our results strengthen the hypothesis that the neural code in the DG and CA1 area of the hippocampus is highly distributed and that it is important to analyze it using a population approach (Fenton et al., 2008; Meshulam et al., 2017; van Dijk and Fenton, 2018). Analysis of the averaged response properties of individual neurons is certainly informative, but it is not sufficient to characterize the neural code of a brain area. Critically, the role of the DG and CA1 area of the hippocampus should be revisited in light of our observations. The methods we propose will shed new light on the general role of other brain areas implicated in high-level cognitive functions, such as spatial navigation, and in which place cells are not observed.

STAR★METHODS

Detailed methods are provided in the online version of this paper and include the following:

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SUPPLEMENTAL INFORMATION

Supplemental Information can be found online at <https://doi.org/10.1016/j.neuron.2020.05.022>.

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AUTHOR CONTRIBUTIONS

Conceptualization, S.F., R.H., M.A.K., F.S., and L.K.; Methodology, M.A.K., R.H., and G.D.S.; Software, F.S. and L.K.; Formal Analysis, F.S., L.K., and S.F.; Investigation, J.H.J., M.A.K., J.C.J., and N.I.W.; Resources, J.H.J., G.D.S., M.A.K., and R.H.; Data Curation, J.C.J., F.S., and M.A.K.; Writing – Original Draft, F.S. and S.F.; Writing – Review & Editing, F.S., S.F., M.A.K., and R.H.; Visualization, F.S.; Supervision, M.A.K., S.F., and R.H.; Funding Acquisition, F.S., M.A.K., S.F., and R.H.

DECLARATION OF INTERESTS

The authors declare no competing interests.

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STAR★METHODS

KEY RESOURCES TABLE

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Bacterial and Virus Strains		
AAVdj-CaMKII-GCaMP6m	Stanford Vector Core	Cat#GVVC-AAV-89
AAV-DJ-CaMKIIa-GCaMP 6f	Stanford Vector Core	Cat#GVVC-AAV-90
AAV1-Syn-GCaMP6f.WPRE.SV40	U Penn Vector Core	Cat#AV-1-PV2822
Experimental Models: Organisms/Strains		
C57BL/6J mice	Jackson Laboratory	CAT#000664; RRID:SCR_004633; http://www.jax.org/index.html
Software and Algorithms		
Ethovision XT 10	Noldus	https://www.noldus.com ; RRID:SCR_000441
Mosaic	Inscopix	https://www.inscopix.com
MATLAB	Mathworks	https://www.mathworks.com/products/matlab.html ; RRID:SCR_001622
CNMF-E	Zhou et al., 2018	https://github.com/zhoup/CNMF_E
Scikit-learn	Pedregosa et al., 2012	https://scikit-learn.org
Decoding Algorithm	This paper	N/A
Spatial information	Skaggs et al., 1992	N/A

RESOURCE AVAILABILITY

Lead Contact

Further information and requests for resources should be directed to and will be fulfilled by the Lead Contact, Stefano Fusi (sf2237@columbia.edu).

Materials Availability

This study did not generate new unique reagents.

Data and Code Availability

The datasets and analysis code supporting the current study are available from the lead contact on request.

EXPERIMENTAL MODEL AND SUBJECT DETAILS

Mice

All procedures were conducted in accordance with the U.S. NIH Guide for the Care and Use of Laboratory Animals and the institutional Animal Care and Use Committees at New York State Psychiatric Institute and UCSF. Adult male C57BL/6J mice were supplied by Jackson Laboratory and were used beginning at 8–12 weeks of age. Mice were co-housed with litter mates (2–5 per cage). Mice were maintained with unrestricted access to food and water on a 12-hour light/dark cycle.

Viral Constructs

For calcium imaging, AAVdj-CaMKII-GCaMP6m was packaged and supplied by Stanford Vector Core at titers of $\sim 4 \times 10^{12}$ vg/ml, and AAV1-Syn-GCaMP6f.WPRE.SV40 was packaged and supplied by U Penn Vector Core at titers of $\sim 2 \times 10^{12}$ vg/ml.

METHOD DETAILS

Calcium imaging

Mice were prepared for *in vivo* calcium imaging as previously described ([Resendez et al., 2016](#)). For dorsal DG imaging, mice were injected with a virus encoding GCaMP6m (AAVdj-CaMKII-GCaMP6m) at the following coordinates: -1.95 AP, 1.4 ML, 2.2 , 2.1 , 2.0 , 1.9 DV, ~ 90 nl per site) and a ~ 1.0 mm diameter, ~ 4 mm long GRIN lens (Inscopix, Palo Alto, CA) was implanted at (-2.0 AP, -1.4 ML,

−1.95 DV). For dorsal CA1 imaging, mice were injected with a virus encoding GCaMP6f (AAV1-Syn-GCaMP6f.WPRE.SV40) at the following coordinates: (−2.15AP, 1.85ML, −1.55, −1.65DV, 256nl per site) and a GRIN lens was implanted at (−2.15AP, 1.30ML, −1.30DV). Three weeks after surgery, mice were checked for GCaMP expression with a miniaturized microscope (Inscopix, Palo Alto, CA) with procedures previously described (Resendez et al., 2016). Anesthetized mice were checked for GCaMP+ neurons and a baseplate was attached to the skull at the optimal imaging plane. For all the mice presented in this report the histology confirmed the adequate placement of the lens (Figure S22). For dorsal DG imaging, one week later, mice were imaged during foraging in an open field task and were habituated to the room and enclosure (30min), then 24 hours later they were imaged as they foraged for sucrose pellets in an open field enclosure (50cm²). For dorsal CA1 imaging, mice were imaged during exploration of an open field enclosure. Mice were habituated to the room and enclosure (10 minutes) and then imaged 30 minutes later. Imaging frames were recorded with nVista acquisition software (Inscopix, Palo Alto, CA), and time-synced behavior was acquired using EthoVision XT 10. Calcium imaging videos were acquired at 15 frames per second with 66.56 ms exposure.

QUANTIFICATION AND STATISTICAL ANALYSIS

Behavior data pre-processing

The behavior was recorded using a webcam (Logitech) mounted on the ceiling about 3 feet above the arena. The instantaneous position of the animal was then extrapolated from the video using custom code written in Python using the Scikit-image library (version 0.13.0). We first applied a 9 points piecewise affine transformation to correct for barrel camera distortions. We then applied a smoothing filter with a Gaussian profile to reduce the effect of pixel intensity noise due to low lighting and low image resolution and applied a threshold to the gray-scale converted image to get a few contiguous regions of pixels as candidate animal tracking. We then used a method based on the determinant of the Hessian to identify blobs in the pre-processed images and verified that the largest blob was consistently found to be corresponding to the animal silhouette. Hence, we used the center of the largest blob as the tracked position of the mouse. We further temporally aligned the position data to the imaging data using linear interpolation and smoothed them with a 7 frames time window. Lastly, we identified the time bins in which the speed of the animal was lower than 2 cm/s for more than 1 s and discarded them from the analysis, unless specified.

Signal extraction and spike deconvolution

All calcium movies were initially processed in Mosaic (Inscopix, Palo Alto, CA) for spatial binning and motion correction and subsequently analyzed using a recently developed software algorithm written in MATLAB (Mathworks) called CNMF-E (Zhou et al., 2018). Briefly, the algorithm separates the large, low-frequency fluctuating background components from the signal produced by multiple sources in the data, allowing the accurate source extraction of cellular signals. It involves a constrained non-negative matrix factorization problem optimized for endoscopic data whereby calcium temporal dynamics and the shape of spatial footprints are used as constraints. It includes 3 main steps which are iterated: obtain a first estimate of spatial and temporal components of single neurons without direct estimation of the background; estimate the background given the estimated neurons' spatio-temporal activity; update the spatial and temporal components of all neurons while fixing the estimated background fluctuations. In each of these steps, manual intervention guided by visual inspection based on temporal profile and spatial footprint shape allowed to further improve the quality of the signal extraction. The result of this process consists of a list of deconvolved calcium events for each cell with associated time-stamp and magnitude and the convolved trace with a calcium decay profile estimated for each cell independently on the basis of the raw trace.

For our decoding analysis, we did not use the original traces, rather we used the events extracted with CNMF-E convolved with an exponential kernel. The time constant of the kernel was optimized to maximize the cross-validated position decoding performance and was equal for all neurons. The results depend only weakly on the kernel time constant, and qualitatively are the same (see Figure S1). All other quantities derived from the calcium traces were computed using the calcium events, unless specified otherwise, and therefore their values do not depend on the shape of the kernel.

Place fields and heading direction tuning

Place fields for each extracted source were constructed in a manner similar to established method applied to electrophysiology data (Leutgeb et al., 2007). We used the calcium events of each cell as its putative spiking activity. We then summed the total number of events that occurred in a given location, divided by the amount of time the animal spent in the location and smoothed using a Gaussian kernel centered on each bin. The rate in each location x was estimated as

$$r(x) = \frac{\sum_{i=1}^n g\left(\frac{s_i - x}{h}\right)}{\int_0^T g\left(\frac{y(t) - x}{h}\right) dt}$$

where g is a Gaussian smoothing kernel, $h = 5$ sets the spatial scale for smoothing, n is the number of events, s_i is the location of the i -th event, $y(t)$ the location of the animal at time t and $[0, T]$ the period of the recording. In this and all subsequent analysis we removed the time bins in which the animal had a speed of less than 2 cm/s for more than 1 s, unless specified otherwise. Similarly, for heading

direction tuning, we first discretized the directions of motion into 8 angular bins of 45 degrees each and then computed the mean event rate for each cell in each of the 8 bins.

Spatial information statistics

To quantify the statistical significance of the rate maps we measured their specificity in terms of the information content of cell activity (Allegra et al., 2019; Danielson et al., 2017; Skaggs et al., 1992). We used a 16x16 square grid and computed the amount of Shannon information that a single event conveys about the animal's location. The spatial information content of cell discharge was calculated as a mutual information score between event occurrence per cell and animal position or equivalently using the formula:

$$SI = \sum_{i=1}^N p_i \frac{r_i}{r} \log_2 \frac{r_i}{r}$$

where i is the spatial bin number, p is the probability for occupancy of bin i , r_i is the mean event rate at bin i and r is the overall mean event rate. We applied the same formula to the direction of motion after discretizing the full angle to 8 bins of 45 degrees. For both measures, we corrected for the sampling bias problem in information measures (Panzeri et al., 2007) using shuffled distributions of event occurrences as follows. For each cell independently, we discretized time, generating a long vector of 0's (no event) and 1's (event). We then randomly permuted the elements of this vector and for each permutation we computed the resulting spatial information. We repeated this procedure 1000 times, therefore obtaining 1000 values of spatial information to which we compared the original information content (Ziv et al., 2013; Danielson et al., 2017; Meshulam et al., 2017; Allegra et al., 2019). We labeled a cell as place cells or a heading direction cell if the original value of spatial information exceeded 3 sigmas from the shuffled distribution (see also Figures S2 and S3 and Table S1).

Decoding position

For all the datasets, unless otherwise specified, we used 10-fold cross validation to validate the performance of the decoders. We divided the trial in 10 temporally contiguous periods of equal size in terms of number of datapoints after excluding datapoints corresponding to immobility. We then trained the decoders using the data from 9 of them and tested on the remaining data. To decode the position of the animal, we first divided the arena into 8x8 equally sized, squared locations. We then assigned at each time bin the label of the discrete location in which the animal was found. For each pair of locations, we trained a Support Vector Machine (SVM) classifier (Cortes and Vapnik, 1995) with a linear kernel to classify the cell activities into either one of the two assigned locations using all the identified cells, unless specified otherwise. We used only the data corresponding to the two assigned locations and to correct for unbalanced data due to inhomogeneous exploration of the arena we balanced the classes with weights inversely proportional to the class frequencies (Pedregosa et al., 2012). The output of the classifiers was then combined to identify the location with the largest number of votes as the most likely location (Bishop, 2006). For each choice of train and test set, we computed the median decoding error as the median of the physical distance between the center of the decoded discrete location and the actual position of the mouse in each time bin of the test set, unless otherwise specified. The final decoding performance was then computed as the mean of all the median errors across the different choices of train and test sets.

Chance level decoding performance

To assess the statistical significance of our decoders, we computed chance distributions of decoding errors from shuffled data. This can be done in different ways and we chose a conservative procedure that maintained some structure of the data while destroying the relation between the behavior, e.g., the animal's position, and the calcium event time series. Briefly, we discretized time obtaining a vector of positions (or other behavioral variables). We then flipped this vector in time (e.g., the last data point of position became the first datapoint and vice versa) and then shifted the whole vector in time by a random amount in a torus, i.e., points that went beyond the time limits of the data were reinserted from the other side. This procedure destroys the relation between behavior and neural activity, but preserves the time correlations of both the time series representing behavior and, of course, the time series of the neural activity (which remains untouched). For each random shift, we trained a new decoder on the data and pooled all the errors obtained. We finally assessed the statistical significance of the decoding error for the 10-fold cross-validation of the original data by comparing it to the distribution of errors obtained from the manipulated data using the non-parametric Mann-Whitney U test, from which we obtained a p value of significance. We implicitly assumed that the 10-folds are statistically independent (the 10 testing time intervals considered for the 10-folds did not have any overlap). This is the procedure we used in all our figures unless specified otherwise.

Another less conservative shuffling strategy is to manipulate the calcium events. We assigned a random time bin to each calcium event for each cell independently while maintaining the overall density of calcium events across all cells, i.e., by choosing only time bins in which there were calcium events in the original data and keeping the same number and magnitude of the events in each time bin. This method destroys spatial information as well as temporal correlations but keeps the overall activity across cells. We verified that our results did not depend on the particular strategy adopted (see Figure S3 and Table S1).

Decoding the direction of motion

One behaviorally relevant quantity that was available to us was the direction of motion of the animal. Unfortunately, the visual tracking didn't allow for a direct estimate of the direction of motion. The head direction was also not easily measurable so we resorted to using the positional information to extract the direction of motion. We computed it by using two subsequent datapoints in the animal x-y trajectory. We discretized the values into 8 angles and then applied similar decoding strategies as for position decoding, i.e., we used a battery of linear-kernel SVM decoders to distinguish between pairs of angles after balancing the dataset through class weighting. We report the median error in radiant on the left-out data of the 10-fold cross validation. We applied the methods described above for position decoding for assessing the statistical significance of the results.

Decoding speed

To decode the speed of movement of the animal we first computed the speed of motion using two consecutive positions and assigned the computed speed to the later time bin among the two. To decode the instantaneous speed of motion we used Lasso (Tibshirani, 1996), a linear regression analysis method that minimizes the sum of squared errors while selecting a subset of the input cells to improve decoding accuracy and interpretability of the results. We applied the methods described above for position decoding for assessing the statistical significance of the results.

Bayesian decoder

The Bayesian decoder is a theoretical optimal probabilistic method to decode information for the activity of the neural population. It is based on the Bayes rule and has been extensively used to decode position from electrophysiological data from the hippocampus (Zhang et al., 1998; Wilson and McNaughton, 1993). Briefly, if x is a discrete position in the arena, we estimate the position using:

$$P(x|r_t) = P(r_t|x)P(x) / P(r_t)$$

where r_t is the activity of the population at time t and assuming independent activity of different neurons. The algorithm computes $P(x|r_t)$ for all discrete positions and assigns the predicted position to the one that maximizes it:

$$\hat{x}_t = \underset{x}{\operatorname{argmax}} P(x|r_t).$$

Importance index

The importance index was introduced to quantify the contribution of each cell in a population to the decoding of a given quantity. We applied a modified version of a traditional method for feature selection in machine learning. In our analysis, a feature of the input space consists of one DG cell. Feature selection is performed using the weights of the decoder after fitting model to the data. In our case, since we employed multiple decoders, one for each pair of physical location in the arena, we introduced a method to combine the weights assigned to the cells by each decoder. We defined the importance index of cell i as:

$$\omega_i = \sum_k \frac{|w_{ik}|}{\sum_j |w_{jk}|}$$

where w_{ik} is the weight of the k -th decoder assigned to the i -th cell (and equivalently w_{jk} is the weight of the k -th decoder assigned to the j -th cell). The indices i, j run through all cells in the population and k runs through all the binary decoders.

Procedure to destroy correlations

To destroy correlations without impacting the spatial information of single neurons, we considered multiple passes through single discrete locations in the arena. We then shuffled the calcium event occurrences between different passes in the same location. Importantly, we corrected the activity of each pass for the different amount of time spent in each pass by randomly sampling events instead of replacing them in order to reduce artifacts. We verified that the correction does not impact decoding when sampling from the same pass (see Figure S14).

Software

The data analysis has been performed using custom code written in Python (version 2.7.12) and routines from the Scipy (ver. 0.19.0), Numpy (ver. 1.11.3) and the Scikit-learn (0.19.1) (Pedregosa et al., 2012) packages. The source extraction has been performed using MATLAB (Mathworks, R2016a) and CNMF-E (Zhou et al., 2018) using the same parameters across animals and minimal manual intervention only for obvious non-cell like sources based on spatial profile shape and temporal profile dynamics.