

Supporting Information

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SI Methods

Reimagine Condition. During the scanning session, 45 reimagine trials were randomly interspersed. This condition (not analyzed as part of the current experiment) consisted of 45 previously constructed imagined future events. In the prescan session a week earlier, participants had constructed future events in response to experimenter-supplied generic person, place, and object cues. In the scanning session, participants were shown these cues and spent the 8-s trial imagining each already-constructed future event, followed by the same 4-s rating scale for detail.

MRI Acquisition. MRI data were collected on a Siemens Avanto 1.5 Tesla MRI scanner. For the anatomical scan, a magnetization-prepared rapidly acquired gradient echo (MP-RAGE) sequence was used, whereas the functional scans were collected with a T2*-weighted echo planar imaging (EPI) sequence (repetition time (TR) = 2,000 ms, echo time (TE) = 23 ms, matrix size = 64 × 64, field of view (FOV) = 200 mm, flip angle = 90°). Twenty-five coronal oblique slices (5 mm thick) were acquired in an interleaved fashion, perpendicular to the long axis of the hippocampus and covering the whole brain. Five functional runs were acquired for each subject, with 270 time points per run (9 min). During the functional scans, the task stimuli were projected onto a screen in the scanner room and reflected into a mirror within the head coil. All participant responses were collected using a four-button response box.

Preprocessing of MRI Data. To allow the longitudinal magnetization to reach equilibrium, the initial four images from each run were discarded. The functional images were preprocessed using SPM8 (Wellcome Trust Centre for Neuroimaging, London, UK), correcting for slice timing differences, adjusting for movement across scans by realigning and unwarping, coregistering with the anatomical scan, normalizing (using normalization parameters derived during segmentation) the images to the Montreal Neurological Institute (MNI) template (resampled at 2 × 2 × 2 mm voxels), and spatial smoothing with an 8-mm full-width half maximum Gaussian kernel. One participant's data contained some small movement artifacts; because a set of five trial-type sequences were generated with Optseq2 (1) and therefore 25 participants were required to maintain a complete counterbalance of these sequences, this participant's data were repaired via interpolation using ArtRepair Software (<http://web.mit.edu/swg/software.htm>). The time-series functional (f)MRI data were high-pass filtered to account for low-frequency drifts; a cutoff value of 128 was used. An AR(1)-model was used to account for possible serial correlations.

Localization and Visualization of fMRI Activations. MNI coordinates of peak voxels were converted to Talairach space for the purposes of localization, and regions of activation were localized in reference to a standard stereotaxic atlas (2). Coordinates in all tables are reported in MNI space. For all figures, thresholded activation maps from SPM8 were overlaid on a standard anatomical template image (ch2better.nii) using in MRICron (3). For those figures depicting activity from analyses focused on hippocampal activity, thresholded whole-brain maps were masked to show only voxels falling within the hippocampus (using an anatomical mask of the hippocampus from MARINA; ref. 4) and then overlaid on a standard anatomical template. Percentage of signal change data

were extracted from clusters of activation using the REX toolbox for SPM8. Note that as the option to plot group level parametric effects is not available in SPM8, a new fixed-effects model was used to compute percentage of signal change data for low detail (ratings 0–1) and high detail (ratings 2–3) future events. From each subject's first-level model, β -values (averaged across all active voxels within a 3-mm sphere) were extracted from each condition of interest in each run. These data were then converted to percentage of signal change by dividing by the value of the constant of that same run and multiplying by 100. Once rescaled, the percentage of signal change values for each condition from each run in that subject were averaged to create one value per condition per subject. These values were used to compute the mean percentage of signal change (and SE) for each condition of interest.

Functional Connectivity: Seed Partial Least Squares Analysis (PLS). PLS is a covariance-based multivariate technique that enables examination of connectivity between regions of interest (“seeds”) and activity across the whole brain over time and whether there are similarities or differences in connectivity across experimental conditions (5–7). For this analysis, we extracted mean percentage of signal change (using REX as described above) from two seed regions within the right hippocampus ($xyz = 20 -12 -16; 34 -26 -8$). These data were entered as seeds in the PLS analysis. First, correlations were computed between the signal in each seed region and all other voxels for each condition across subjects. The resulting correlation maps were stacked and analyzed with singular value decomposition, producing a set of orthogonal latent variables (LVs), each containing three matrices: (i) a singular value indicating the amount of covariance for which the LV accounts; (ii) a linear contrast between the seeds and the conditions that codes the effect depicted by voxels; and (iii) the singular image of voxel weights or “saliences” (akin to a component loadings in principle components analysis) that are proportional to the covariance of activity with the linear contrast. Each extracted latent variable successively accounted for a smaller portion of the covariance (as indicated by the singular value) and are thus determined by the strength of effects in the dataset.

The statistical significance of each LV was assessed by use of a permutation test. This procedure involved randomly reassigning each subject's data to experimental conditions, rerunning the PLS analysis, and determining the new singular value for each reordering; this was done 500 times. Thus, significance reflects the probability on the basis of the number of times the singular value from the permuted data exceeds the original singular value (7). A threshold of $P < 0.05$ was used. Note that unlike univariate analyses, the significance of whole-brain patterns of activity are determined in one single analytic step, and thus correcting for multiple comparisons is not necessary.

The reliability of the voxel saliences was computed using bootstrap estimation of the SE. This procedure involves randomly resampling subjects with replacement, rerunning the PLS analysis, and determining new saliences for each sampling. After carrying this procedure out 300 times, the SE of the saliences was computed (7). Clusters of five or more voxels in which bootstrap ratios were greater than ± 4.5 (roughly equal to a Z score, or a P value of $P < 0.0001$), were considered to represent reliable voxels.

