

Supplementary Information

Connectome as Compiler: Reading Computation
from Connectivity and then Writing it Back

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1 Overview

This Supplementary Information provides the exact first-order identity underlying the response geometry used in the main text and fourteen supplementary figures supporting Figs. 2–6. The proposition below makes explicit the relation among the finite-horizon controllability Gramian, response covariance, and orthogonal response modes under the task-aligned response window used throughout the analyses.

2 The first-order Gramian–covariance–mode identity

At a specified operating point s^* , let

$$D = \text{diag}(1 - s^{*2}), \quad F = D\alpha A, \quad g = Db.$$

Here, the square of s^* is taken elementwise. The following proposition concerns the first-order local system and is exact for the finite response horizon stated below.

Proposition 1 (First-order Gramian–covariance–mode identity). For $p = 1, \dots, K$, define the task-aligned propagated-input responses

$$h_p = F^{p-1}g, \quad R^{(1)} = \begin{bmatrix} h_1^\top \\ \vdots \\ h_K^\top \end{bmatrix} \in \mathbb{R}^{K \times N}.$$

Let u_t be a zero-mean, temporally white scalar input satisfying $\mathbb{E}[u_{t-p}u_{t-q}] = \delta_{pq}$, and define the truncated first-order state

$$\tilde{s}_t^{(K)} = \sum_{p=1}^K h_p u_{t-p}.$$

The node-space Gram matrix is $W_c^{(1)} = R^{(1)\top} R^{(1)}$. Its target-space counterpart is $R^{(1)} R^{(1)\top}$. These matrices satisfy the following identities.

(i) **Finite-horizon controllability Gramian.**

$$W_c^{(1)} = \sum_{j=0}^{K-1} F^j g g^\top (F^\top)^j,$$

which is the K -step controllability Gramian of the local propagated-input pair (F, g) .

(ii) **Response covariance.**

$$\text{Cov}\left(\tilde{s}_t^{(K)}\right) = W_c^{(1)}.$$

(iii) **Orthogonal response modes and effective dimension.** If the thin singular-value decomposition is $R^{(1)} = V\Sigma U^\top$, then

$$W_c^{(1)} = U\Sigma^2 U^\top, \quad R^{(1)} R^{(1)\top} = V\Sigma^2 V^\top.$$

Thus $W_c^{(1)}$ and $R^{(1)} R^{(1)\top}$ have the same nonzero eigenvalues σ_r^2 . The columns of U are orthogonal state-space response modes, the columns of V are orthogonal input-history target modes, and

$$\text{Cov}\left(U^\top \tilde{s}_t^{(K)}\right) = \Sigma^2$$

on the nonzero response subspace. Consequently, the first-order response dimension can be evaluated in either space:

$$\kappa_1 = \text{tr}\left[W_c^{(1)}(W_c^{(1)} + \epsilon I_N)^{-1}\right] = \text{tr}\left[R^{(1)} R^{(1)\top} (R^{(1)} R^{(1)\top} + \epsilon I_K)^{-1}\right] = \sum_r \frac{\sigma_r^2}{\sigma_r^2 + \epsilon}.$$

The response-mode coordinates are uncorrelated under the stated white-input assumption. Their statistical independence would additionally require an appropriate distributional assumption, such as Gaussian input in the linearized system.

Proof. Because $h_{j+1} = F^j g$, direct substitution gives

$$R^{(1)\top} R^{(1)} = \sum_{p=1}^K h_p h_p^\top = \sum_{j=0}^{K-1} F^j g g^\top (F^\top)^j,$$

establishing the finite-horizon controllability identity in (i)¹. The white-input assumption gives

$$\begin{aligned} \text{Cov}\left(\tilde{s}_t^{(K)}\right) &= \mathbb{E}\left[\tilde{s}_t^{(K)} \tilde{s}_t^{(K)\top}\right] \\ &= \sum_{p=1}^K \sum_{q=1}^K h_p h_q^\top \mathbb{E}[u_{t-p} u_{t-q}] \\ &= \sum_{p=1}^K h_p h_p^\top = W_c^{(1)}, \end{aligned}$$

which proves (ii). Finally, $R^{(1)} = V\Sigma U^\top$ implies $R^{(1)\top} R^{(1)} = U\Sigma^2 U^\top$ and $R^{(1)} R^{(1)\top} = V\Sigma^2 V^\top$.

Rotating the state into the columns of U therefore diagonalizes its covariance on the response subspace, and applying the ridge filter $x/(x + \epsilon)$ to the shared nonzero eigenvalues gives the stated expression for κ_1 , proving (iii).

For a temporally white scalar input with variance σ_u^2 rather than one, the same calculation gives

$$\text{Cov}\left(\tilde{s}_t^{(K)}\right) = \sigma_u^2 W_c^{(1)}.$$

The simulations use $u_t \sim \text{Uniform}[-1, 1]$, for which $\sigma_u^2 = 1/3$; the unit-variance statement in the proposition isolates the response geometry from this scalar input normalization.

Task-aligned response window. The implemented window begins with $h_1 = g$ and ends with $h_K = F^{K-1}g$. Under the state convention in the main text, h_p is the response of s_t to the target u_{t-p} . The response window therefore aligns exactly with the simulated targets $u_{t-1}, \dots, u_{t-K}$ and yields the K -step Gramian of (F, g) . A shifted window beginning with Fg would omit the response to the most recent target and is not used in the reported analyses.

Second-order qualification. Once the variance-scaled second-order response matrix $R^{(2)}$ has been constructed, its node-space Gram matrix is $W_c^{(2)} = R^{(2)\top} R^{(2)}$. The target-space matrix $R^{(2)} R^{(2)\top}$ has the same nonzero eigenvalues, so the corresponding singular-value identity for κ_2 is exact. However, $R^{(2)}$ itself is obtained from a finite degree-two local expansion over the 36 delayed-product targets. It is therefore a truncated second-order response representation, not a standard linear controllability Gramian or a claim about the full covariance of the nonlinear reservoir state.

3 Supplementary figures

The fourteen figures below support the results in Figs. 2–6. Figures S1–S6 report the raw associations, test sensitivity to the stated model conditions and input maps, assess response-order specificity, replicate the analysis in an independent human cohort, and compare the response dimensions with conventional graph descriptors. Figures S7 and S8 show the individual targets underlying the nonlinear-mixing profile and test the reproducibility of held-out recovery profiles across input streams. Figures S9 and S10 test regional prediction and the sensitivity of regional capacity shifts to more closely strength-matched controls. Figures S11 and S12 test response-gradient specificity and resolve the resulting capacity changes across individual delayed targets. Figures S13 and S14 test whether targeted response changes produce corresponding simulated-capacity changes and replicate sparse gain recovery in HCP-Aging.

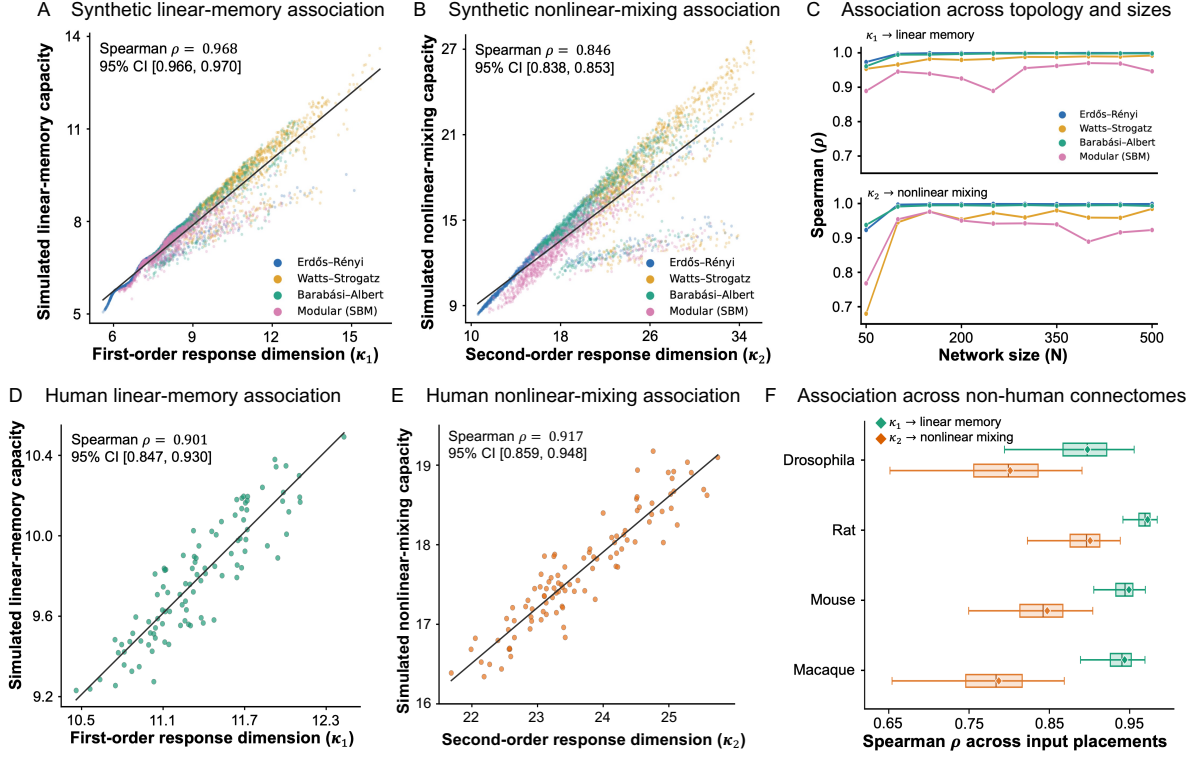


Figure S1: Response dimensions are associated with their matched simulated capacities. Each response dimension is associated with its corresponding simulated capacity across synthetic reservoirs, human connectomes, and input maps within non-human connectomes. **A. Synthetic linear-memory association.** κ_1 is associated with simulated linear-memory capacity across 4,000 synthetic reservoirs (Spearman $\rho = 0.968$). **B. Synthetic nonlinear-mixing association.** κ_2 is associated with simulated nonlinear-mixing capacity in the same reservoirs ($\rho = 0.846$). **C. Association across topology and sizes.** Spearman ρ exceeds zero for both matched associations in all 40 topology-by-size groups. **D. Human linear-memory association.** κ_1 is associated with simulated linear-memory capacity across 100 HCP-YA connectomes ($\rho = 0.901$). **E. Human nonlinear-mixing association.** κ_2 is associated with simulated nonlinear-mixing capacity across the same connectomes ($\rho = 0.917$). **F. Association across non-human connectomes.** Across 60 Gaussian input maps within each fixed connectome, ρ ranges from 0.898 to 0.972 for κ_1 and linear memory and from 0.787 to 0.901 for κ_2 and nonlinear mixing. Diamonds show observed correlations, boxes show the interquartile range of 10,000 input-map bootstrap estimates, and whiskers show 95% intervals.

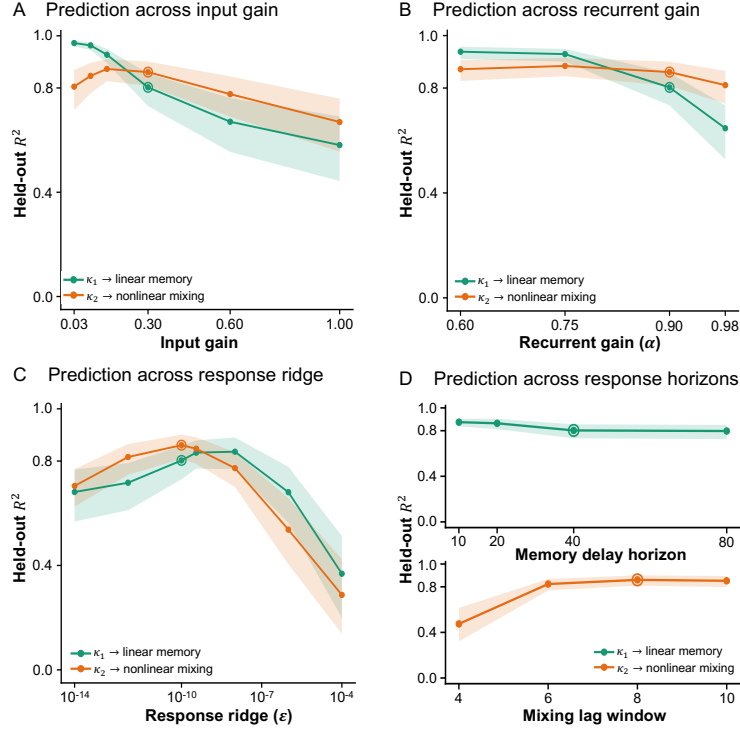


Figure S2: Response dimensions predict matched simulated capacities across model conditions. Both response dimensions predict their matched simulated capacities across the tested model conditions, although predictive accuracy varies among settings. **A. Prediction across input gain.** Held-out prediction is shown as input gain varies from 0.03 to 1.00 around the Fig. 2 value of 0.30. **B. Prediction across recurrent gain.** Held-out prediction is shown as recurrent gain varies from 0.60 to 0.98. **C. Prediction across response ridge.** Held-out prediction is shown as the response ridge varies from 10^{-14} to 10^{-4} . **D. Prediction across response horizons.** Memory horizons span 10, 20, 40, and 80 delays, and mixing horizons span 4, 6, 8, and 10 lags. Green denotes κ_1 predicting linear memory and orange denotes κ_2 predicting nonlinear mixing across 100 HCP-YA connectomes. Points show participant-held-out R^2 , bands show 95% participant-bootstrap intervals, and open rings mark the Fig. 2 settings.

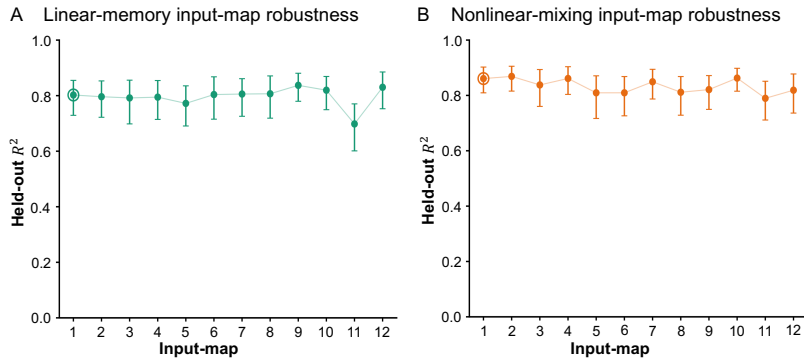


Figure S3: Response dimensions predict matched simulated capacities across input maps. Both response dimensions predict their matched simulated capacities across 12 prespecified spatial input maps. **A. Linear-memory input-map robustness.** κ_1 predicts simulated linear-memory capacity across all input maps. **B. Nonlinear-mixing input-map robustness.** κ_2 predicts simulated nonlinear-mixing capacity across the same maps. Points show participant-held-out R^2 , error bars show 95% participant-bootstrap intervals, and open rings mark the Fig. 2 input map.

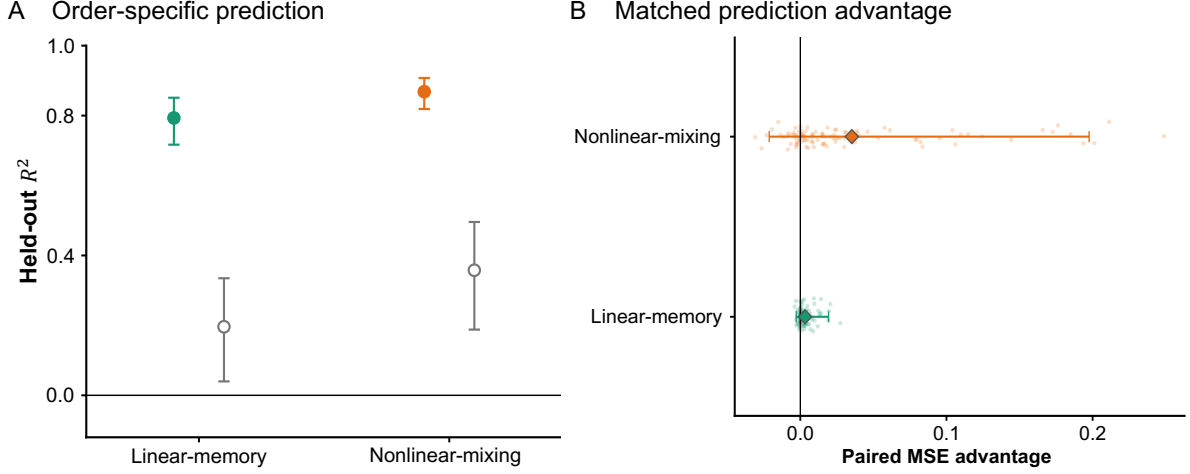


Figure S4: Response dimensions preferentially predict functions of the corresponding input order. For each capacity, the response dimension of the corresponding input order predicts more accurately than the response dimension of the other order. **A. Order-specific prediction.** For linear memory, held-out R^2 is 0.793 with κ_1 and 0.196 with κ_2 ; for nonlinear mixing, it is 0.868 with κ_2 and 0.358 with κ_1 . **B. Matched prediction advantage.** The corresponding response order has lower participant-level squared error for both capacities ($p = 4.0 \times 10^{-5}$ for each). Filled and open symbols in **A** denote corresponding and other response orders, and error bars show 95% participant-bootstrap intervals. In **B**, paired MSE advantage is $\text{MSE}_{\text{other}} - \text{MSE}_{\text{corresponding}}$, so positive values favor the corresponding response order; pale points represent participants, diamonds show means, and error bars span the 2.5th–97.5th percentiles.

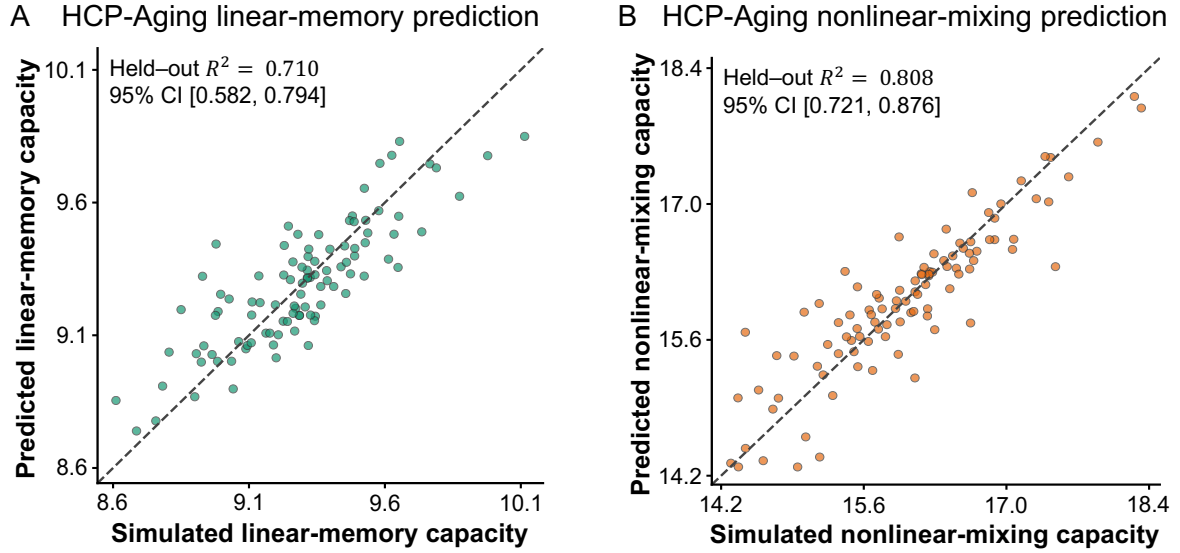


Figure S5: Response dimensions predict matched simulated capacities in an independent human cohort. Both matched predictions replicate in 100 HCP-Aging connectomes. **A. HCP-Aging linear-memory prediction.** κ_1 predicts simulated linear-memory capacity (held-out $R^2 = 0.710$, 95% CI [0.582, 0.794]). **B. HCP-Aging nonlinear-mixing prediction.** κ_2 predicts simulated nonlinear-mixing capacity (held-out $R^2 = 0.808$, 95% CI [0.721, 0.876]). Dashed lines mark equality. Models are fitted without the evaluated participant, and 95% intervals resample participants while retaining their held-out predictions.

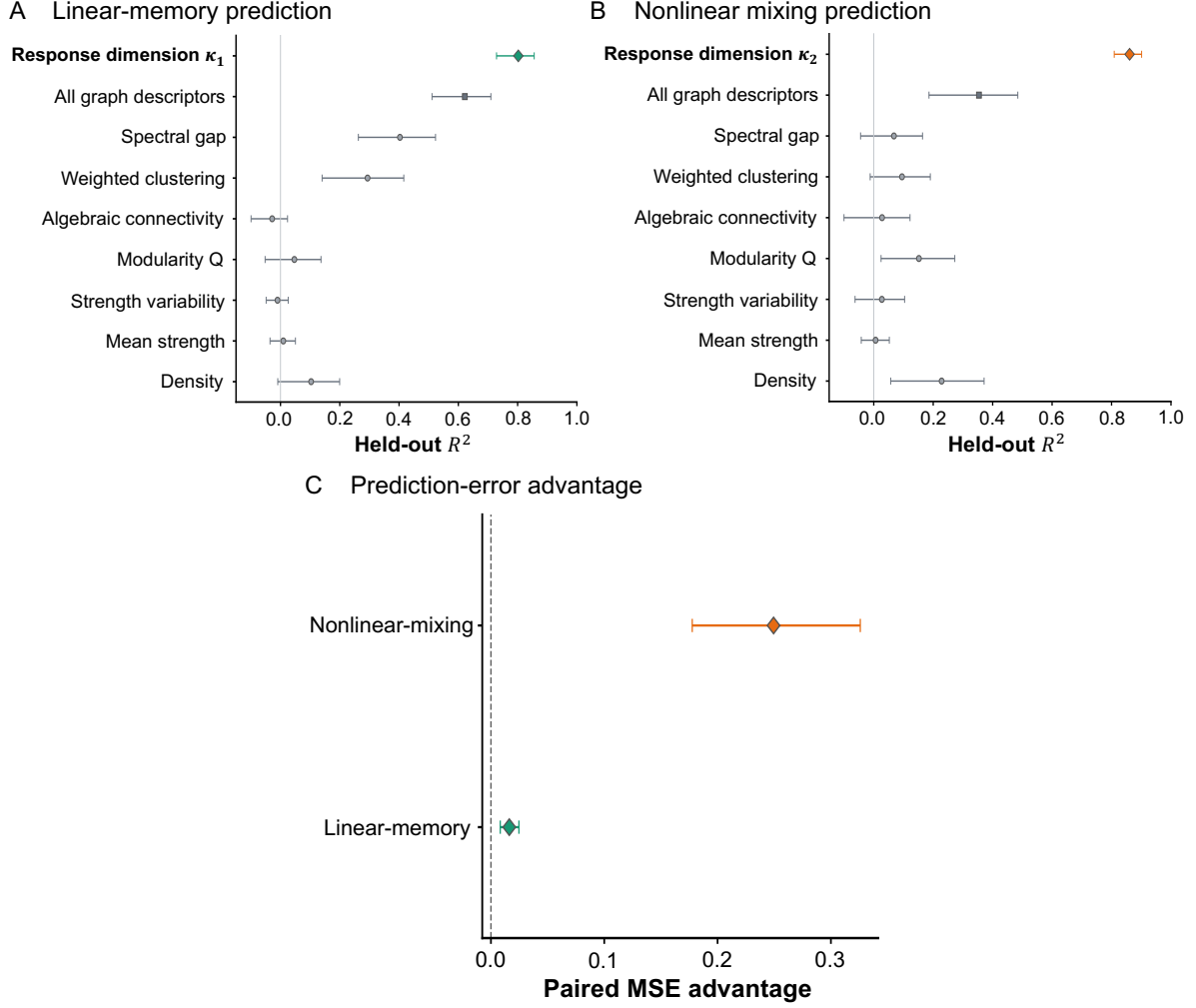


Figure S6: Response dimensions predict simulated capacities more accurately than graph descriptors. Across 100 HCP-YA connectomes, each response dimension yields higher held-out R^2 than the tested graph models and lower participant-level squared error than the combined graph model. **A. Linear-memory prediction.** κ_1 predicts linear-memory capacity more accurately than the graph models. **B. Nonlinear mixing prediction.** κ_2 predicts nonlinear-mixing capacity more accurately than the graph models. **C. Prediction-error advantage.** Both response dimensions have lower mean participant-level squared error than the combined graph model. In **A** and **B**, points show held-out R^2 ; error bars in all panels show 95% participant-bootstrap intervals. Paired MSE advantage is $\text{MSE}_{\text{graph}} - \text{MSE}_{\text{response}}$, so positive values favor the response dimension ($p = 2.0 \times 10^{-4}$ for linear memory and $p = 2.0 \times 10^{-5}$ for nonlinear mixing).

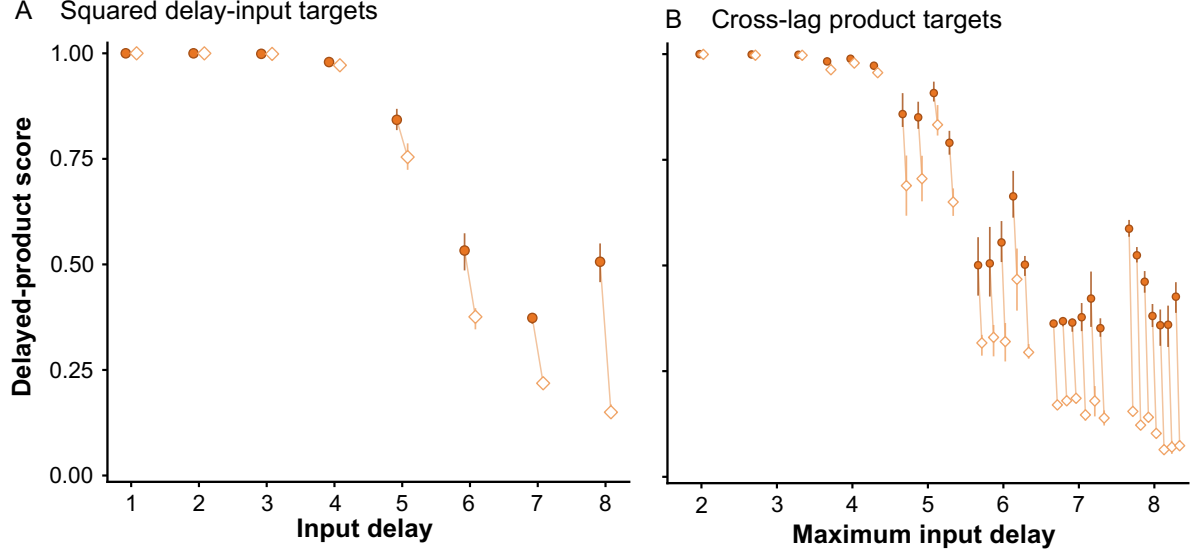


Figure S7: Individual delayed-product targets underlying the nonlinear-mixing profile. Across 100 HCP-YA connectomes, analytic contributions and held-out recovery are resolved for all 36 second-order targets summarized in Fig. 3D. **A. Squared delay-input targets.** The eight centered squared-input targets (p, p) are shown by input delay p . **B. Cross-lag product targets.** The 28 targets (p, q) with $p < q$ are grouped by maximum input delay q ; within each group, p increases from left to right. Filled circles show cohort-mean analytic contributions, open diamonds show cohort-mean held-out recovery, vertical bars show participant interquartile ranges, and pale lines join the two means for each target.

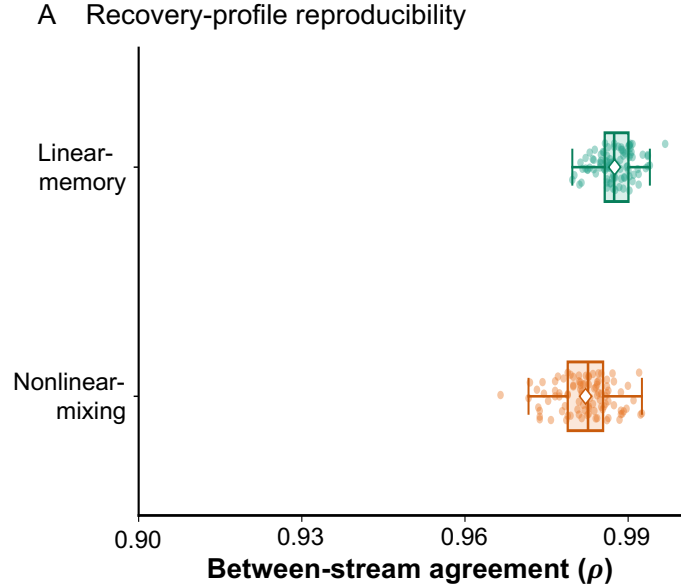


Figure S8: Held-out recovery profiles are reproducible across input streams. Held-out target-recovery scores retain a consistent ordering across the two independent temporal input streams used in Fig. 3. **A. Recovery-profile reproducibility.** Within each participant, ρ compares the two stream-specific profiles across 40 delayed-input targets or 36 delayed-product targets; mean ρ is 0.988 for linear memory and 0.982 for nonlinear mixing. Points represent 100 HCP-YA participants, boxes show interquartile ranges, center lines show medians, whiskers extend to $1.5\times$ the interquartile range, and white diamonds show means.

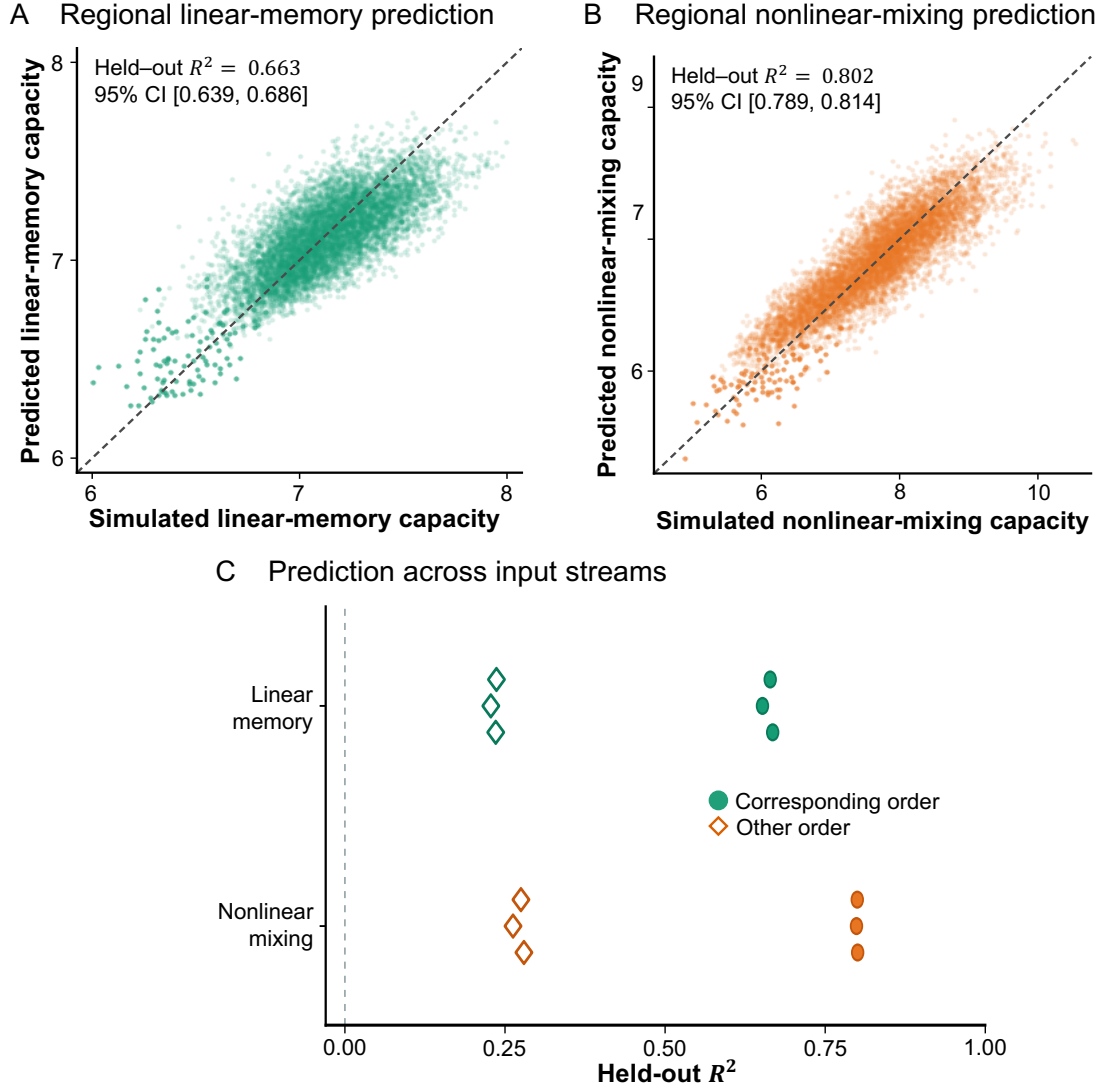


Figure S9: Regional response dimensions predict simulated capacities. Across 100 HCP-YA connectomes, response dimensions restricted to regional readouts predict the simulated capacities accessible from the same locations. **A. Regional linear-memory prediction.** Restricted κ_1 predicts simulated linear-memory capacity with participant-held-out $R^2 = 0.663$ (95% CI [0.639, 0.686]). **B. Regional nonlinear-mixing prediction.** Restricted κ_2 predicts simulated nonlinear-mixing capacity with participant-held-out $R^2 = 0.802$ (95% CI [0.789, 0.814]). **C. Prediction across input streams.** The corresponding response order predicts its matched capacity more accurately than the other order for each of three independent temporal input streams. Dashed lines in **A** and **B** mark equality. In **C**, filled circles denote the corresponding response order and open diamonds denote the other order. Reported 95% intervals resample participants while retaining their held-out predictions.

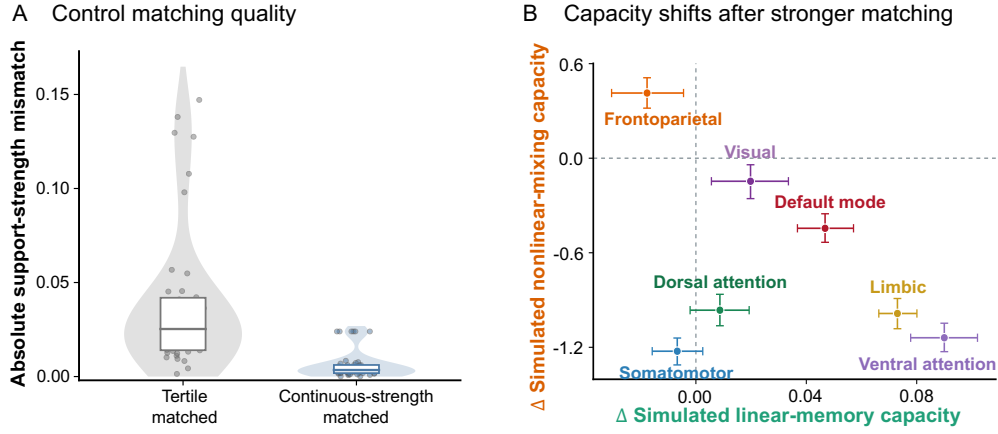


Figure S10: Regional capacity shifts under more closely strength-matched controls. More closely matching outside-network controls on continuous node strength preserves the nonlinear-mixing direction in all seven Yeo networks and the linear-memory direction in five of seven. **A. Control matching quality.** Across 42 regional conditions, continuous-strength matching reduces mean absolute support-strength mismatch from 0.039 to 0.006 and improves 41 of 42 conditions. **B. Capacity shifts after stronger matching.** Points show the mean system-minus-control changes in simulated linear-memory and nonlinear-mixing capacities across 100 HCP-YA connectomes; horizontal and vertical bars show 95% participant-bootstrap intervals for the respective capacities. In **A**, points are support pairs, boxes show interquartile ranges and medians, and violins show the distributions. Grey and blue denote tertile- and continuous-strength-matched controls. In **B**, marker colors identify Yeo networks.

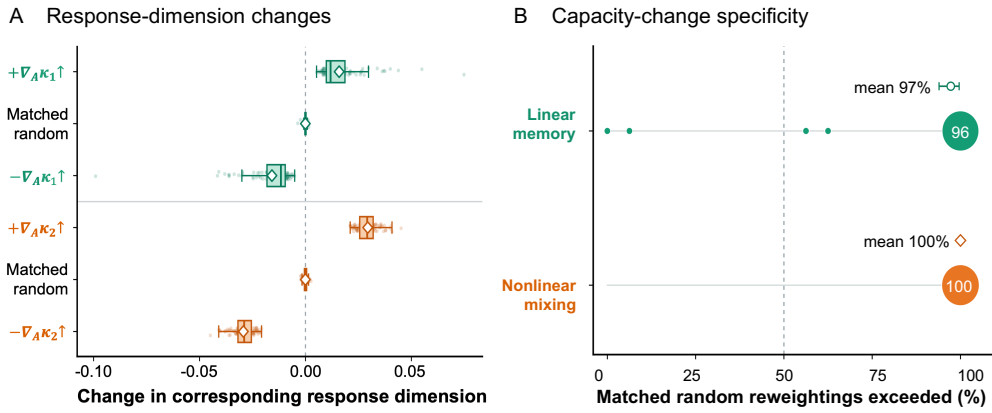


Figure S11: Response-gradient reweightings move their analytic objectives and matched simulated capacities. Across 100 HCP-YA connectomes, directed reweightings change the corresponding response dimensions and produce capacity changes that typically exceed matched random reweightings. **A. Response-dimension changes.** Participant-level changes in κ_1 and κ_2 are shown after reweighting along their positive and negative gradients; each matched-random value is the participant mean across eight random reweightings of the corresponding order. **B. Capacity-change specificity.** For each direction, the percentage of eight matched random reweightings producing a smaller change in the requested direction was calculated, then averaged across the positive and negative directions. Cohort means were 97% for linear-memory capacity and 100% for nonlinear-mixing capacity. In **A**, pale points represent participants, boxes show interquartile ranges and medians, whiskers extend to $1.5\times$ the interquartile range, and diamonds show means. In **B**, marker size and labels give participant counts, open markers and bars show cohort means and 95% participant-bootstrap intervals, and the dashed line marks the 50% random expectation.

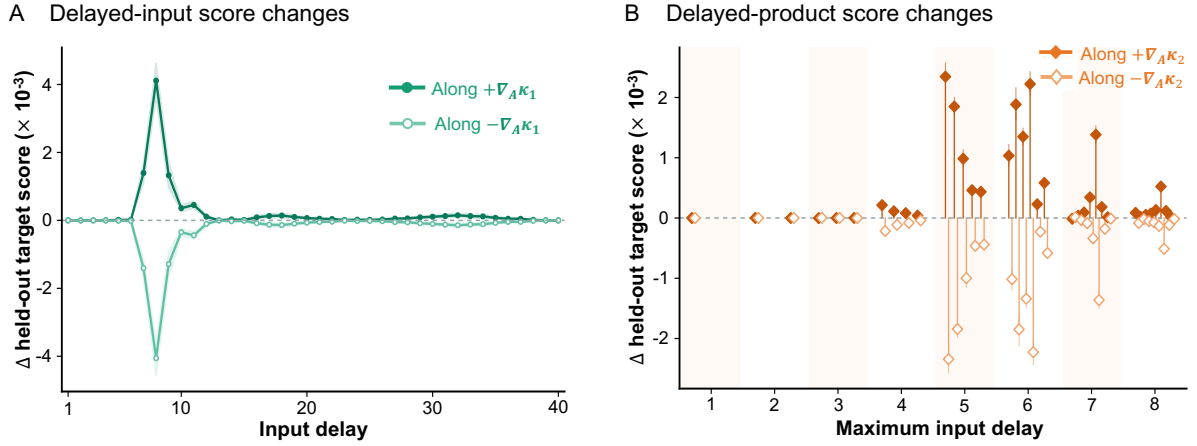


Figure S12: Simulated-capacity changes decompose across delayed targets. The total changes in Fig. 5A are resolved across the held-out target scores whose sums define linear-memory and nonlinear-mixing capacities. **A. Delayed-input score changes.** Changes in all 40 delayed-input scores are shown after reweighting along the positive and negative gradients of κ_1 . **B. Delayed-product score changes.** Changes in all 36 delayed-product scores are shown after reweighting along the positive and negative gradients of κ_2 ; targets are grouped by their maximum input delay. Curves, stems, and markers show cohort means; bands and thin intervals show 95% participant-bootstrap intervals. Filled and open markers denote positive- and negative-gradient directions, respectively.

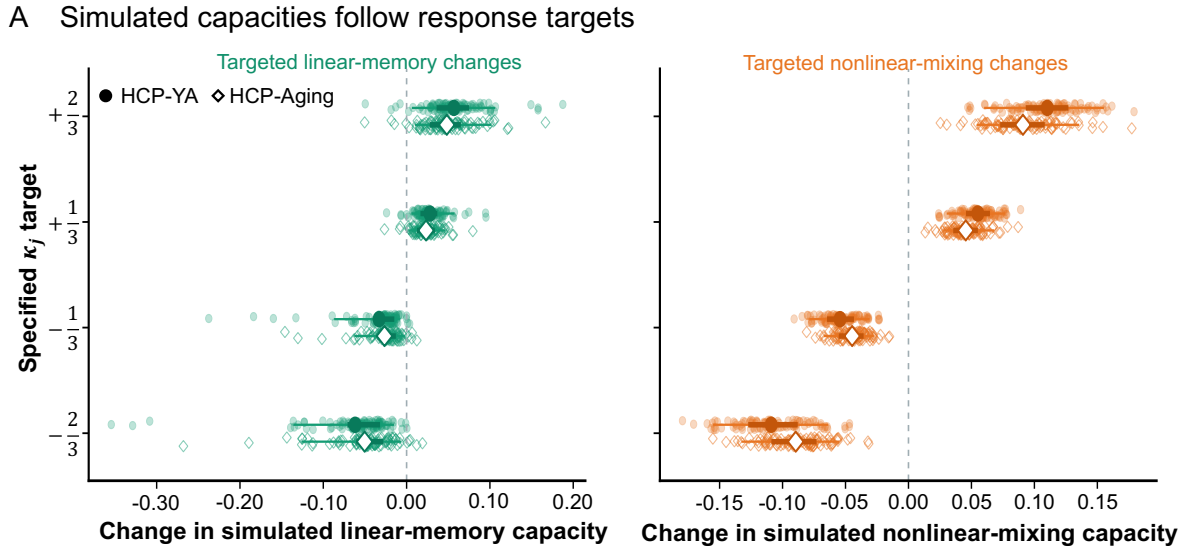


Figure S13: Simulated capacities follow response targets. Target-directed changes in the response dimensions produce ordered changes in their matched simulated capacities across HCP-YA and HCP-Aging. **A. Simulated capacities follow response targets.** First-order targets are evaluated by changes in simulated linear-memory capacity and second-order targets by changes in simulated nonlinear-mixing capacity; targets are set to one-third and two-thirds of each participant's response change after ten constrained steps in the corresponding direction. Filled circles denote HCP-YA and open diamonds denote HCP-Aging. Large markers show cohort means, thick horizontal intervals show interquartile ranges, thin horizontal intervals show 5th–95th percentiles, and vertical dashed lines mark zero capacity change.

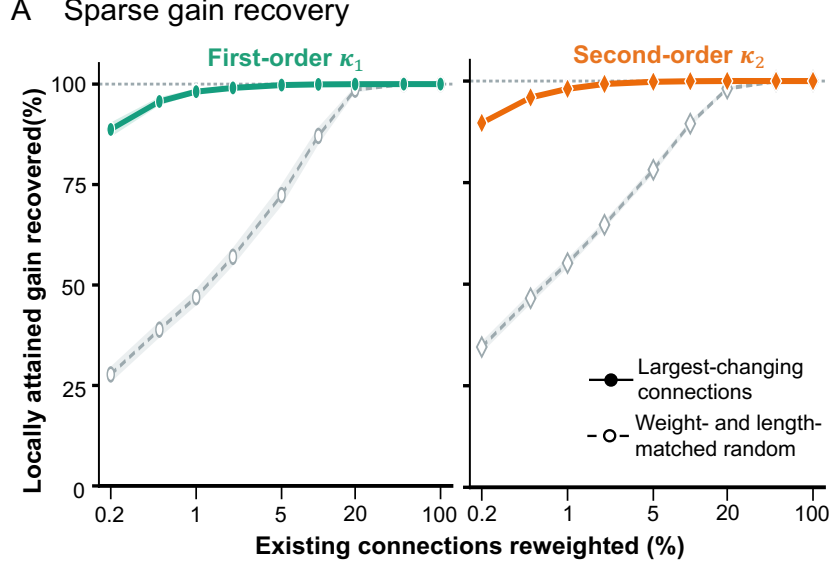


Figure S14: Sparse gain recovery replicates in HCP-Aging. The concentration of locally attained response gain in a small fraction of existing connections replicates across 100 HCP-Aging connectomes. **A. Sparse gain recovery.** Searches restricted to the largest-changing 0.2% of existing connections recover 88.9% of the locally attained κ_1 gain and 91.9% of the κ_2 gain, compared with 26.4% and 33.8% for weight- and length-matched random subsets. Solid colored curves show cohort means for the largest-changing subsets, dashed grey curves show means across two matched-random subsets per participant, bands show 95% participant-bootstrap intervals, and the horizontal dashed line marks complete recovery.

References

- [1] Pasqualetti, F., Zampieri, S. & Bullo, F. Controllability metrics, limitations and algorithms for complex networks. *IEEE Transactions on Control of Network Systems* **1**, 40–52 (2014).