Online Resource 1

How one brain substrate generates many ideas. A Geometro-Diffusion Theory model

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This Online Resource collects the parameters of every model used in the paper (Section S1), the results for all the thresholds, substrates and settings that the main text summarizes in one sentence (Sections S2–S9), and the list of codes that produce each result (Section S10). Unless stated otherwise, the substrate is the Schaefer-100 connectome of Hansen et al. (100 regions, 1136 connections, unit mean strength), the dynamics is the coupling model at $G = 0.96$, the reading time is $t^* = 0.217$ s, and the effective network is defined by the rule "is or has been" with $\theta = 0.01$. Figures cited are those of the main text.

S1 Parameters

Table S1: Coupling model and effective networks.

Symbol	Value	Meaning
λ_0	5.952 s^{-1}	leak of a region with zero strength
κ_0	7.287 s^{-1}	diffusion rate per unit of global coupling, $\kappa = \kappa_0 G$
ϑ	0.357	fraction of long-range excitation not compensated by feedback inhibition
G	0.96 (0.85–1.15 in S5)	global coupling; awake value of the propofol volunteers
t^*	0.217 s	reading time, $t_{\max}$ of the whole substrate (Hansen, $G = 0.96$)
	0.218 / 0.211 / 0.200 s	t^* of HCP cortex / HCP with subcortex / HCP-MMP1
θ	0.01 (0.005, 0.02, 0.05)	threshold of the effective network (inputs of unit mass)
	$0.01 \times 100/360$	threshold on the 360 parcels of HCP-MMP1
time grid	61 / 121 points	times in $[0, t^*]$ for the repertoire / for all other analyses

Table S2: Readers.

Reader	Parameter	Value
Reader of items (recurrent network)	units	200, leak $a = 0.35$
	recurrent weights	density 0.10, spectral radius 0.88
	input weights / biases	uniform in $[-0.65, 0.65]/\sqrt{n}$ / uniform in $[-0.15, 0.15]$
	input signal	24 log-spaced times in $[t^*/10, t^*]$, noise 0.06 of the rms activity
	readout	ridge regression, parameter 10^{-4}
	items, presentations	8 items; 60 pictures and 60 names each (40 train, 20 test); 10 seeds
Geometric reader (learns propagation)	operator	one-step least squares, $\widetilde{M} = -\log(A)/\Delta t$, $\Delta t = 5$ ms
	single run	50, 250, 1000 relaxation times (43 s, 3.6 min, 14 min)
	episodes	43 steps of 5 ms ($\approx t^*$); 100–4000 episodes
	observation noise	0, 1, 2, 3, 6% of the rms activity
	smoothing	moving average of 10, 20, 40 ms

Table S3: Full dynamic mean-field model and serial reader (rivalry).

Model	Parameter	Value
DMF	a_E, b_E, d_E	310 nC^{-1}, 125 Hz, 0.16 s
	a_I, b_I, d_I	615 nC^{-1}, 177 Hz, 0.087 s
	τ_E, τ_I, γ	0.1 s, 0.01 s, 0.641
	$I_0, W_E, W_I, w_+, J_{\mathrm{NMDA}}$	0.382 nA, 1, 0.7, 1.4, 0.15 nA
	noise σ	0.01 nA
	feedback inhibition	J_i set for 3.06 Hz in every region, at each coupling
	couplings	0.96, 1.5, 2.0
	inputs	0.02, 0.05, 0.1 nA (separate regions); 0.01, 0.02, 0.05 nA (same 17 regions)
	integration	Euler–Maruyama, 0.1 ms; 20 s per run, first 6 s discarded
Serial reader	items	effective networks of 12–30 regions, up to 60 per frequency class
	fidelity	$f(n) = 1 - \exp[-(n/70)^{0.87}]$, $n = 10\times$ frequency
	drive	Sørensen–Dice overlap $\times\, I_{\mathrm{sig}}^{\max} \times f(n)$
	τ, τ_a	10 ms, 80 ms
	inhibition β, adaptation g	2, 1.5
	transfer	logistic, centre 0.3, width 0.08; noise 0.05
	reading criterion	unit above 0.5 and above the other by 0.3

S2 Repertoire at four thresholds

Table S4 gives, for each threshold, the quantities that the main text reports for $\theta = 0.01$ (Figs. 3a–d). "Repeated" means produced by two or more different inputs.

Table S4: Repertoire of effective networks. Localized: 15,073 different inputs; distributed: 18,105.

Inputs	θ	different networks	median regions	repeated networks	repeated from different regions	max. sets of starting regions	max. frequency
Localized	0.005	12,802	43	1,308	438	10	16
	0.01	12,438	23	1,441	956	14	21
	0.02	10,606	5	1,910	1,106	23	41
	0.05	9,991	3	1,986	58	2	15
Distributed	0.005	18,028	57	71	8	2	3
	0.01	18,022	17	68	46	5	5
	0.02	17,899	6	188	32	3	4
	0.05	17,733	5	325	4	2	4

Growth of the repertoire with the number of sampled localized inputs (before removal of duplicates; 2,500, 5,000, 10,000 and 20,000 inputs): 1,912, 3,619, 6,874 and 12,802 networks ($\theta = 0.005$); 1,866, 3,509, 6,708 and 12,438 (0.01); 1,783, 3,260, 5,963 and 10,606 (0.02); 1,796, 3,232, 5,750 and 9,991 (0.05). For distributed inputs: 2,353, 4,607, 9,110 and 18,028 (0.005) and 2,351, 4,597, 9,092 and 18,022 (0.01). At every threshold the number of networks nearly doubles when the number of inputs doubles.

Distribution of frequencies. Localized inputs: power-law exponent 3.6 ($\theta = 0.005$), 3.4 (0.01) and 2.9 (0.02), each preferred to an exponential; at $\theta = 0.01$ an exponential cutoff does not improve the fit ($p = 0.39$), and at $\theta = 0.05$ the fit requires a cutoff.

Connectivity. For 3,000 inputs of each family and each threshold, every component of every effective network contained a starting region. Networks with several components: localized inputs, 0 at $\theta = 0.005$, 0.01 and 0.02 and 1 at 0.05; distributed inputs, 8, 788, 2,192 and 2,349 at $\theta = 0.005$, 0.01, 0.02 and 0.05, always from inputs with distant starting regions. With the effective network defined by the activity at t^* alone (16,706 inputs), inputs on a connected set of regions (8,091) gave 0 disconnected networks at $\theta = 0.005$ and 0.01, 8 (0.1%) at 0.02 and 609 (7.5%) at 0.05, and every component again contained an entry region.

Geometric richness. Mean $I_{\text{sig}}^{\max}$ 0.0204 (localized) and 0.0172 (distributed); mean $t_{\max}$ 0.215 s and 0.223 s; whole brain 0.093 and 0.217 s. Networks with $I_{\text{sig}}^{\max}$ above and $t_{\max}$ below their means: 2,884 of 12,438 and 5,454 of 18,022; with the means taken within each network size, 2,929 and 3,923.

S3 Inputs of different origin

Table S5: Search for an input that reproduces a perceived visual network: linear program at the tested crossing times (for the rule "is or has been", the reading time or the peak time under the visual input); 600 visual inputs. For the rule "is or has been" at $\theta = 0.01$, the exhaustive search over all crossing times of the grid (main text) proves impossibility for all 447 networks from control and default regions and for 428 from all non-visual regions, reproduces 2 from non-visual regions and leaves 17 undecided.

	"is or has been"				activity at t^*			
θ	perceived networks	from visual regions	from control and default	from all non-visual	perceived networks	from visual regions	from control and default	from all non-visual
0.005	448	448	0	0	448	448	0	0
0.01	447	447	0	2	449	449	0	10
0.02	408	408	0	0	400	400	0	0
0.05	403	403	0	0	–	–	–	–

Table S6: Forward simulation: number of different effective networks per origin (about 41,000 different inputs per origin) and networks shared by two origins (visual and non-visual, visual and somatomotor, visual and control+default, somatomotor and control+default).

Rule	θ	visual	non-visual	somatomotor	control+default	shared
"is or has been"	0.005	15,010	37,128	19,169	31,948	0
	0.01	10,948	36,821	20,499	31,498	0
	0.02	16,526	33,358	11,277	26,439	0
	0.05	15,687	32,170	10,233	23,741	0
activity at t^*	0.005	15,015	37,135	19,179	31,948	0
	0.01	10,686	36,756	20,230	31,397	0
	0.02	15,462	32,699	9,896	25,353	0
	0.05	1,107	6,326	564	2,304	empty network only

Substrate with subcortex. HCP connectome (ENIGMA toolbox), Schaefer-100 cortex with and without 14 subcortical regions; $t^* = 0.218$ s ($I_{\text{sig}}^{\max} = 0.081$) and 0.211 s (0.171); 30,000–33,000 different inputs per origin. Visual and auditory inputs shared 0 effective networks in both substrates, for $\theta = 0.005$, 0.01 and 0.02 and with both rules. Linear program ($\theta = 0.01$, activity at t^*): visual networks reproduced from visual regions 435 of 435 (cortex) and 463 of 463 (with subcortex), from auditory regions 0, and from auditory regions with hippocampus and amygdala 0 of 463.

S4 Reader of items

Table S7: Reader of the picture and the name of eight items: mean over ten seeds (range). Correct item for new pictures and new names, and same output for a picture and a name of the same item. Chance: 12.5%.

	HCP with subcortex			Hansen cortex		
Reader	pictures	names	same output	pictures	names	same output
Real activity	98.6 (97–100)	97.3 (94–99)	95.9 (91–99)	97.6	97.7	95.3 (93–97)
Active regions only	94.1	89.7	84.4	91.6	94.0	86.1
Rewired connectome	98.3	96.5	94.9	97.1	97.7	94.8
Trained real, tested rewired	94.7	82.7	78.2	87.2	83.2	73.6
Trained on pictures only	–	13 (3–42)	–	–	8 (0–24)	–
Names paired with wrong items	–	0.8	–	–	0.4	–

Same output for a picture and a name of different items: 0.6% in both substrates. Effective networks per item and modality: about 26 (HCP with subcortex) and 32 (Hansen); overlap between picture and name networks (shared regions divided by regions in either) 0.02 and 0.04. Relations between items (16 items, single-region pictures, no training): rank correlation between the true distances between items and the distances between the activities that reach the reader, 0.997 in both substrates; between the reader's final states, 0.13 (HCP with subcortex) and 0.18 (Hansen).

S5 Effective networks along the coupling axis

Table S8: Same 4,614 localized and 5,495 distributed inputs at every coupling; t^* and $I_{\text{sig}}^{\max}$ of the whole brain at each coupling; median size and median $I_{\text{sig}}^{\max}$ of the effective networks, localized (distributed).

G	t^* (s)	whole-brain $I_{\text{sig}}^{\max}$	median regions	median $I_{\text{sig}}^{\max}$
0.85	0.227	0.080	19 (12)	0.0132 (0.0098)
0.913 (loss of responsiveness)	0.221	0.088	21 (15)	0.0166 (0.0137)
0.963 (awake)	0.217	0.094	23 (18)	0.0199 (0.0172)
1.103 (psilocybin)	0.207	0.111	29 (26)	0.0303 (0.0298)
1.15	0.203	0.117	30 (29)	0.0339 (0.0347)

S6 Reading the geometry

Reference: the geometry of the whole substrate restricted to a network agrees with diffusion on the network itself with a rank correlation of 0.994 (10th–90th percentiles 0.990–0.996). Single response to the creating input, rank correlation between read and true distances 0.01 (percentiles −0.17 to 0.24). Ongoing activity of the network's regions: 0.55 (0.46–0.65) for 43 s, 0.82 (0.75–0.86) for 3.6 min and 0.95 (0.93–0.96) for 14 min. Learning by repetition, whole brain and effective networks: with ongoing episodes, 0.35 and 0.38 (100 episodes), 0.66 and 0.68 (500), 0.80 and 0.81 (1,000), 0.94 and 0.95 (4,000); with responses to localized inputs, 0.03 and −0.04 (100), 0.77 and 0.74 (500), 0.85 and 0.91 (1,000), 0.98 and 0.98 (4,000).

Table S9: Identification of the effective network from one episode (200 new inputs): percentage identified exactly, and median number of extra regions in parentheses, for each observation noise (percentage of the rms activity) and smoothing window. No region was missed in any case, and the rank correlation between read and true geometry of the identified regions was 0.976–0.977 in every case.

Noise	no smoothing	10 ms	20 ms	40 ms
0%	100 (0)	98.5 (0)	93.5 (0)	84.0 (0)
1%	29.5 (1)	51.5 (0)	66.5 (0)	78.5 (0)
2%	11.5 (3)	20.5 (2)	42.5 (1)	64.5 (0)
3%	4.5 (5)	10.5 (3)	25.0 (1)	50.5 (0)
6%	0.0 (12)	3.0 (7)	8.5 (4)	20.5 (1)

S7 Comparison with stimulation data (F-TRACT)

The three thresholds are $\theta = 0.0015$, 0.0028 (main case, $0.01 \times 100/360$) and 0.0050, about half and twice the main value; c is the probability that defines a responding parcel. Enrichment: fraction of the pairs inside the model networks that respond, divided by that of all measured pairs, pooled over the 339 stimulated parcels.

Table S10: Overlap between model effective networks and responding parcels (339 stimulated parcels). Dice: median Sørensen–Dice index for the model, for 200 random sets of the same size and for the rewired connectome; above random: parcels where the model exceeds the mean of the random sets (and their 95th percentile); nearest: Dice of the model and of the nearest measured parcels of the same size, on the pairs with known distance.

c	θ	enrichment model	enrichment rewired	Dice: model / random	above random (95th pct.)	Dice: rewired	nearest: model / nearest
0.90	0.0015	1.21	1.00	0.67 / 0.57	321 (208)	0.28	0.77 / 0.77
	0.0028	1.29	1.00	0.59 / 0.46	331 (224)	0.13	0.67 / 0.67
	0.0050	1.34	1.00	0.48 / 0.36	332 (207)	0.12	0.56 / 0.58
0.95	0.0015	1.24	0.98	0.62 / 0.50	309 (171)	0.26	0.70 / 0.70
	0.0028	1.35	0.98	0.55 / 0.42	323 (194)	0.12	0.63 / 0.63
	0.0050	1.43	0.98	0.47 / 0.34	327 (187)	0.12	0.56 / 0.56
0.99	0.0015	1.14	0.93	0.51 / 0.45	250 (60)	0.22	0.55 / 0.54
	0.0028	1.21	0.96	0.46 / 0.37	266 (78)	0.12	0.52 / 0.50
	0.0050	1.27	0.97	0.38 / 0.30	272 (66)	0.11	0.44 / 0.45

Table S11: Graded comparisons over all measured pairs: rank correlation of each predictor with the response probability (all pairs; beyond Euclidean distance, partial rank correlation; median over stimulated parcels), rank correlation with the response amplitude (15,772 pairs), and area under the ROC curve for separating the pairs with $p_{ij} \geq 0.9$, 0.95 and 0.99 from the others.

	probability		amplitude	AUC		
Predictor	all	beyond distance	per parcel	all	$c = 0.9$	$c = 0.95$	$c = 0.99$
Coupling model (peak up to t^*)	0.27	0.10	0.27	0.27	0.68	0.65	0.57
Communicability	0.26	0.09	0.27	0.26	0.68	0.65	0.57
Shortest path	0.25	0.08	0.26	0.25	–	–	–
Direct connection	0.23	0.10	0.24	0.27	0.61	0.60	0.55
Rewired connectome	−0.03	–	–	−0.01	0.50	0.49	0.48
Euclidean distance	0.28	–	–	0.31	0.70	0.67	0.59

Peak latency against the time of the model peak: rank correlation 0.16, and 0.35 for the Euclidean distance; latencies depend on conduction delays, which are outside the coupling model.

S8 Rivalry

Full DMF. Inputs on different visual regions (four pairs, three input strengths, three couplings; 36 runs): both sets of regions active together in every run (for example about 20 Hz in both at $G = 0.96$ and 0.02 nA); dominance δ constant within ± 0.02 (standard deviation over time 0.002–0.023), unimodal (bimodality coefficient 0.32–0.34), and never beyond $|\delta| = 0.5$; correlation between the activities of the two sets +0.03 to +0.13. Inputs as different graded patterns on the same 17 visual regions (36 runs): stable mixture in every run, with weights α 0.33–0.67 and β 0.49–0.82 on the two pure patterns, standard deviation of δ 0.002–0.039 (with a single input, 0.002–0.023), never beyond $|\delta| = 0.5$, unimodal (0.32–0.37).

Table S12: Serial reader, 300 pairs of items: pairs that alternate (both items read more than 5% of the time) and median share of reading time of the weaker item, by ratio of the drives (weaker divided by stronger).

Ratio of drives	pairs that alternate	reading time of the weaker item
0.9–1.0	34 of 34	31%
0.8–0.9	23 of 23	23%
0.7–0.8	35 of 35	17%
below 0.7	38 of 208	0.04%

Composition of the sample: of the 11,087 effective networks of 12–30 regions, 9,823 have frequency 1, 1,041 frequency 2–3, 179 frequency 4–7 and 44 frequency 8 or more; up to 60 items per class were used, and the classes of the two items of each pair were drawn uniformly. Rank correlations of the log ratio of reading time with the log ratios of $I_{\mathrm{sig}}^{\max}$, frequency and fidelity: 0.49, 0.57 and 0.59. Fusion (40 pairs with the union of the two networks learned as a third item): the union was read more than the two components together in all 40 pairs.

S9 Normalization of the weights

Hansen connectome, raw mean strength 12.6; 3,000 localized inputs. Pure diffusion, e^{-tL}, in arbitrary time units: $t^* = 2.07$ with normalized and 0.165 with raw weights (12.6 times shorter), $I_{\mathrm{sig}}^{\max} = 1.048$ in both, median network of 30 regions in both, and the same effective network for all 3,000 inputs. Coupling model: normalized weights at $G = 0.96$ and raw weights at $G = 0.96/12.6$ give the same $t^* = 0.217$ s, $I_{\mathrm{sig}}^{\max} = 0.0935$, median network of 23 regions and 2,199 different networks.

S10 Software

The MATLAB codes that reproduce the results are provided in Online Resource 2 (`ESM_2_JCompNeuro.zip`), whose `README.txt` explains where to place the data and how to run each code (MATLAB R2020b or later, Optimization Toolbox, Statistics and Machine Learning Toolbox). The results were obtained with the same computations in Python (NumPy, SciPy, scikit-learn). Input data: `sc_weighted.npy` (Hansen connectome), `strucMatrix_with_sctx_schaefer_100.csv` and `strucMatrix_ctx_glasser_360.csv` (ENIGMA toolbox), and the F-TRACT tables `probability.csv`, `amplitude.csv`, `peak_latency.csv` and `euclidian_distance.csv`.

Code	Result
`common/`	coupling model, t^*, distances, I_{sig}, inputs, effective networks, rewiring
`effnet.m`	repertoire, repeated networks, connectivity, frequencies (Fig. 3; S2)
`effnet_isig.m`	geometric richness of the networks (Fig. 4; S2)
`actual_conn.m`	connectivity with the activity at t^* (S2)
`imagine_lp.m`, `imagine_actual.m`	exact search over inputs (S3)
`imagine_exhaustive.m`	exhaustive search over crossing times (S3)
`shared.m`	shared repertoire of origins (S3)
`mtl.m`	substrate with subcortex (S3)
`reader_test.m`, `reader_geom.m`, `reader_relations.m`, `reader_rsa.m`	reader of items and its controls (Fig. 5c; S4)
`states.m`	coupling axis (Fig. 5a,b; S5)
`readA.m`, `readAB.m`, `readID.m`	reading the geometry, learning, identification (Fig. 6; S6)
`ftract.m`, `ftract_cmp.m`, `ftract_amplitude.m`, `ftract_overlap.m`, `ftract_dice.m`	comparison with F-TRACT (Fig. 7; S7)
`rivalry.m`, `rivalry_same.m`	full DMF with two inputs (Fig. 8a; S8)
`run_queue.m`	serial reader (Fig. 8b–d; S8)
`norm_check.m`	normalization of the weights (S9)
`run_all.m`	all of the above in order