

Supplementary materials

This file accompanies “Precision-weighted updating shows cross-task consistency as a bounded computational marker when precision gain is sufficiently large.” Source data remain on OpenNeuro (ds000030, ds004636, ds008083). Large EEG/fMRI volumes are not duplicated here.

S0. Package layout

Item	Path
Main text	manuscripts/gamma_endophenotype/manuscript.md
This file	manuscripts/gamma_endophenotype/supplementary_materials.md
Download	manuscripts/gamma_endophenotype/code/download_openneuro.py
Analyses	manuscripts/gamma_endophenotype/code/analysis_pipeline.py (calls analysis_htcv_extras.py and analysis_gamma_positivity.py)
Post-review numbers	manuscripts/gamma_endophenotype/results/
Archived HTCV	openneuro_validation/derivatives_htcv/
Archived Stage 4 MAP/NUTS	openneuro_validation/derivatives_stage4/
Simulator	openneuro_validation/stageD_repair/d1c_sim.py

S1. Preregistration timestamps (all earlier than the original HTCV figures)

Document	Timestamp
Stage 4 scope	2026-08-24T07:31:00+08:00
HTCV v2	2026-08-24T08:24:30+08:00
D1d	2026-08-23T19:56:00+08:00
D1e	2026-08-23T20:46:00+08:00
M3	2026-08-23T21:04:00+08:00
M1_1920	2026-08-23T22:36:50+08:00
HTCV run	2026-08-24T08:44:01 → 08:45:07

Post-review grids (ROPE, conjugate sensitivity, WAIC/LOO, IPW, non-null family separability) were computed 2026-08-29 and did not change H1–H4 decision rules.

S2. Archived numerical sources

Object	Path
HTCV results	openneuro_validation/derivatives_htcv/htcv_result.json
D1 / D5 posterior extracts	openneuro_validation/derivatives_htcv/d1_posterior_extract.csv, d5_posterior_extract.csv
D1 subject MAP+SE	openneuro_validation/derivatives_stage4/d1_fits/d1_subject_map.npz (keys: y, se, group, pid)
D5 subject MAP+SE	openneuro_validation/derivatives_stage4/d5_fits/d5_subject_map.npz (keys: y, se, pid)
D2 γ MAP	openneuro_validation/derivatives_htcv/d2_gamma_extract.csv
D1e nested BF	archived D1e (e1_ok=false, e2_ok=false, BF $\approx$ 1.05–1.09)
M3 / M1-1920	openneuro_validation/recovery_m3/m3_result.json, recovery_m1_1920/m1_1920_result.json

S3. Post-review products (verbatim files)

Object	Path
Non-null grid summary	results/pw_gamma_positivity_result.json
Non-null cell log	results/pw_gamma_positivity_cells.jsonl
HTCV sensitivity + WAIC + IPW	results/pw_htcv_sensitivity_waic_demo.json
All conjugate cells	results/pw_htcv_sensitivity_cells.json
Age/sex joined table	results/pw_subject_gamma_demographics.csv

Non-null grid: $\gamma \in \{0.25, 0.5, 1.0, 1.5, 2.0\} \times \text{trials} \in \{480, 960, 1920\} \times \text{seeds} \{42, 7, 123\} \times 10 \text{ cohorts} \times 100 \text{ subjects} = 450 \text{ cells}$. Nested BIC-BF of γ -free vs $\gamma=0$. First $P(\text{BF}>3) \geq 0.5$: $\gamma=1.0$ at 960 trials (0.741); at 480 trials the 0.5 line is first crossed at $\gamma=1.5$ (0.810).

Conjugate grid: 8 parameters $\times$ 3 priors $\times$ 3 SE floors $\times$ 4 pooling rules = 288 cells. γ : 0/36 HDI $\square$ 0. t_0 : 36/36 HDI $\square$ 0.

WAIC (MAP+SE layer, N=277): shared 1565.3 vs task-specific 1418.7.

S4. Degrade sentence (verbatim)

Precision-gated delta-rule: individual γ is recoverable; family-inseparable from RW at the family level when the generator is the RW limit ($\gamma=0$); mechanism absence is not detectable (one-sided: presence can be justified, absence cannot be justified). Non-null probes show family separability when true $\gamma \geq 1.0$ at ≥ 960 trials (or $\gamma \geq 1.5$ at 480 trials); they do not show it at $\gamma \leq 0.5$.

S5. How to reproduce

```
py -3 manuscripts/gamma_endophenotype/code/download_openneuro.py py -3
manuscripts/gamma_endophenotype/code/analysis_pipeline.py
```

analysis_pipeline.py runs the conjugate/WAIC/IPW analyses then the 450-cell non-null grid. Event files already on disk are not re-downloaded. OpenNeuro accessions: ds000030, ds004636, ds008083.

Combined numerical appendix

Precision-weighted updating (CPSP-8). This file also prints figures, post-review tables, full preregistration text, and archived HTCV extracts so the old extra folders are not needed.

S1. Package and degrade sentence

Download and analysis: code/download_openneuro.py and code/analysis_pipeline.py. OpenNeuro: ds000030, ds004636, ds008083. Binary NUTS npz files stay with the code folder (not printable).

Degrade: individual gamma is recoverable; family-inseparable from RW at gamma=0; non-null probes separate when gamma ≥ 1.0 at 960+ trials (or gamma ≥ 1.5 at 480 trials); not at gamma ≤ 0.5 .

S2. Figures

Figures are printed at the end of this PDF.

S3. Non-null family separability (450 cells)

Grid: gamma [0.25, 0.5, 1.0, 1.5, 2.0]; trials [480, 960, 1920]; seeds [42, 7, 123]; 10 cohorts $\times$ 100 subjects. BF = $\exp[0.5(\text{BIC}_{\text{nested}} - \text{BIC}_{\text{free}})]$. Threshold $P(\text{BF}>3) \geq 0.5$ first at gamma=1.0.

gamma	trials	median BF	P(BF>3)	P(BF>10)
0.25	480	0.02265	0.012	0.002
0.25	960	0.01798	0.018	0.009

0.25	1920	0.0208	0.038	0.020
0.5	480	0.07089	0.071	0.033
0.5	960	0.1273	0.160	0.101
0.5	1920	0.9228	0.389	0.301
1.0	480	2.241	0.466	0.351
1.0	960	93.26	0.741	0.652
1.0	1920	3.314e+05	0.929	0.887
1.5	480	340.1	0.810	0.729
1.5	960	4.692e+06	0.960	0.931
1.5	1920	4.852e+08	0.995	0.993
2.0	480	2.044e+05	0.942	0.902
2.0	960	4.852e+08	0.993	0.985
2.0	1920	4.852e+08	1.000	1.000

S4. Conjugate HTCV sensitivity, ROPE, WAIC, demographics

Priors: archived / half / double. SE floors: 0.02, 0.05, 0.10. Pooling: n-weighted, equal, CONTROL-only, SCHZ-only. 36 cells per parameter.

param	n_cells	frac HDI contains 0	archived contains 0	frac match archived
threat	36	0.000	False	1.000
baseline	36	0.000	False	1.000
alpha0	36	0.000	False	1.000
gamma	36	0.000	True	0.000
beta	36	0.000	False	1.000
v_gain	36	0.000	False	1.000
a	36	0.028	False	0.972
t0	36	1.000	True	1.000

Archived NUTS BART-pool minus CCT:

param	mean	95% HDI	contains 0
threat	-0.8759	[-1.1610, -0.5991]	False
baseline	0.9067	[0.7704, 1.0487]	False
alpha0	0.1413	[0.1128, 0.1698]	False
gamma	0.3803	[-0.0299, 0.7662]	True
beta	1.7660	[1.5840, 1.9496]	False
v_gain	1.8808	[1.7585, 2.0050]	False
a	0.2843	[0.1705, 0.3936]	False
t0	-0.0795	[-0.1647, 0.0020]	True

ROPE on archived NUTS delta-gamma: mean 0.3789, HDI [-0.0110, 0.7747], contains0=True. mass $|d| < 0.10/0.15/0.20 = 0.0786/0.1244/0.1824$. HDI+ROPE: {'0.1': 'undecided', '0.15': 'undecided', '0.2': 'undecided'}.

WAIC shared 1565.28 vs task-specific 1418.70; delta (shared-specific) 146.58. LOO-IC delta 146.74. Computed on subject-level MAP+SE as observations of the hierarchical mean (HTCV measurement-error layer), not trial-level CPSP-8 likelihoods.

task	N	age mean	age SD	frac female	MAP gamma
BART	173	33.01	9.10	0.410	1.4908
CCT	103	23.95	5.67	0.650	1.7574

EEG	42	24.95	4.43	0.643	1.4850
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IPW delta BART-CCT MAP gamma = -0.3327; bootstrap HDI [-0.7890, 0.1922]. Meta-regression is_BART = -0.2808.

S5. Archived HTCV extracts

D1 hierarchical means

param	group	mean	median	hdi_lo	hdi_hi	contains0
threat	BART_CONTROL	-0.8649	-0.8650	-1.0316	-0.7116	0
baseline	BART_CONTROL	0.9369	0.9369	0.7752	1.0984	0
alpha0	BART_CONTROL	0.1911	0.1908	0.1648	0.2191	0
gamma	BART_CONTROL	1.4836	1.4835	1.2412	1.7340	0
beta	BART_CONTROL	1.8927	1.8926	1.6786	2.1134	0
v_gain	BART_CONTROL	1.9180	1.9181	1.7746	2.0653	0
a	BART_CONTROL	0.5244	0.5242	0.4388	0.6019	0
t0	BART_CONTROL	0.1754	0.1754	0.1491	0.2006	0
threat	BART_SCHZ	-0.7363	-0.7362	-0.9650	-0.4935	0
baseline	BART_SCHZ	0.9398	0.9406	0.6882	1.1872	0
alpha0	BART_SCHZ	0.1784	0.1784	0.1403	0.2169	0
gamma	BART_SCHZ	1.4795	1.4770	1.0838	1.8491	0
beta	BART_SCHZ	1.4555	1.4533	1.1557	1.7719	0
v_gain	BART_SCHZ	1.8545	1.8536	1.6305	2.0780	0
a	BART_SCHZ	0.5478	0.5467	0.4176	0.6734	0
t0	BART_SCHZ	0.1852	0.1852	0.1432	0.2286	0
threat	BART_pool	-0.8284	-0.8287	-0.9610	-0.6939	0
baseline	BART_pool	0.9377	0.9375	0.8077	1.0796	0
alpha0	BART_pool	0.1875	0.1873	0.1652	0.2095	0
gamma	BART_pool	1.4825	1.4828	1.2725	1.6916	0
beta	BART_pool	1.7689	1.7687	1.5905	1.9521	0
v_gain	BART_pool	1.9000	1.9003	1.7836	2.0255	0
a	BART_pool	0.5311	0.5309	0.4619	0.6033	0
t0	BART_pool	0.1782	0.1781	0.1567	0.2003	0

D5 hierarchical means

param	group	mean	median	hdi_lo	hdi_hi	contains0
threat	CCT	0.0494	0.0430	-0.1834	0.3023	1
baseline	CCT	0.0318	0.0305	0.0026	0.0610	0
alpha0	CCT	0.0461	0.0460	0.0286	0.0627	0
gamma	CCT	1.1012	1.0945	0.7720	1.4474	0
beta	CCT	0.0010	0.0010	-0.0100	0.0118	1
v_gain	CCT	0.0187	0.0185	-0.0058	0.0428	1
a	CCT	0.2475	0.2443	0.1634	0.3352	0
t0	CCT	0.2576	0.2564	0.1801	0.3414	0

D2 gamma MAP (first 20 rows)

participant_id	accuracy	prior_bias_index	n_scored_trials	alpha0_map	gamma_map	alpha0_se	gamma_se	ok	mu_gamma_mean
sub-001	0.6305	0.0187	320.0000	0.1278	1.1000	0.0300	0.3826	True	1.4227
sub-002	0.6409	0.0128	312.0000	0.1383	1.0493	0.0300	0.3764	True	1.4227
sub-003	0.7935	0.0750	320.0000	0.3116	1.6119	0.0322	0.4769	True	1.4227
sub-004	0.7745	0.0559	313.0000	0.2868	1.4337	0.0317	0.4409	True	1.4227
sub-005	0.7168	0.0340	294.0000	0.2184	1.2337	0.0307	0.4029	True	1.4227
sub-006	0.7705	0.0615	317.0000	0.2819	1.4860	0.0314	0.4516	True	1.4227
sub-007	0.6720	0.0597	293.0000	0.1703	1.4693	0.0300	0.4482	True	1.4227
sub-008	0.8146	0.0969	320.0000	0.3404	1.8083	0.0332	0.5086	True	1.4227
sub-009	0.7267	0.0633	316.0000	0.2297	1.5027	0.0300	0.4550	True	1.4227
sub-010	0.7083	0.0375	320.0000	0.2091	1.2650	0.0300	0.4083	True	1.4227
sub-011	0.6771	0.0541	296.0000	0.1756	1.4165	0.0300	0.4374	True	1.4227
sub-012	0.7686	0.0619	315.0000	0.2795	1.4896	0.0314	0.4524	True	1.4227
sub-013	0.7177	0.0469	309.0000	0.2195	1.3507	0.0301	0.4243	True	1.4227
sub-014	0.6844	0.0531	311.0000	0.1833	1.4072	0.0300	0.4355	True	1.4227
sub-015	0.7919	0.0655	313.0000	0.3093	1.5233	0.0324	0.4593	True	1.4227
sub-016	0.8214	0.1053	304.0000	0.3492	1.8784	0.0343	0.5160	True	1.4227
sub-017	0.9053	0.0789	304.0000	0.4898	1.6484	0.0405	0.4837	True	1.4227
sub-018	0.7740	0.0379	290.0000	0.2855	1.2689	0.0328	0.4090	True	1.4227
sub-019	0.8409	0.1102	295.0000	0.3773	1.9175	0.0358	0.5191	True	1.4227
sub-020	0.8515	0.0710	303.0000	0.3944	1.5743	0.0361	0.4695	True	1.4227

(Showing first 20 rows.)

HTCV written 2026-08-24T08:45:07+08:00; D2 N=43.

S6. Archived main-text tables

param	BART_mu	CCT_mu	delta	hdi_lo	hdi_hi	includes0	verdict	source
threat	-0.8284	0.0494	-0.8775	-1.1533	-0.5882	False	Inconsistent	htcv_result.js on tests/gamma.mma.bart_cc t...
baseline	0.9377	0.0318	0.9064	0.7670	1.0473	False	Inconsistent	htcv_result.js on tests/gamma.mma.bart_cc t...
alpha0	0.1875	0.0461	0.1414	0.1140	0.1711	False	Inconsistent	htcv_result.js on tests/gamma.mma.bart_cc t...
beta	1.7689	0.0010	1.7690	1.5839	1.9488	False	Inconsistent	htcv_result.js on tests/gamma.mma.bart_cc t...
v_gain	1.9000	0.0187	1.8822	1.7572	2.0054	False	Inconsistent	htcv_result.js on tests/gamma.mma.bart_cc t...
gamma	1.4825	1.1012	0.3835	-0.0084	0.7826	True	Consistent	htcv_result.js on tests/gamma.mma.bart_cc t...

contrast	mean	hdi_lo	hdi_hi	includes0
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BART vs CCT	0.3835	-0.0084	0.7826	True
BART vs EEG	0.0586	-0.2028	0.2982	True
CCT vs EEG	-0.3236	-0.6901	0.0405	True

task	layer	CPSP8	RW	HGF2	DDM	logistic
D1 BART	choice RMSE	3.6253	1.6158	2.8699	nan	nan
D1 BART	RT RMSE	0.0712	nan	nan	0.0615	nan
D5 CCT	choice RMSE	1.1783	0.1272	0.5215	nan	0.0082
D5 CCT	RT RMSE	0.3591	nan	nan	0.3167	nan

S7. Preregistration lock (English summary of the Chinese working notes)

The original lock files in `openneuro_validation/preregistration/` were written in Chinese. The locked content, restated in English, is:

HTCV v2 (2026-08-24T08:24:30+08:00)

Written before any cross-task contrast, D2 probe, PPC, or fair RMSE. No Stage 4 NUTS refit. Core files untouched. OU frozen at group means; H3 is untestable on BART/CCT/EEG-summary data. Consistency = shortest 95% HDI of $\mu_{\text{BART}} - \mu_{\text{CCT}}$ contains 0. H1: threat, baseline, α_0 , β , v_{gain} . H2: γ on BART-CCT, BART-EEG, CCT-EEG. H4: layer-wise RMSE, never a mixed score. Degrade sentence: individual γ is recoverable; family-inseparable from RW; mechanism absence is not detectable (one-sided).

D1d (2026-08-23T19:56:00+08:00)

Locked before any D1d simulation. Trial-length extension only (480 vs 960), seeds 42/7/123, MDN hyperparameters frozen. Claim set $\{\alpha_0, \gamma, \beta\}$. Subject-level scatter arrays were not required to be archived.

D1e (2026-08-23T20:46:00+08:00)

Locked before any D1e scan. Nested $\gamma=0$ versus γ -free; Savage-Dickey / nested BF; E1/E2/E3 gates. Instrument prior $\gamma \sim U(0, 2.8)$ for this test only.

Gamma paper / endophenotype folder (2026-08-24)

No refit. Figures from archived JSON only. Figure 4 plots Pearson r , not fabricated clouds. Must not claim CPSP beats RW/DDM/logistic. OU awaits external anchors.

Subject demographics (first 40 rows)

task	pid	age	female	gamma	se	group
BART	sub-10159	30.0000	1.0000	1.5110	1.6505	0
BART	sub-10171	24.0000	0.0000	1.3756	1.3970	0
BART	sub-10189	49.0000	0.0000	1.5198	2.5079	0
BART	sub-10193	40.0000	0.0000	1.8033	1.7911	0
BART	sub-10206	21.0000	0.0000	1.4331	1.9461	0
BART	sub-10217	33.0000	1.0000	1.5031	1.6943	0
BART	sub-10225	35.0000	0.0000	1.5262	2.0379	0
BART	sub-10227	31.0000	1.0000	1.5385	1.5881	0
BART	sub-10228	40.0000	1.0000	1.5000	0.8949	0
BART	sub-10235	22.0000	0.0000	1.5879	2.3010	0
BART	sub-10249	28.0000	0.0000	1.5917	1.2936	0
BART	sub-10269	38.0000	0.0000	1.4916	1.4707	0
BART	sub-10271	41.0000	1.0000	1.6661	1.4341	0

BART	sub-10273	30.0000	1.0000	1.5489	1.3307	0
BART	sub-10274	43.0000	0.0000	1.5467	1.4409	0
BART	sub-10280	27.0000	0.0000	1.4954	1.0113	0
BART	sub-10290	48.0000	0.0000	1.3905	1.6118	0
BART	sub-10292	49.0000	0.0000	1.4971	1.5200	0
BART	sub-10304	23.0000	1.0000	1.4594	1.2427	0
BART	sub-10316	29.0000	0.0000	1.1676	1.5978	0
BART	sub-10321	34.0000	0.0000	1.3425	1.0391	0
BART	sub-10325	29.0000	1.0000	1.4990	1.2224	0
BART	sub-10329	22.0000	0.0000	1.4907	1.5864	0
BART	sub-10339	45.0000	1.0000	1.5516	1.1090	0
BART	sub-10340	32.0000	0.0000	1.4559	1.1561	0
BART	sub-10347	25.0000	1.0000	1.5092	1.8846	0
BART	sub-10356	43.0000	1.0000	1.5661	2.8024	0
BART	sub-10361	42.0000	1.0000	1.5003	1.7591	0
BART	sub-10365	24.0000	1.0000	1.4941	2.6075	0
BART	sub-10376	42.0000	1.0000	1.5885	1.8572	0
BART	sub-10377	49.0000	0.0000	1.4849	1.3142	0
BART	sub-10388	50.0000	1.0000	1.5208	1.4924	0
BART	sub-10429	36.0000	1.0000	1.5018	1.8452	0
BART	sub-10438	25.0000	0.0000	1.5033	1.3881	0
BART	sub-10440	26.0000	1.0000	1.4948	0.8964	0
BART	sub-10448	37.0000	0.0000	1.4486	1.4970	0
BART	sub-10455	25.0000	0.0000	1.2600	1.0281	0
BART	sub-10460	40.0000	0.0000	1.5628	4.7219	0
BART	sub-10471	30.0000	1.0000	1.5024	1.4812	0
BART	sub-10478	21.0000	1.0000	1.5279	2.1153	0

(Showing first 40 rows.)

Figures

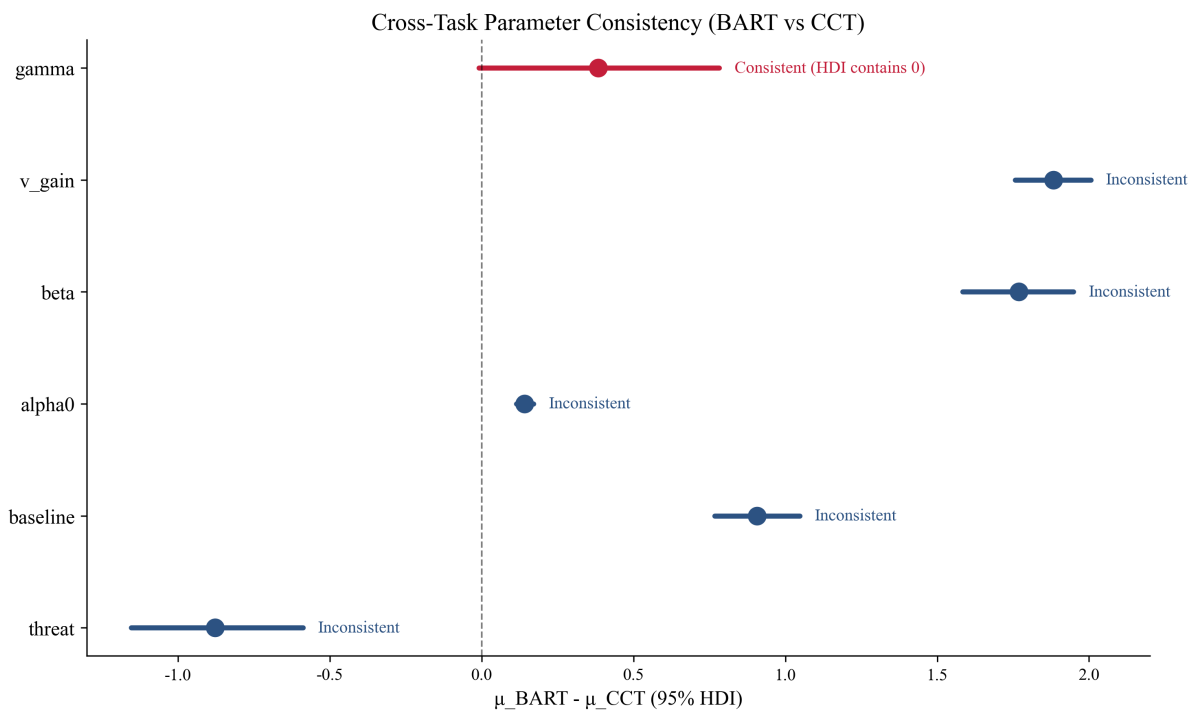


Figure 1. HTCV forest, BART vs CCT.

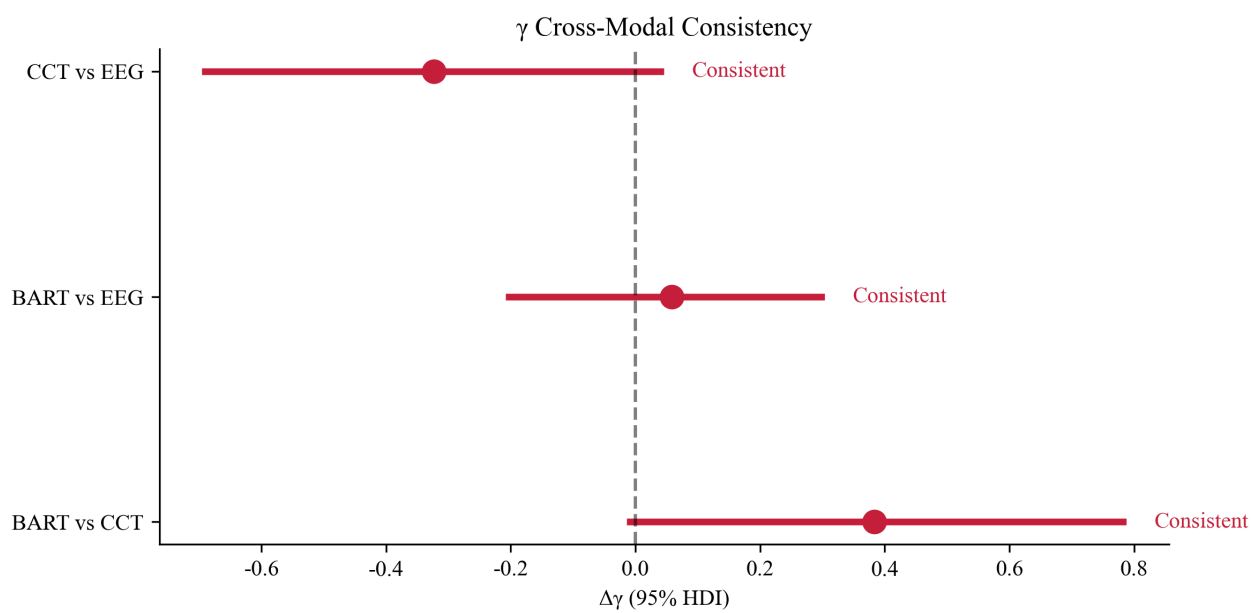


Figure 2. Gamma cross-task / cross-probe HDI.

Fair Comparison: CPSP-8 vs Specialized Models (by layer)

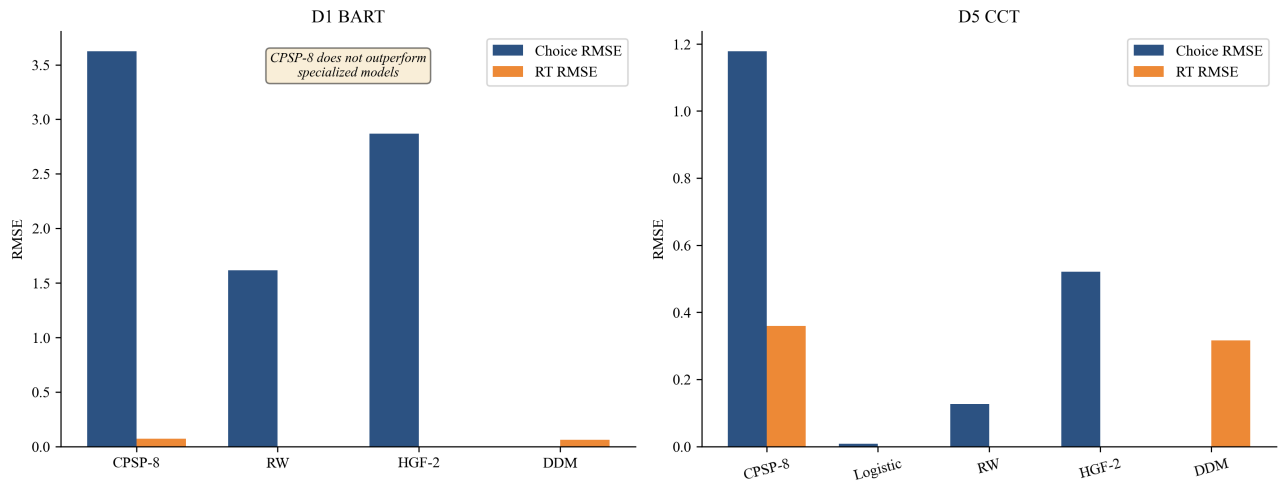


Figure 3. Layer-wise fair RMSE.

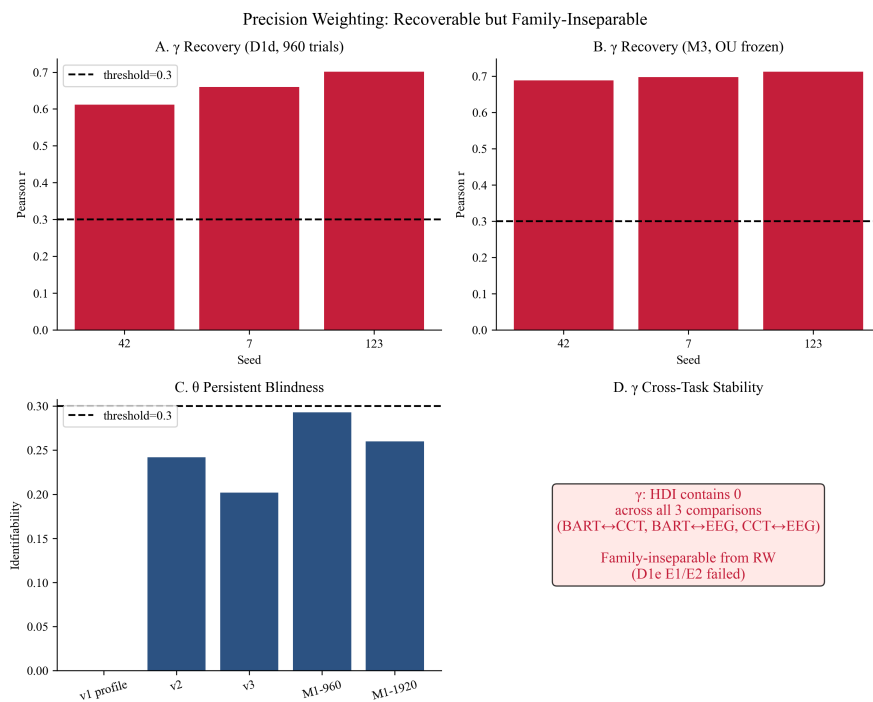


Figure 4. Gamma recovery vs theta blindness.

Task-mapping audit (post hoc; original analysis unchanged)

CCT action	CPSP option	Rationale	Risk
hot / draw	risky	High P(loss) as threat-context risk	Medium
safe / end	safe	No loss = safety	Low
pass (no independent code)	exploratory	Information search	High

CCT pass has no independent event code in this dataset; Stage 4 mapped non-draw to safe.

Figure 4b. Mapping audit.

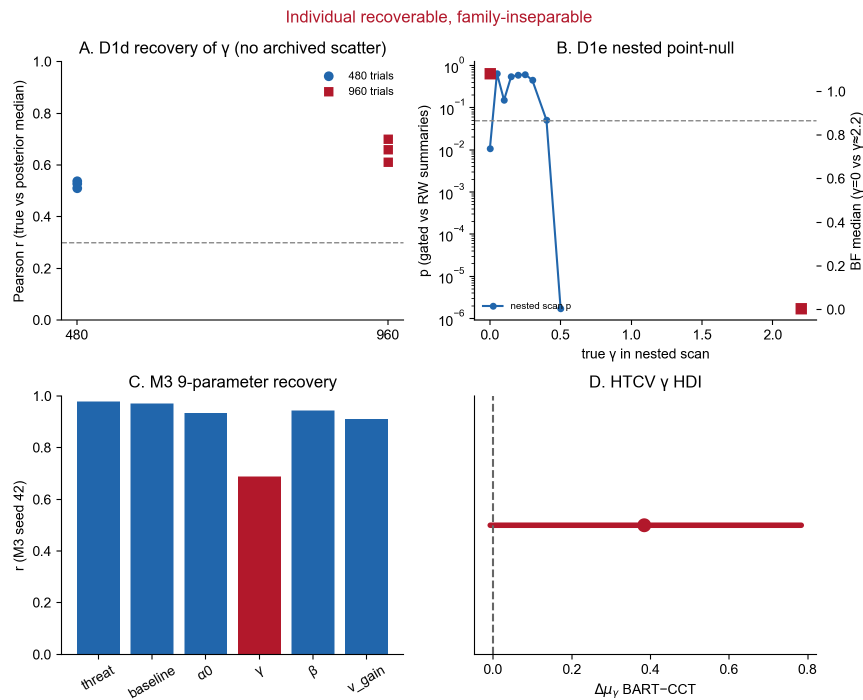


Figure 5. Gamma recovery (alternate panel).

CPSP three-layer verdict (read-only archived results; no refit)

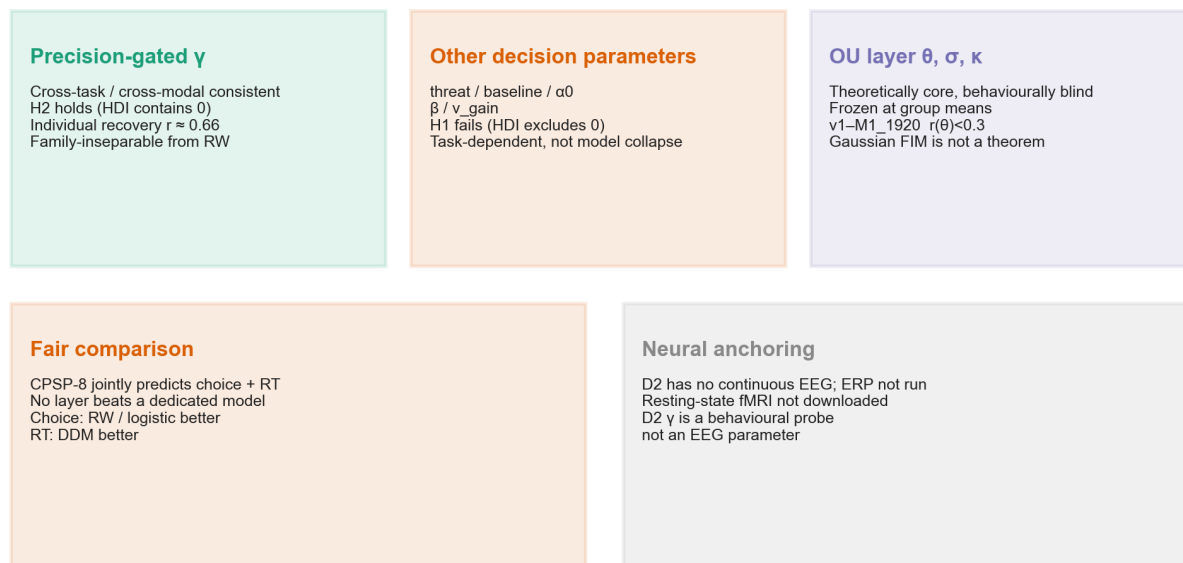


Figure S1. Three-layer verdict.

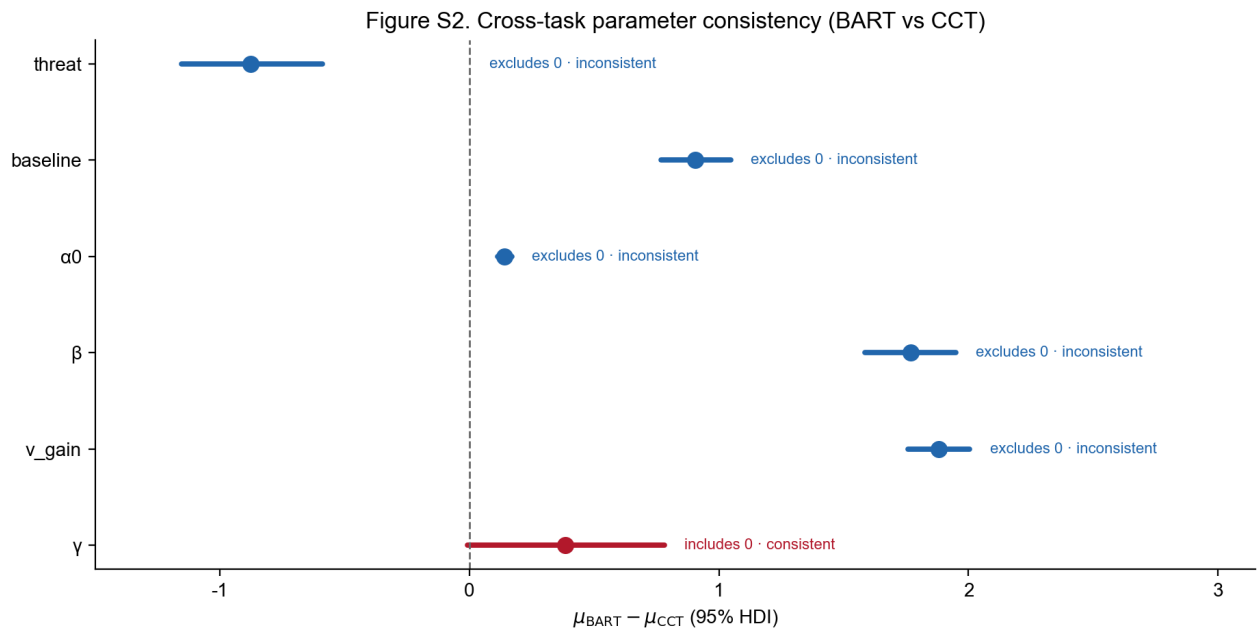


Figure S2. HTCv forest (synthesis).

Figure S3. Layer-wise fair comparison: CPSP-8 does not beat dedicated models

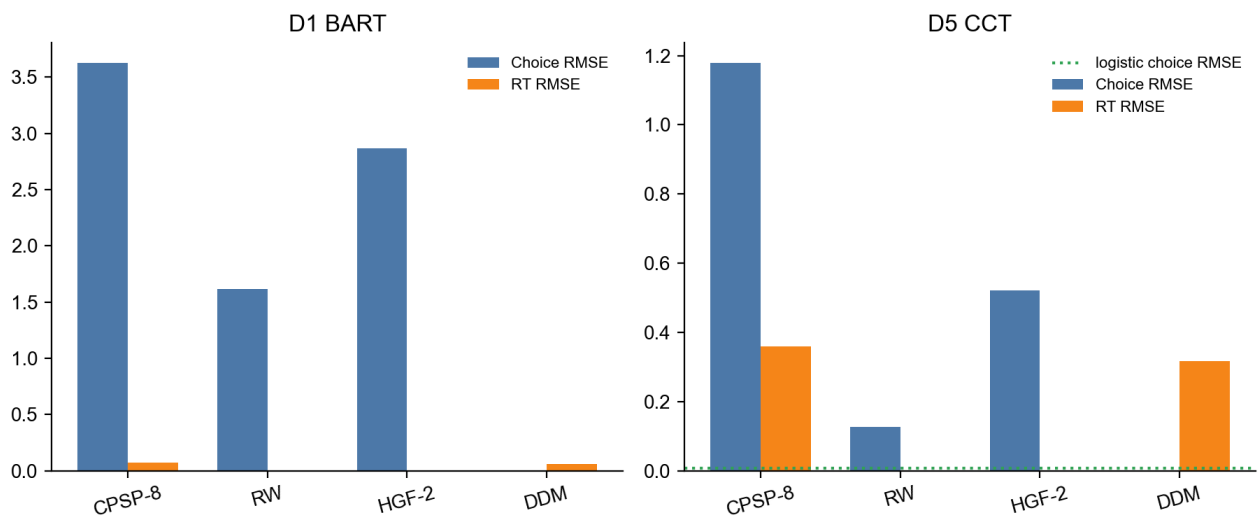


Figure S3. Layer-wise fair RMSE (synthesis).

Figure S4. γ recoverable vs θ behaviourally blind (still family-inseparable from RW)

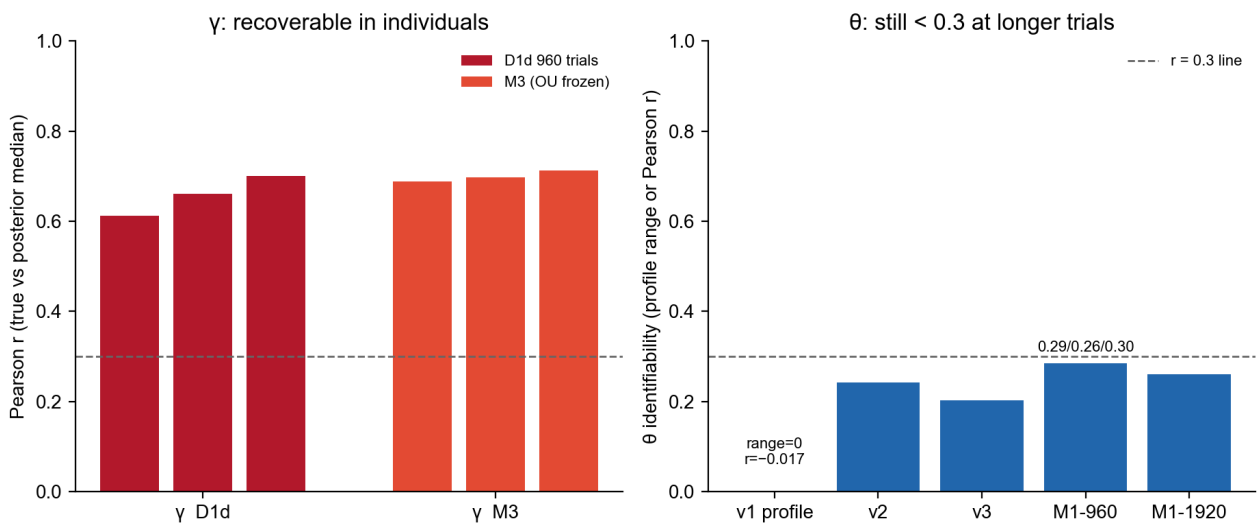


Figure S4. Gamma recovery vs theta blindness (synthesis).