

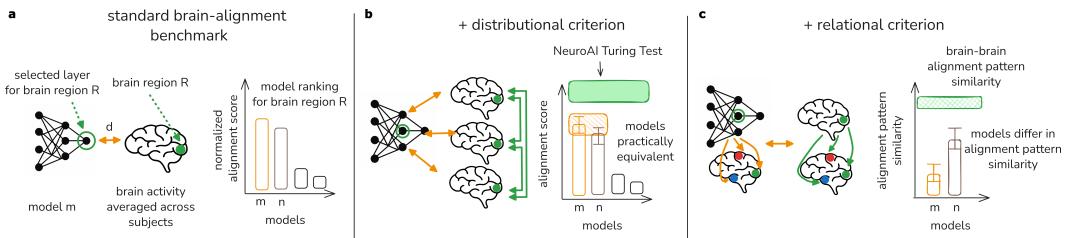
ONLY BRAINS ALIGN WITH BRAINS: CROSS-REGION PATTERNS EXPOSE LIMITS OF NORMATIVE MODELS

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ABSTRACT

011 Neuroscientists and computer vision scientists alike have relied on model-brain
 012 alignment benchmarks to find parallels between artificial and biological vision
 013 systems. These benchmarks rank models according to alignment measures (AM)
 014 such as representational similarity analysis (RSA) and linear predictivity (LP).
 015 However, recent works have revealed a number of problems with these rankings,
 016 such as their sensitivity towards the choice of AM, raising the deeper conceptual
 017 question of what it means for a model to be “brain-aligned.” Here, we introduce
 018 the notion of *alignment patterns* - characteristic patterns of alignment between
 019 brain regions - and posit that models should reproduce these patterns in order to
 020 be considered brain-aligned. First, we apply a standard benchmarking pipeline to
 021 a broad spectrum of vision models on the BOLD-Moments video fMRI dataset
 022 across visual regions of interest (ROIs). We find that, while this pipeline can iden-
 023 tify nominally best predictive models, many other models fall within subject-level
 024 variability and are therefore practically equivalent in terms of brain alignment. We
 025 then apply our complementary relational criterion: a ROI-aligned model should
 026 reproduce that ROIs cross-region alignment pattern. We find that, while these pat-
 027 terns are highly stable across brains of different subjects, even top-ranked models
 028 fail to capture them. Notably, models that appear practically equivalent in pre-
 029 dictive accuracy diverge sharply under the relational criterion, revealing both the
 030 limitations with respect to discriminative power of existing evaluation pipelines,
 031 as well as alignment pattern analysis as a way of increasing this discriminative
 032 power. Finally, we argue for a principled distinction between brain-predictivity
 033 and brain-alignment. For applications such as digital twins, prediction perfor-
 034 mance may suffice; but for understanding the inductive biases of the visual system,
 035 models should satisfy stricter distributional and relational criteria.



044 **Figure 1: Extending brain-alignment benchmarks with distributional and relational criteria.**
 045 (a) Standard brain-alignment benchmarks report model rankings based on normalized and averaged
 046 scores obtained from some alignment measure d , obscuring both the gap to ceiling performance, as
 047 well as the degree of variability in predictivity across the population. (b) In addition to assessing the
 048 distribution of brain-brain alignment scores across the population (“NeuroAI Turing Test”)(Feather
 049 et al., 2025; Thobani et al., 2025), we assess the distribution of model-brain alignment scores to
 050 define equivalence classes of models in terms of brain-alignment. (c) To distinguish between equiv-
 051 alently aligned models, we introduce alignment pattern similarity as a relational criterion that as-
 052 sesses whether a model reproduces the cross-region alignment patterns of visual regions of interest
 053 (ROIs).

054

1 INTRODUCTION

055
 056 A central aim of vision research is to understand which evolutionary and developmental inductive bi-
 057 ases have shaped the biological - and, in particular, the primate - visual system in a way that supports
 058 robust visual behaviors. Over the last ten years, researchers have leveraged increasingly powerful
 059 artificial vision models to probe candidate inductive biases Yamins et al. (2014); Yamins & DiCarlo
 060 (2016). In this line of research, models trained on a variety of tasks from computer vision are eval-
 061 uated with regard to how well they *align* to functional recordings from visual brain areas according
 062 to a variety of measures (Klabunde et al., 2025), and high alignment is typically interpreted as ev-
 063 idence that a model’s task, architecture, or training dataset reflect biologically relevant constraints.
 064 Recent progress in computer vision, including large-scale self-supervised and multi-modal models
 065 (e.g. Bear et al., 2023; Assran et al., 2025), along with the systematic collection of large-scale fMRI
 066 datasets (Lahner et al., 2024; Allen et al., 2022) now allow to scale these efforts towards compre-
 067 hensive brain-alignment benchmarks of vision models (Schrimpf et al., 2018; 2020; Conwell et al.,
 068 2024; Sartzetaki et al., 2024). The conclusions drawn from such benchmarks, however, rest on the
 069 assumption that alignment score rankings reflect differences in brain-alignment in some meaningful
 070 way. Recent work has challenged this assumption, showing that commonly used measures yield
 071 inconsistent results, and thus may not capture alignment in a principled way (Bowers et al., 2022;
 072 Schaeffer et al., 2024; Soni et al., 2024). This raises a deeper question: *What does it actually mean*
 073 *for a model to be “brain-aligned”?* Previous works (Feather et al., 2025; Thobani et al., 2025) have
 074 posited that a model should only be considered truly brain-like if its internal representations are
 075 indistinguishable - under a similarity transform - from those of other brains. The authors suggest a
 076 *distributional* criterion to assess this: if the model-brain alignment score is within the distribution
 077 of brain-brain alignment scores, the model is considered indistinguishable from other brains under
 078 the similarity transform that generated the score, thereby passing the *NeuroAI Turing Test* (Fig. 1
 079 a). The authors apply their distributional criterion to a range of static, i.e. image-based model-brain
 080 alignment benchmarks and conclude that many of them are saturated, i.e., models pass the Neu-
 081 roAI Turing Test (Feather et al., 2025). Here, we make three major contributions on top of existing
 082 benchmarks and the NeuroAI Turing Test:

082

1. Benchmarking

083 First, we evaluate a broad family of state-of-the-art vision models on a naturalistic video
 084 fMRI dataset spanning the entire visual hierarchy (Lahner et al., 2024), resolving brain-
 085 alignment to individual visual ROIs (Fig. 1a). We apply the NeuroAI Turing test and find
 086 that many models pass the NeuroAI Turing test when evaluated with Linear Predictivity
 087 (LP), but most fail when evaluated with Representational Similarity Analysis (RSA). This
 088 highlights the *lack of robustness* of standard benchmarking pipelines to the choice of align-
 089 ment measure.

090

2. Defining practical equivalence in brain-alignment

091 Second, using a distributional criterion to analyze alignment-score rankings, we show that
 092 for most visual ROIs, models that differ substantially in architecture, training data, and
 093 objective are still *practically equivalent* in their brain-alignment (Fig. 1b). This challenges
 094 the discriminative power of current benchmarks.

095

3. Alignment pattern similarity to distinguish among equivalently aligned models

096 Third, we introduce a *relational* criterion to distinguish among equivalently aligned mod-
 097 els: We posit that a model should only be considered aligned to a brain region if it repro-
 098 duces the *cross-region alignment pattern* of this brain region (Fig. 1c).

099 We conclude with a discussion where we argue to make a distinction between *brain-aligned* models
 100 in this stricter sense, and *brain-predictive* models, where high LP-scores in suffice.

102

2 RELATED WORK

104 **Alignment benchmarks.** Kicked off by work on explaining visual object recognition (Yamins
 105 et al., 2014), neural network models have been compared to the brain on large-scale benchmarks.
 106 Brain-Score (Schrimpf et al., 2018) originally focused on static image processing along the ventral
 107 stream, later adding language regions (Schrimpf et al., 2021). It provided a first large-scale platform

108 for model evaluation. The Algonauts challenge brought this approach to whole-brain responses
 109 to naturalistic stimuli, beginning with static images and later extending to dynamic movie-based
 110 paradigms (Gifford et al., 2024; 2023; Cichy et al., 2021). Most recently, the challenge has empha-
 111 sized multimodal video inputs, pushing alignment analyses into richer and more ecologically valid
 112 contexts (see e.g. d’Ascoli et al., 2025).

113 Beyond these community benchmarks, several studies have systematically examined factors shaping
 114 model–brain alignment. Conwell et al. (2024) showed that vastly different architectures can
 115 achieve similar alignment, with variation in “visual diet” emerging as the most consistent deter-
 116 minant. Tang et al. (2025) further found that a single predictive objective generalizes well across
 117 cortical areas when evaluated with LP, suggesting shared computational principles across the hierar-
 118 chy. In contrast, Sartzetaki & Groen (2025) used RSA to reveal stream-specific alignment: modular
 119 architectures preferentially aligned with dorsal versus ventral pathways, consistent with a division
 120 of labor between motion and object processing. Sartzetaki et al. (2024) find that while video models
 121 achieve highest RSA-alignment in early visual regions, for both ventral and dorsal regions, semantic
 122 objectives seem key.

123 **Alignment metrics.** Conclusions about brain–model alignment strongly depend on the choice of
 124 alignment metric. Several recent studies have shown that different metrics can yield inconsistent
 125 model rankings, highlighting the instability of current benchmarking practices (Soni et al., 2024; Bo
 126 et al., 2024). In particular, LP has drawn substantial criticism: Schaeffer et al. (2024) argue that
 127 LP primarily reveals biases of the regression framework rather than genuine alignment, while Soni
 128 et al. (2024); Bo et al. (2024); Wu et al. (2025) show that LP offers low discriminability between
 129 models. More broadly, Bowers et al. (2022) contend that such metrics do not provide a reliable basis
 130 for drawing conclusions about brain alignment at all. Together, these findings underscore the need
 131 for stricter and more interpretable criteria when assessing model–brain correspondence.

132 **Alignment patterns.** A number of works have evaluated whether the visual hierarchy of regions or
 133 voxels is reflected in the order of their best-matching layers within a DNN, e.g., Güçlü & Van Gerven
 134 (2015); Cichy et al. (2016); Bersch et al. (2025); Thobani et al. (2025). Nonaka et al. (2021) suggest
 135 using such hierarchical correspondence as an alignment criterion. This evaluates whether entire
 136 models match to entire visual streams, while we look at alignment of models to individual regions.
 137 Thobani et al. (2025) also correlate layer dissimilarity scores to known distances between layers,
 138 and repeat the same analysis for visual brain regions, which they assign to integer hierarchy levels 1
 139 to 5. This serves to compare alignment methods, not to evaluate model-brain similarity.

141 3 METHODS

142 3.1 DATASET

143 We base our analyses on the BOLDMoments dataset (Lahner et al., 2024), a 3T fMRI dataset
 144 recorded from 10 subjects watching over 1000 different 3-second video clips. We chose this dataset
 145 to ensure stimulation of motion-responsive brain areas (Grossman & Blake, 2002; Sunaert et al.,
 146 1999). Each of the 1000 stimuli in the train split was shown three times to each subject, each of
 147 the 102 stimuli in the test split was shown ten times. Stimulus repetitions were presented in random
 148 order across 4 sessions. We use beta values (GLMSingle regression coefficients of each voxel and
 149 video shown), projected to fslr32k surface space, as they are output from the preprocessing pipeline
 150 (specifically, version B) of Lahner et al. (2024). Please refer to Lahner et al. (2024) for more details.
 151 We use the original train-test split, dropping data for 2 (4) stimuli from the train (test) set because of
 152 frame extraction issues, and average the fMRI activity over repetitions, leading to a higher signal-to-
 153 noise ratio on the test split, compared to the train split. While the voxel-wise beta values provided by
 154 Lahner et al. (2024) are already centered and normalized across individual sessions, we normalize
 155 and center them once more across the train set, and use the same standard deviation and mean per
 156 feature to approximately center and normalize the test split.

157 We analyze ROIs from the Glasser HCP-MMP atlas (Glasser et al., 2016): early visual areas
 158 (V1,V2,V3), dorsal stream (V3A, V3B, V6, V6A, V7, IPS1, MST, MT, FST, LO1–LO3), and ventral
 159 stream (V4, V8, PIT, FFC).

162 3.1.1 NOISE CEILINGS
163

164 Because fMRI data are noisy, neither perfect predictivity nor perfect representational similarity can
165 be expected (Walther et al., 2016). We compute two noise ceilings for each ROI in the following
166 ways: **Upper noise ceiling**. We average the fMRI data of N-1 subjects for the given ROI. Then we
167 use this average as predictor feature space and compute RSA/LP score between the average map
168 and the remaining subject’s ROI data. This yields one upper noise ceiling per subject, from which
169 we can compute a mean, and a 95% confidence interval of the mean, across the ten subjects. **Lower**
170 **noise ceiling**. As suggested in the Neuro-AI Turing test Feather et al. (2025), we compute a noise
171 ceiling based on pairwise alignment scores between subjects. For a given ROI, we sample five other
172 subjects per target subject, excluding previously sampled pairs, for a total of 50 subject pairs. For
173 each pair we compute the RSA/LP score between the regions’ fMRI features of the two subjects,
174 and again compute mean and 95% confidence interval across all pairs.

175 3.2 MODELS
176

177 We evaluate 47 state-of-the-art pretrained image and video deep learning models that cover a broad
178 range of architectures, objectives and datatsets:

179 **Taskonomy model bank.** A collection of 26 models based on ResNet-50 and trained on the same
180 dataset of 4 million indoor scenes, but for different tasks (Sax et al., 2018; Zamir et al., 2018).
181 **Supervised image models.** We include ResNet (He et al., 2016) and ConvNext (Liu et al., 2022b)
182 models from the timm library (Wightman, 2019), all trained for object recognition on ImageNet-
183 1K. **Self-supervised image models.** As counterpart to the supervised image models, we include
184 ResNets trained on ImageNet-1K with the self-supervised SimCLR objective (Chen et al., 2020), as
185 provided by VISSL (Goyal et al., 2021). **CLIP.** We consider the ResNet-50 and Vision Transformer
186 based CLIP models from the original codebase, all trained to align image and text representation
187 on a large dataset of 400M image-text pairs (Radford et al., 2021). **Supervised video models.**
188 We use three video transformers from the mmaction2 toolkit (Contributors, 2020): MViT (Li et al.,
189 2022), Video Swin Transformer (Liu et al., 2022a), TimeSformer (Bertasius et al., 2021). All models
190 were trained for action recognition on the Kinetics-400 dataset. **Unsupervised video models.** We
191 include the ViT-based counterfactual world model (CWM) (Stojanov et al., 2025) which was trained
192 on Kinetics-400 using an adapted MAE objective (He et al., 2022). Further, we consider the V-
193 JEPA 2 model (Assran et al., 2025) that was trained on a large-scale video dataset using a variant of
194 the MAE objective in feature space. **VGG Transformer (VGG-T).** We include the 3D foundation
195 model VGG-T (Wang et al., 2025) as comparison to the dominantly semantic models described
196 above. This ViT-based model was trained to simultaneously predict multiple key 3D attributes from
a variable number of views of a scene.

197 For all models, we extract representations for the last layer of up to 15 blocks (e.g., a residual block
198 in a ResNet). For models with more blocks, we use 15 equally spaced blocks. We apply image
199 models to each frame individually, and video models and VGG-T to the entire video clip (3s), and
200 average representations over time. The resulting feature vectors are reduced using sparse random
201 projection (Achlioptas, 2003) to 5919 dimensions, following the Johnson-Lindenstrauss Lemma
202 with an epsilon of 0.1 (Achlioptas, 2001).

203 3.3 MEASURING MODEL-BRAIN ALIGNMENT
204

205 For every combination of model and ROI, we select the best layer on the training set by averaging the
206 alignment scores over subjects. Using the selected layer for all subjects, we then report alignment
207 scores on the test set. We consider the following two alignment metrics:

208 **Representational Similarity Analysis (RSA)** compares representations based on representational
209 dissimilarity matrices (RDMs), which are sufficient statistics for the representational geometry of
210 a system (Kriegeskorte & Wei, 2021; Kriegeskorte et al., 2008). RDMs are constructed for the
211 model and brain representation by computing the pairwise correlation distances of the representation
212 (1 – Pearson correlation) for all samples. The overall RSA alignment score is then the Pearson
213 correlation of the brain and model RDMs.

214 **Linear predictivity (LP)** measures alignment by fitting a linear model that predicts brain activity
215 from model features (e.g., Yamins et al. (2014)). We fit ridge regression models predicting the

216 preprocessed fMRI signals on the training set using 5-fold cross-validation. We use the RidgeCV
 217 implementation from the scikit-learn package (Pedregosa et al., 2011), which selects the optimal
 218 alpha value using leave-one-out cross-validation from 19 candidate values on a logarithmic scale
 219 spanning 10^{-9} to 10^9 . Given the respective linear models fitted on the training set, we report the
 220 residual sum of squares (R^2) on the test set.

222 3.4 DETERMINING PRACTICAL EQUIVALENCE BETWEEN MODELS

224 To determine when models are practically indistinguishable in terms of brain alignment, we defined a
 225 practical equivalence criterion based on bootstrap estimates of variability in model-brain alignment
 226 scores. For a given model m with feature space X_m , we generated a bootstrap distribution of
 227 mean brain-alignment scores under a measure \mathcal{M} by resampling subject indices with replacement.
 228 Specifically, we defined a bootstrap index vector

$$229 I^* = (i_1^*, \dots, i_{10}^*), \quad i_k^* \sim \text{Unif}(I) \text{ with replacement}, \quad I = \{1, \dots, 10\},$$

230 and computed the corresponding bootstrap estimate of the mean alignment score as

$$232 233 234 \frac{1}{10} \sum_{k=1}^{10} \mathcal{M}(X_m, Y_{i_k^*}).$$

235 We then derived 95% confidence intervals for the model's mean brain-alignment score from the
 236 resulting distribution. A model m was deemed practically equivalent to the top-ranking model t if
 237 its empirical mean alignment score $\langle \mathcal{M}(X_m, Y_i) \rangle_i$ fell within the 95% confidence interval of the top
 238 ranking model.

240 3.5 ALIGNMENT PATTERN ANALYSIS

242 We define an alignment pattern α under a similarity transform \mathcal{M} between a predictor feature space
 243 ϕ_p and N target feature spaces $\Psi_t = [\psi_t^1, \dots, \psi_t^N]$ as

$$244 \alpha(\phi_p, \Psi_t) = [\mathcal{M}(\phi_p, \psi_t^1), \mathcal{M}(\phi_p, \psi_t^2), \dots, \mathcal{M}(\phi_p, \psi_t^N)] \quad (1)$$

246 3.5.1 FMRI-DERIVED ALIGNMENT PATTERNS

248 For fMRI-derived alignment patterns, both the predictor and the target feature spaces are sourced
 249 from brain activity from the BOLDMoments dataset. fMRI-derived alignment patterns are defined
 250 between pairs of subjects p, t , where the brain activity of subject p functions as the predictor feature
 251 space ϕ_p and the brain activity of subject t functions as the target feature space Ψ_t . The alignment
 252 pattern for a given ROI $r \in N$ and a pair of subjects p, t is then defined as

$$253 254 \alpha_r(\phi_p, \Psi_t) = [\mathcal{M}(\phi_p^r, \psi_t^1), \mathcal{M}(\phi_p^r, \psi_t^2), \dots, \mathcal{M}(\phi_p^r, \psi_t^r), \dots, \mathcal{M}(\phi_p^r, \psi_t^N)] \quad (2)$$

255 We detail in the Appendix Section S3.1 how the variance of fMRI-derived alignment patterns is
 256 estimated.

257 3.5.2 MODEL-DERIVED ALIGNMENT PATTERNS

259 For model-derived alignment patterns, the predictor feature space is defined as the activations in one
 260 layer l of the model, ϕ_m^l , and the target feature spaces are analogous to the case of fMRI-derived
 261 alignment patterns. A model-derived alignment pattern between model m and subject t for a given
 262 ROI $r \in N$ is then

$$263 264 \alpha_l(\phi_m, \Psi_t) = [\mathcal{M}(\phi_m^l, \psi_t^1), \mathcal{M}(\phi_m^l, \psi_t^2), \dots, \mathcal{M}(\phi_m^l, \psi_t^N)] \quad (3)$$

266 3.5.3 STRUCTURAL CONNECTIVITY-DERIVED ALIGNMENT PATTERNS

268 For comparing alignment patterns to structural connectivity patterns, we use a network based on
 269 diffusion-weighted tensor imaging (DTI) Pierpaoli et al. (1996) streamline-density from the Human
 Connectome Young Adult full dataset (Caron & Pestilli, 2023) as provided through brainlife Hayashi

et al. (2024) (provided as ‘conmat’ datatype). The procedure fits streamlines - white-matter trajectory candidates Smith et al. (2012) - to diffusion MRI data. The number of streamlines intersecting both ROIs of a pair of regions is divided by the volume of both regions to obtain the ‘density’-based connectivity matrix we use. For more information, see Hayashi et al. (2024), section *dMRI processing*. We average the connectivity matrices of 1065 subjects to obtain a single connectivity matrix, $C = (c_{r,t})_{r,t=1\dots N}$ where $c_{r,t}$ is the streamline density between regions r and t . The structural connectivity-derived alignment pattern for a given ROI r is then

$$\alpha_{struct}(r) = [c_{r,1}, \dots, c_{r,r-1}, c_{r,r+1}, \dots, c_{r,N}] \quad (4)$$

where we exclude the ROI r since self-similarity is not defined for streamline-density as alignment measure.

3.5.4 ALIGNMENT PATTERN SIMILARITY

Alignment pattern similarity between two alignment patterns, e.g. a fMRI-derived alignment pattern $\alpha_r(\phi_p, \Psi_t)$ and a model-derived alignment pattern $\alpha_l(\phi_m, \Psi_t)$ is calculated as

$$\rho(\alpha_r(\phi_p, \Psi_t), \alpha_l(\phi_m, \Psi_t)) \quad (5)$$

where ρ is Pearson’s correlation coefficient.

4 RESULTS

4.1 BENCHMARKING ALIGNMENT OF VISION MODELS TO THE VISUAL CORTEX

4.1.1 V-JEPA ACHIEVES HIGHEST OVERALL BRAIN-ALIGNMENT SCORES

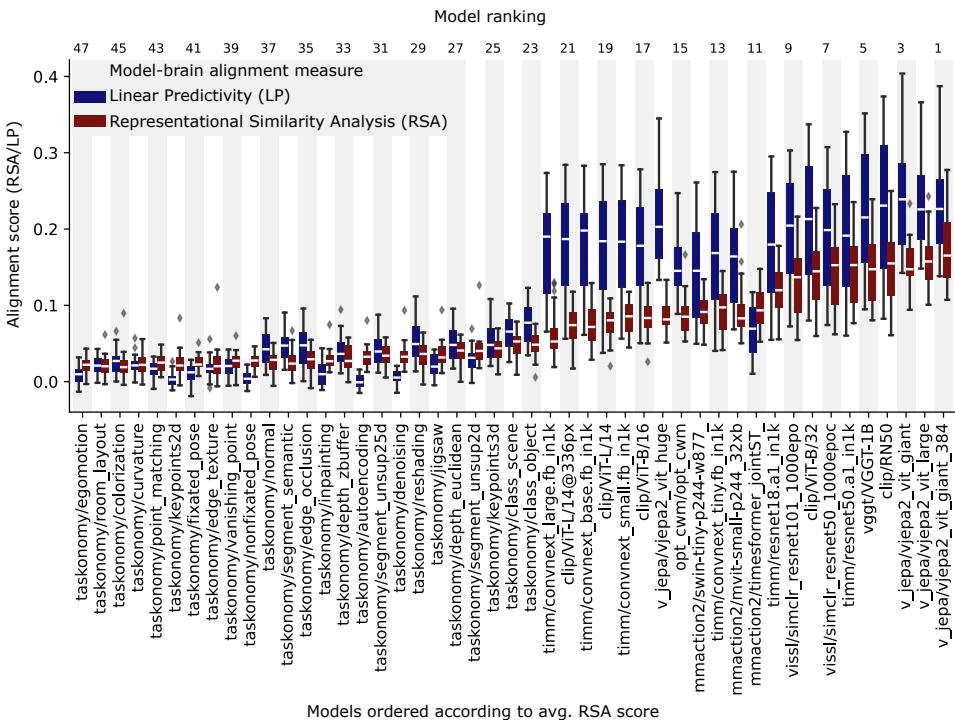


Figure 2: **Standard benchmarking results for the BOLDMoments dataset.** Boxplots depict the distribution of subject-averaged alignment scores (RSA/LP) across ROIs.

We evaluated a broad range of vision models with respect to their alignment to visual cortex—including early, ventral, and dorsal regions—using two complementary alignment measures: RSA and LP. The models varied with respect to architecture (CNNs and Transformers), training objective

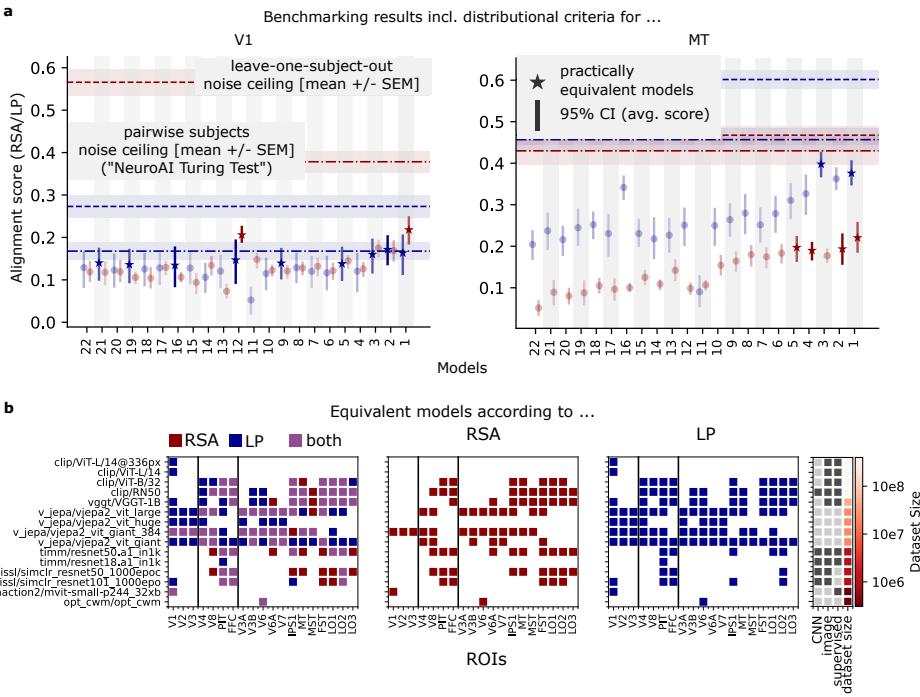


Figure 3: ROI-wise benchmarking results including noise ceilings and practical equivalence assessment **a** Benchmarking results for the top 22 models for two example regions, including upper and lower noise ceilings (see Sec.3.1.1), as well as 95% CIs about the mean alignment score for each model. Practically equivalent models (see Sec. 3.4 are indicated by stars. **b** Overview of all models that are practically equivalent for a given ROI according to RSA, LP or both. The right-most box shows properties of the models.

(various supervised and self-supervised objectives), modality (image and video), as well as model size and training dataset (Methods 3.2).

Consistent with previous work (Tang et al., 2025), we found that the self-supervised V-JEPA 2 model family (Assran et al., 2025), achieved the strongest overall alignment scores across visual cortex, according to both RSA and LP (Fig. 2). Notably, however, the best aligned models included CLIP with a ResNet-50 backbone and the VGG-Transformer—which differ in several important aspects from V-JEPA 2 and each other, such as the training data, training objective and overall architecture. LP appeared to primarily separate poorly aligned models (largely from the Taskonomy family) from the rest, while offering limited discrimination among better-aligned models. RSA, by contrast, produced a more graded ranking that distinguished among high-performing models.

4.1.2 MODELS PASS THE NEUROAI TURING TEST ON LP, BUT NOT ON RSA

We compared model-brain alignment scores to an upper and a lower noise ceiling derived from inter-subject (i.e., brain-brain) alignment distributions. The lower noise ceiling is defined as the 95% confidence interval (CI) of the average alignment of brain activity of any two subjects in the population(Feather et al., 2025; Thobani et al., 2025) (“NeuroAI Turing Test”). The upper noise ceiling is defined as the 95% confidence interval (CI) of the average alignment of the leave-one-subject-out average brain activity to the left-out subject. We find that for LP, many models reach or even surpass the lower noise ceiling for many ROIs, thereby passing the NeuroAI Turing test. However, both the noise ceiling and the absolute model performance are relatively low. In contrast, for RSA this is rarely the case - namely, for the ROI-model combinations V-JEPA ViT-giant-384 - V3A, V-JEPA ViT-giant-384 - V6, V-JEPA ViT-large - V6, and Opt-CWM - V6 (Fig. 3a, Figs. S4.1–S4.7).

378 4.2 DIFFERENT MODELS ARE PRACTICALLY EQUIVALENT IN MODEL-BRAIN ALIGNMENT
379380 Next, we further assessed the robustness of model rankings and the discriminability between mod-
381 els in terms of brain alignment by checking for models that were practically equivalent in brain-
382 alignment (see Methods 3.4), i.e., whose scores fell within the 95% CI of the mean score of the
383 top-ranking model. This analysis revealed that many models were practically equivalent in terms
384 of brain alignment (Fig. 3 a, b; Figs. S4.1 - S4.7), but results differed between LP and RSA. For
385 example, in primary visual cortex (V1), LP grouped nine models as practically equivalent to the best
386 model, whereas RSA reduced this set to just two. We found a similar pattern in ventral regions such
387 as PIT, where LP identified ten models as equivalent compared to five with RSA. Dorsal regions, by
388 contrast, showed broader equivalence classes under both metrics. Overall, RSA yielded sharper dis-
389 tinguishes than LP, classifying on average 4.1 models as practically equivalent per region, compared
390 to 5.6 with LP.391 These findings demonstrate the lack of discriminative power of alignment-measure based model
392 rankings, motivating the need for additional criteria to distinguish between equivalently aligned
393 models.394
395 4.3 ALIGNMENT PATTERN SIMILARITY AS A NECESSARY CRITERION FOR
396 BRAIN-ALIGNMENT
397398 We propose a necessary (though not sufficient; see Discussion) criterion for alignment to a brain re-
399 gion: a model should not only match that region locally, but also preserve its pattern of relationships
400 to other regions. First, we estimated fMRI-derived cross-region alignment patterns. These patterns
401 are highly consistent *within* each ROI for both RSA and LP (RSA: Fig. 4a,b, black lines and boxes;
402 LP: Suppl. Fig. S4.9). Moreover, whereas RSA yields clearly distinct alignment patterns for differ-
403 ent ROIs, LP does not: LP-based cross-region patterns are substantially more homogeneous across
404 ROIs (Suppl. Fig. S4.9).405 Next, we examined *model*-derived alignment patterns for all models in the equivalence class of
406 each ROI (Section 4.2). RSA produces strongly model-specific alignment patterns, enabling dis-
407 crimination among models that are otherwise equivalent (Fig. 4a,b, colored lines and boxes). In
408 contrast, LP yields uniformly high pattern similarity across models, providing little discriminability
409 (Suppl. Fig. S4.9). Training further increases alignment-pattern similarity (APS) for RSA—often
410 substantially—but has little to no effect on LP-based APS (Suppl. Fig. S4.10).411 Finally, applying a lenient criterion that a model’s alignment-pattern similarity to its ROI’s pattern
412 must at least be positive, RSA-based APS excludes three V-JEPA variants as candidate models
413 across ten (mostly dorsal) ROIs (Fig. 4c). In contrast, LP-based APS excludes only three out of nine
414 candidate models, and only for a single ROI (V1).415 Overall, these results show that RSA-based fMRI-derived APs are highly reliable and ROI-specific,
416 whereas LP-derived patterns are both more homogeneous across ROIs and similarly high for nearly
417 all models, trained or untrained. Consequently, LP offers limited ability to distinguish between
418 models on the basis of cross-region alignment structure.420
421 4.4 RSA-BASED BUT NOT LP-BASED ALIGNMENT PATTERNS TRACK STRUCTURAL
422 CONNECTIVITY
423424 To better understand the factors determining brain-brain alignment patterns, and the role of the align-
425 ment measure used to calculate APs, we estimated APs from an independent dataset of structural
426 connectivity from N=1065 humans(Caron & Pestilli, 2023). The similarity measure used to cal-
427 culate connectivity-derived APs is streamline density(Pierpaoli et al., 1996), which takes the role
428 of RSA/LP in the fMRI-based APs. We then compared these connectivity-derived APs with RSA-
429 based and LP-based fMRI-derived APs. We found that RSA-based fMRI-derived APs were similar
430 to connectivity-derived APs for most early, ventral and late dorsal regions (Fig. 5, 12/19 ROIs sig-
431 nificant; Methods), whereas the same analysis for LP-based APs revealed much lower similarity
432 between fMRI-derived and connectivity-derived APs (Suppl. Fig. S4.11, 5/19 ROIs significant).

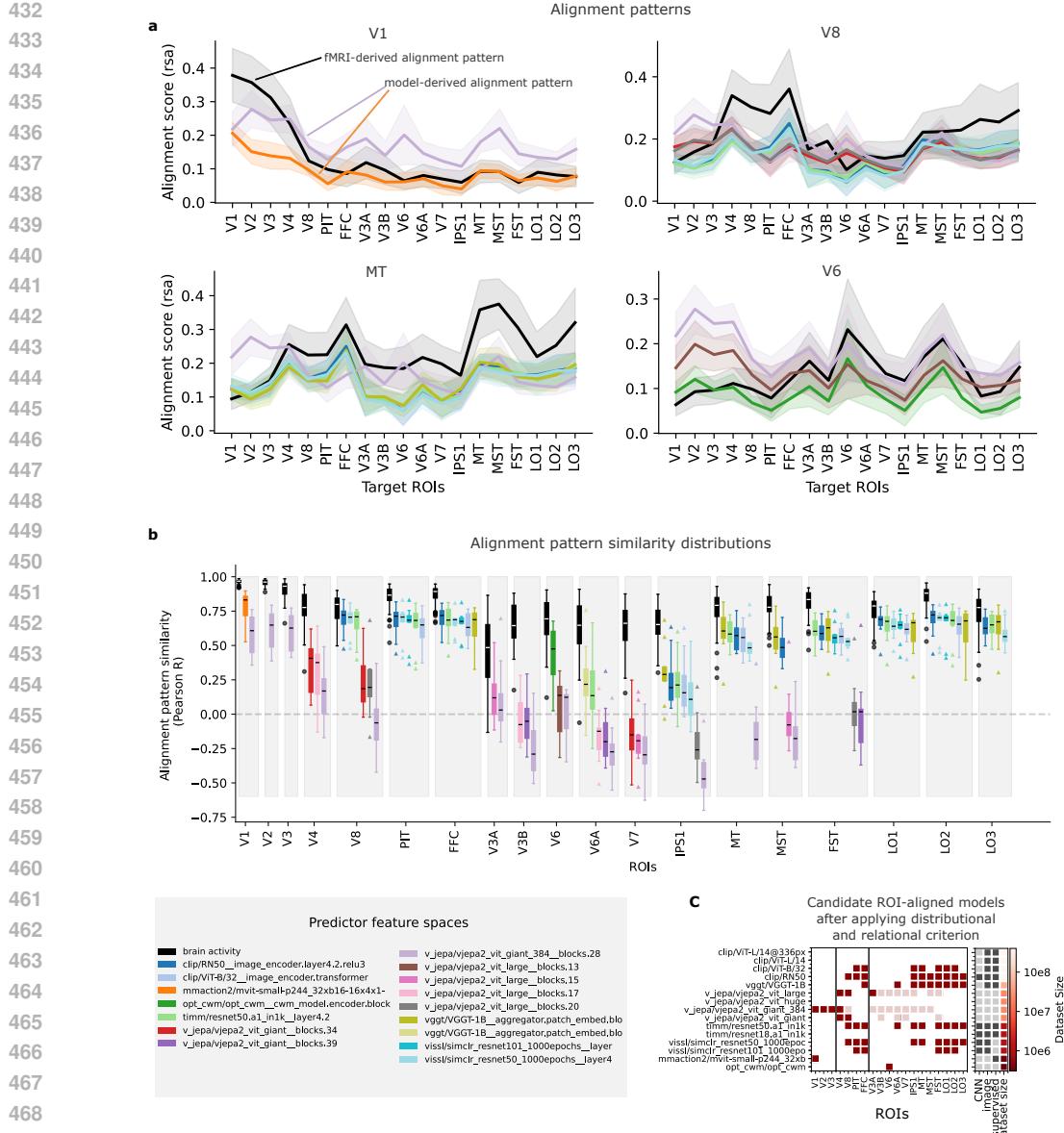
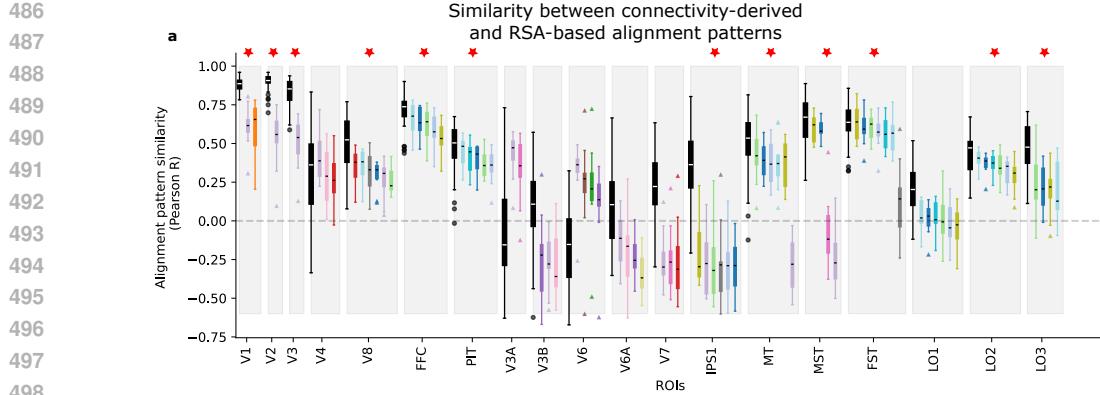


Figure 4: Alignment patterns are consistent within ROIs and distinguish equivalently aligned models. **(a)** RSA-based fMRI-derived (black) and model-derived (coloured) alignment patterns for four example ROIs. Shaded area indicates \pm SD (see Appendix Sec. S3.1). **(b)** Distributions of alignment pattern similarities within a ROI (black box-plots) and between a ROI and its equivalently aligned models (coloured box-plots). **(c)** Same plot as Fig. 3b, but graying out models whose 95% CI of the mean APS includes zero.

5 DISCUSSION

In this work, we show that model rankings produced by standard brain-alignment benchmarking pipelines are insufficient both for identifying the most brain-aligned models as well as for distinguishing them from merely brain-predictive models. To alleviate this problem, we introduce and apply a relational criterion - alignment pattern similarity - and propose to use it as an additional criterion in alignment benchmarks to increase their discriminative power.



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Figure 5: Connectivity-derived alignment pattern similarity across ROIs and models. Colour code as in previous plots. APS is calculated between RSA-based fMRI-derived and connectivity-derived APs (black box-plots), and between RSA-based model-derived and connectivity-derived APs (coloured box-plots) (see Methods Sec. 3.5.2). Stars indicate significantly higher fMRI-connectivity APS than with random connectivity-derived APs (see Appendix Sec. S3.2).

What does it mean to be “brain-aligned”? As pointed out by Schaeffer et al. (Schaeffer et al., 2024), “NeuroAI lacks canonical definitions of neural similarity”. This lack of canonical definitions, among other factors, underlies recent discussions about common practices of brain-alignment benchmarking and the kinds of conclusions that can (or cannot) be drawn about model-brain similarity based on the results of such benchmarks (e.g. Dujimovi et al. (2024); Bowers et al. (2023)). At the core of the discussion is the repeated finding that models often achieve high brain-alignment according to some measure while diverging from the brain in other aspects that neuroscientists consider relevant to “true” brain-alignment (Schaeffer et al., 2022; Malhotra & Bowers, 2024), without the field agreeing on what those aspects are. Here, we propose alignment pattern similarity as an additional *necessary, but not sufficient criterion* for brain-alignment: low APS excludes models from the pool of potentially brain-aligned models, but high APS does not confirm brain-alignment of a model.

Alignment patterns reveal additional implicit biases of alignment measures Consistent with recent work (e.g. Soni et al. (2024)), our results highlight systematic differences between linear predictivity (LP) and representational similarity analysis (RSA) for state-of-the-art vision models trained on large-scale internet image and video datasets. It has been conjectured that LP implicitly rewards higher-dimensional predictor feature spaces (Schaeffer et al., 2024), which warrants caution in drawing conclusions about brain-alignment from LP-based model rankings. Our results are consistent with this conjecture: LP-based rankings mostly separate models with richer feature spaces from those with less rich feature spaces. Here, in addition to this, we find that LP-based alignment patterns are similar in shape (Suppl. Fig.S4.8), leading to a second conjecture: LP scores carry implicit biases not only about the richness of the predictor feature spaces, but also about the *predictability of the target feature spaces*.

Distinguishing between brain-predictivity and brain-alignment These findings motivate a clear distinction: LP may be effective at identifying brain-predictive models - which can be very useful e.g. as digital twins in a variety of settings such as BMI-applications - but insufficient for discriminating between more and less brain-aligned models in a stricter sense of the term. Recent works have made progress towards narrowing down the set of candidate brain-aligned models by increasing the discriminative power of benchmarks. A promising approach relies on combining complementary measures (Wu et al., 2025). We propose APS in a similar spirit: as a biologically motivated complementary measure for brain-alignment.

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756 **S1 DISCLOSURE OF LLM USE**
757758 We have used LLMs to assist in the code writing process, including for plot creation, to discuss ideas
759 and concepts, in literature search, for searching information in a given work, and for refining text in
760 this paper.
761762 **S2 SUPPLEMENTARY DISCUSSION**
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765 **Relation to prior benchmarks** Our results replicate and refine conclusions from prior benchmarks.
766 We replicate the finding by Sartzetaki et al. (2024) that modeling temporal dynamics is
767 key for RSA-alignment to early visual regions, whereas models trained with semantic objectives
768 are more aligned to higher-level regions. Tang et al. (2025) found that a single predictive objective
769 generalized across cortical areas under LP. Using both LP and RSA, we likewise identify the same
770 best-performing model overall. However, our results suggest that rather than reflecting a single unifying
771 objective, this apparent generalization may instead arise from the flexibility of large feature
772 spaces. In particular, distinct subspaces within a model’s representation may be selectively exploited
773 by linear readouts, each supporting different tasks across cortical areas. A closer analysis of these
774 subspaces could clarify whether cross-regional alignment reflects genuine commonalities or simply
775 the representational versatility of large models. Finally, large-scale efforts such as BrainScore
776 (Schrimpf et al., 2018) and the Algonauts challenges (Gifford et al., 2024; 2023; Cichy et al., 2021)
777 have advanced the field, but their reliance on LP may systematically overstate alignment.
778779 **S3 DETAILED METHODS**
780781 **S3.1 ALIGNMENT PATTERN SIMILARITY DISTRIBUTIONS**
782783 **S3.1.1 ALIGNMENT PATTERN SIMILARITY DISTRIBUTIONS**
784785 To assess whether model-brain alignment pattern similarities fall within or outside the distribution
786 of brain-brain alignment pattern similarities, we first define a subject-specific reference alignment
787 pattern.
788789 For a given ROI r and a subject t_0 , we compute the mean brain-brain alignment pattern across all
790 pairs of subjects (p, t) in which t_0 does not participate, i.e., $p \neq t_0$ and $t \neq t_0$. The subject-specific
791 reference pattern for p_0 is then obtained by averaging over all such alignment patterns that exclude
792 p_0 :
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$$\bar{\alpha}_r^{(t_0)} = \frac{1}{|P \setminus \{t_0\}| \cdot |T \setminus \{t_0\}|} \sum_{\substack{p \in P \setminus \{t_0\} \\ t \in T \setminus \{t_0\}}} \alpha_r(\phi_p, \Psi_t), \quad (S1)$$

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796 where P and T denote the sets of all predictor and target subjects.
797798 The brain-brain alignment pattern similarity distribution for subject t_0 , ROI r is then defined as the
799 set of similarities between the reference pattern $\bar{\alpha}_r^{(t_0)}$ and all individual alignment patterns **in which**
800 t_0 **functions as the target**:
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$$\mathbf{D}_{\text{brain}}^{(t_0)} = \left\{ \rho(\bar{\alpha}_r^{(t_0)}, \alpha_r(\phi_p, \Psi_{t_0})) \mid p \in P \setminus \{t_0\} \right\}. \quad (S2)$$

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804 Analogously, the model-brain alignment pattern similarity distribution for subject t_0 is computed
805 using the model feature space ϕ_m as predictor:
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$$\mathbf{D}_{\text{model}}^{(t_0)} = \left\{ \rho(\bar{\alpha}_r^{(t_0)}, \alpha_{r_0}(\phi_m, \Psi_{t_0})) \right\}. \quad (S3)$$

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812S3.2 SIGNIFICANCE OF fMRI-DERIVED-TO-STRUCTURAL ALIGNMENT PATTERN
SIMILARITY813
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To determine whether an APS value between a structural and an fMRI-derived alignment pattern is meaningful and not due to random chance, we create a null distribution of structural patterns, and compute APS between the fMRI-derived pattern to those random patterns.

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We create random patterns by sampling 18 regions $\mathbf{k} = (k_1, \dots, k_{16})$ at random from all regions contained in the full structural connectivity matrix $\tilde{C} = (\tilde{c}_{i,j})_{i,j=1\dots M}$, $M > N$, containing additional regions to the ones included in our analysis. This yields one random alignment pattern per region,

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$$\alpha_{rand,\mathbf{k}}(r) = [\tilde{c}_{\sigma(r),k_1}, \dots, \tilde{c}_{\sigma(r),k_{16}}] \quad (S4)$$

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where $\sigma(r)$ is the index of region r in matrix \tilde{C} . We then compute the APS to fMRI-derived alignment pattern $\alpha(\phi_p^r, \Psi_t)$ as

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$$\rho(\alpha(\phi_p^r, \Psi_t), \alpha_{rand,\mathbf{k}}(r))$$

according to equation 3.5.4.

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We repeat this 100 times to get a 95% percentile range of APS values due to random chance. We consider a fMRI-derived-to-structural APS value significant if it falls outside this range.

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S4 SUPPLEMENTARY RESULTS

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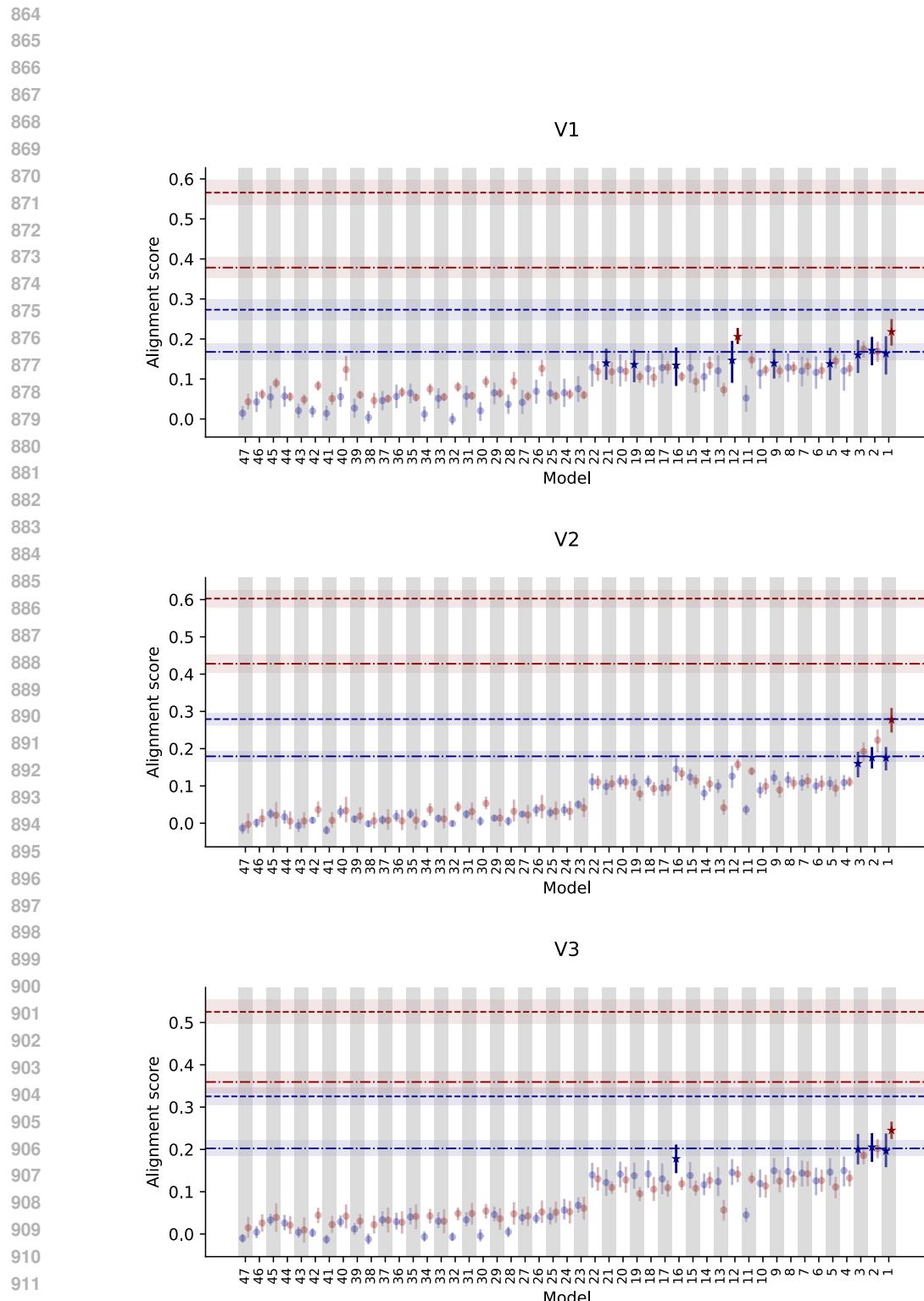


Figure S4.1: Benchmarking results for each ROI. Legend see main Figure 2

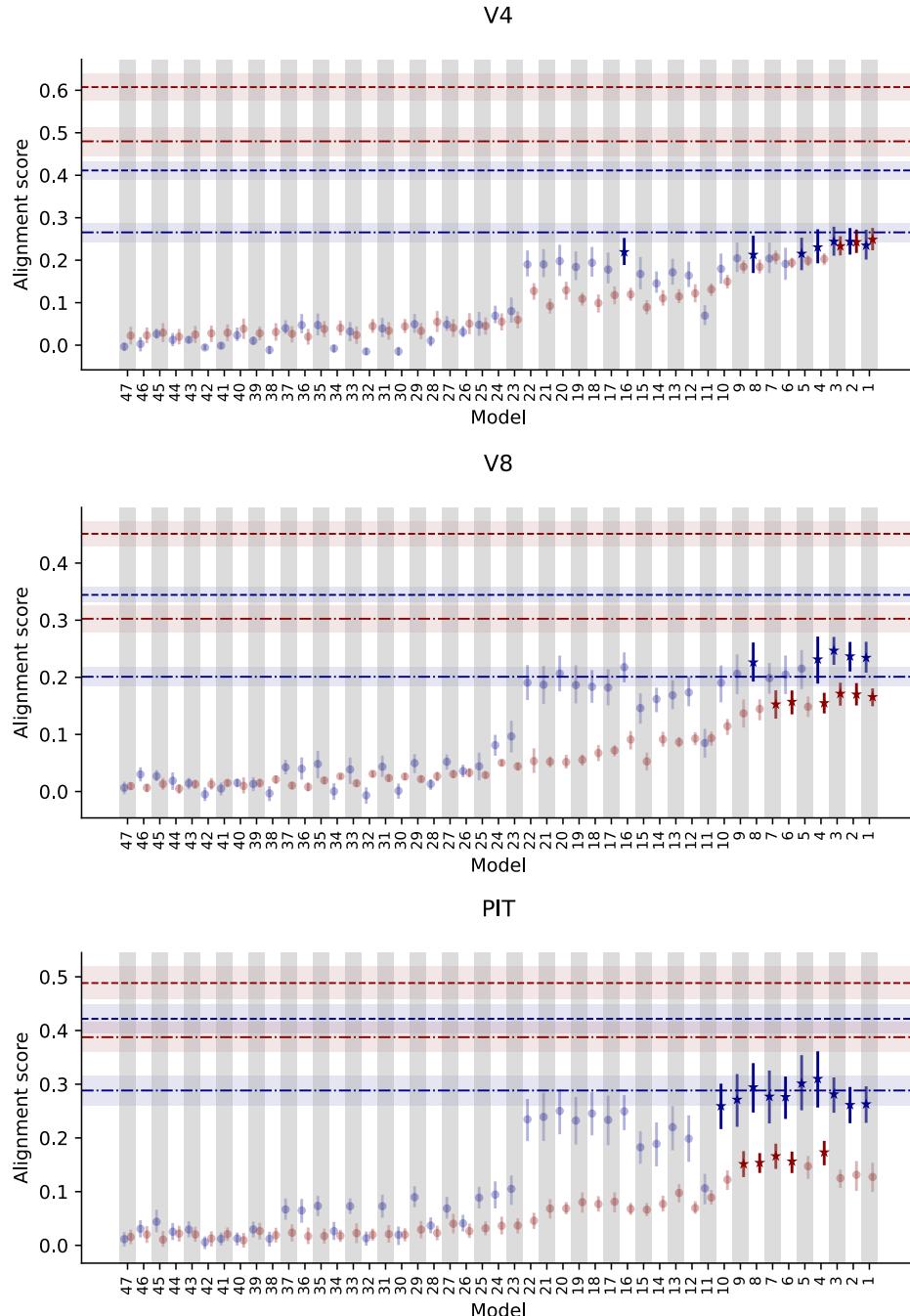


Figure S4.2: Benchmarking results for each ROI. Legend see main Figure 2

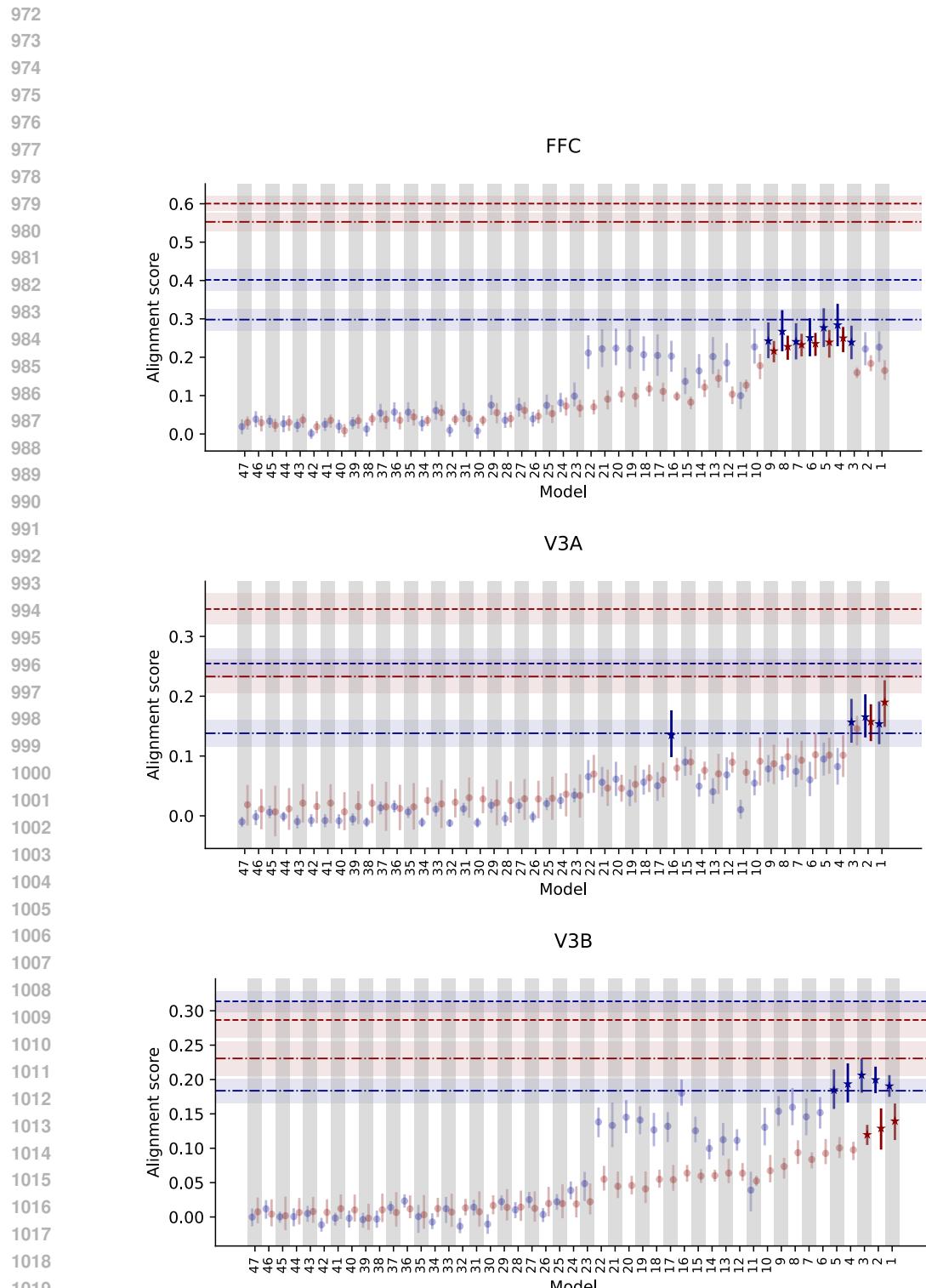


Figure S4.3: Benchmarking results for each ROI. Legend see main Figure 2

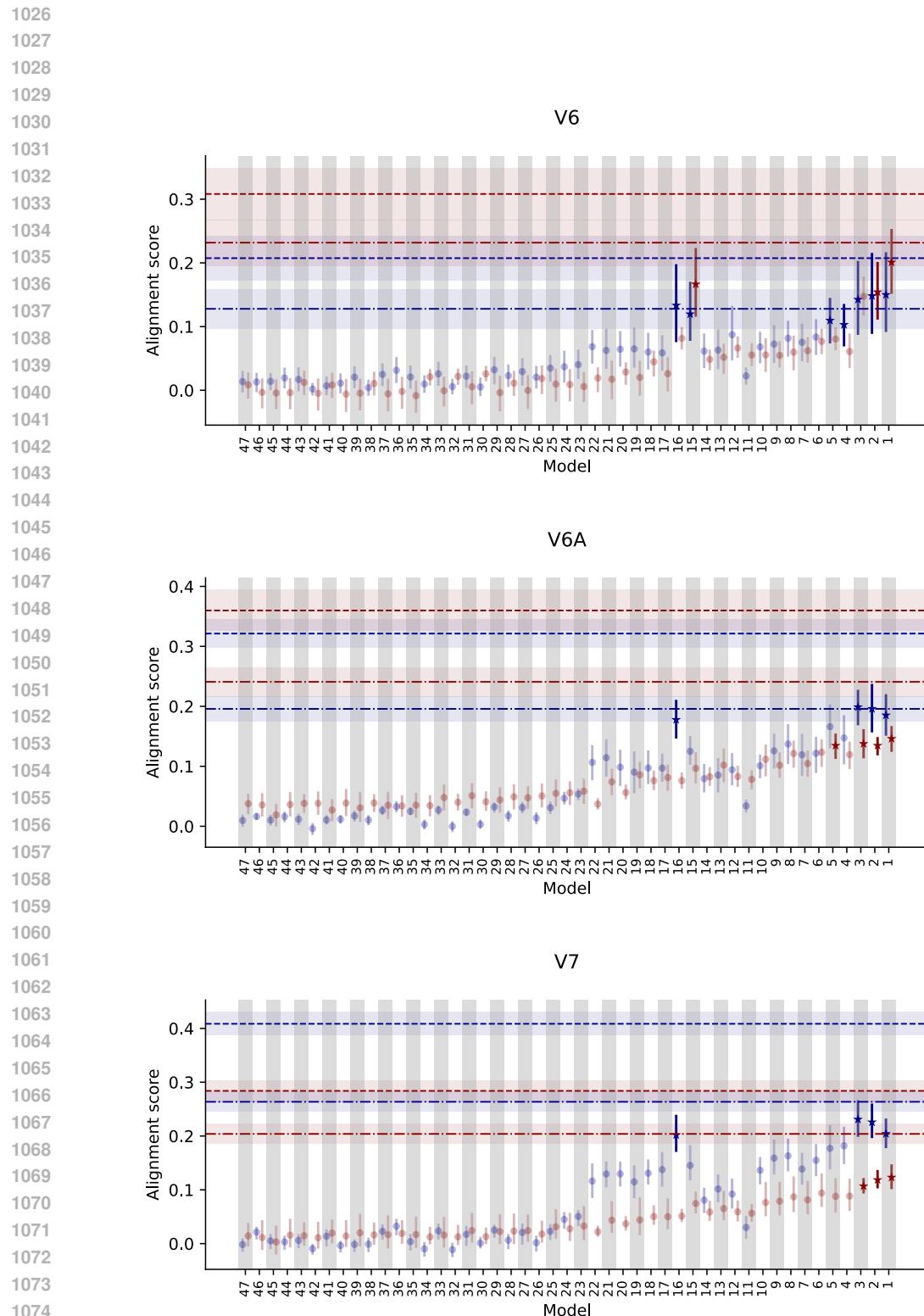


Figure S4.4: Benchmarking results for each ROI. Legend see main Figure 2

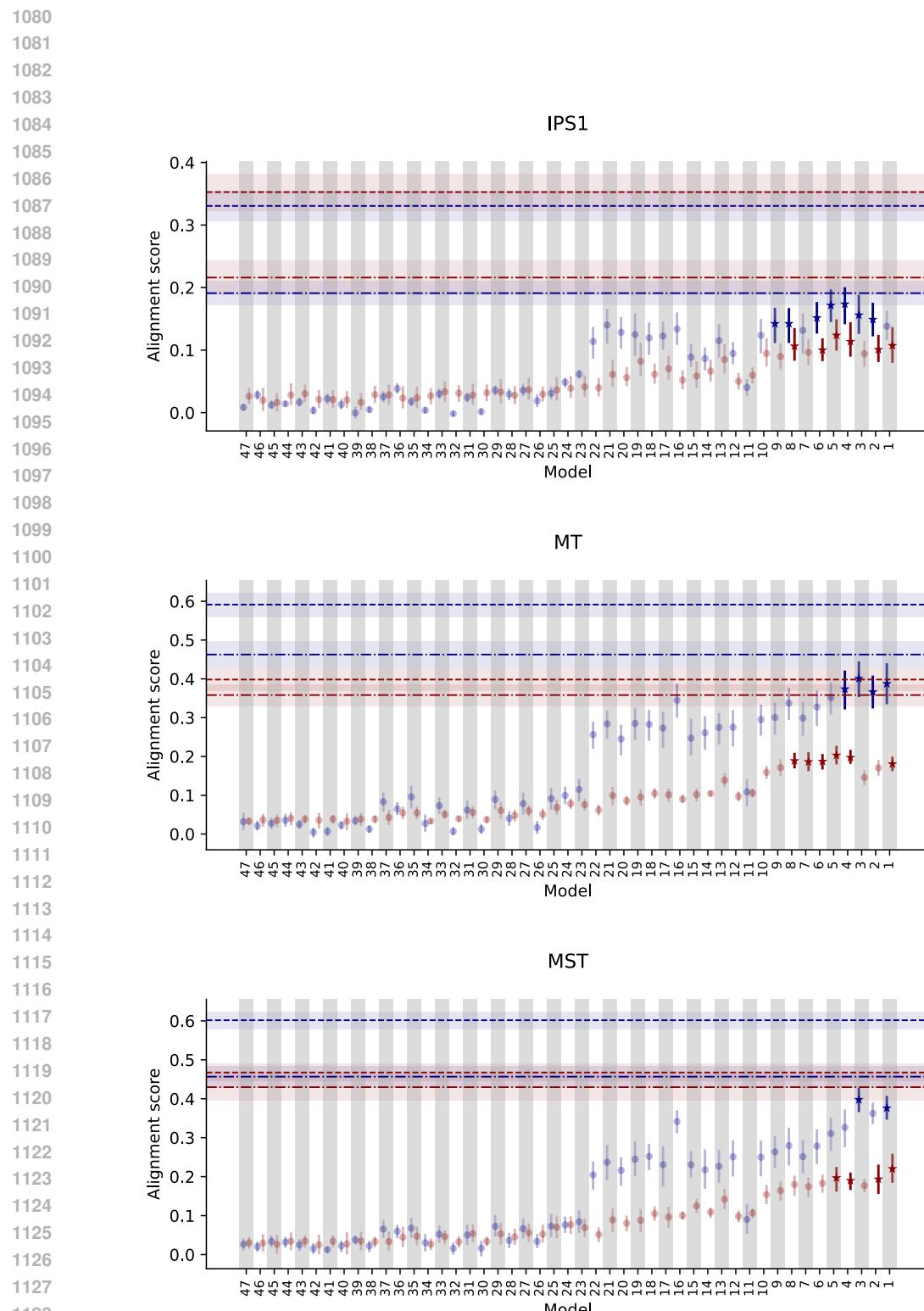
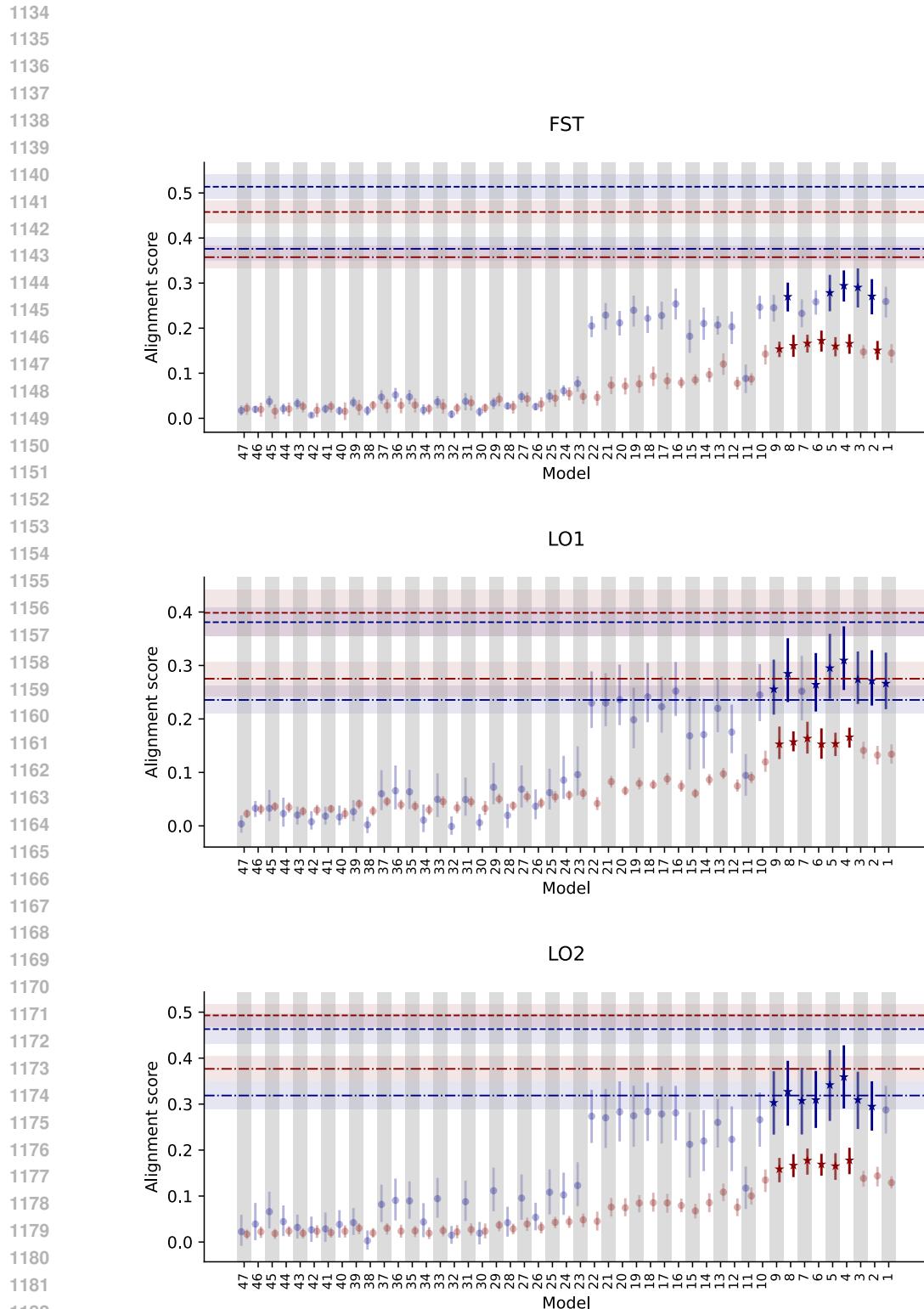
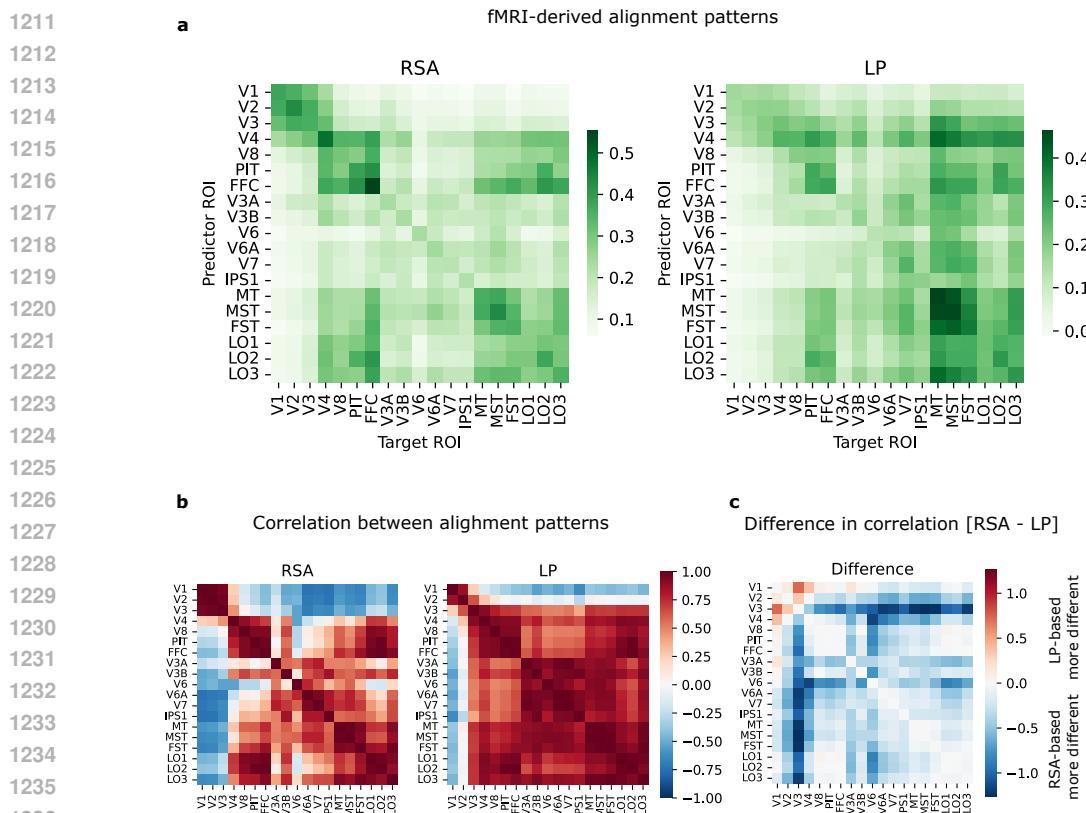
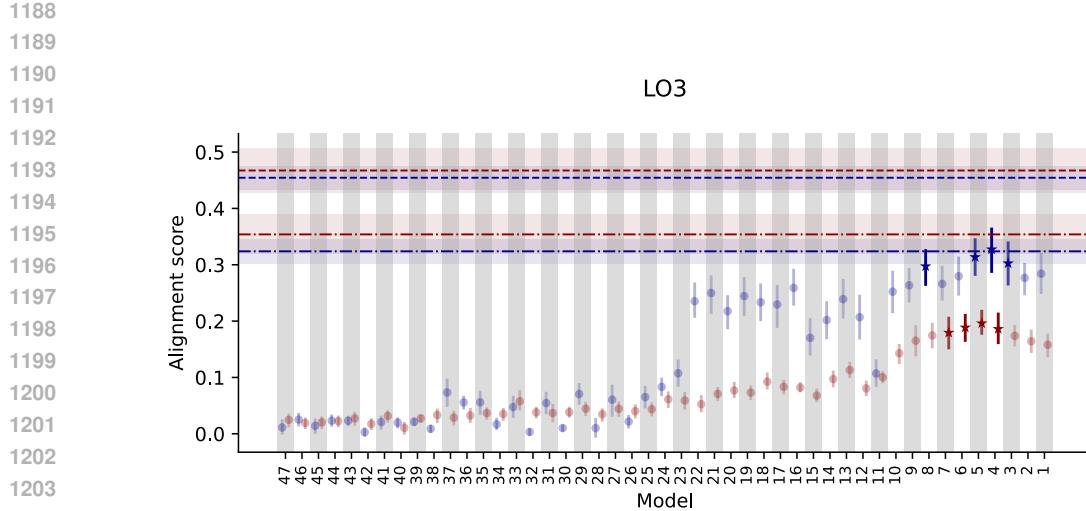


Figure S4.5: Benchmarking results for each ROI. Legend see main Figure 2





1238 Figure S4.8: fMRI-derived alignment patterns and their similarities, RSA-based vs. LP-based. **(a)**
1239 Alignment patterns as heatmaps. **(b)** Confusions matrices based on pairwise correlations between
1240 alignment patterns. **(c)** Difference in correlation (RSA-titled panel in (b) - LP-titled panel in (b)).

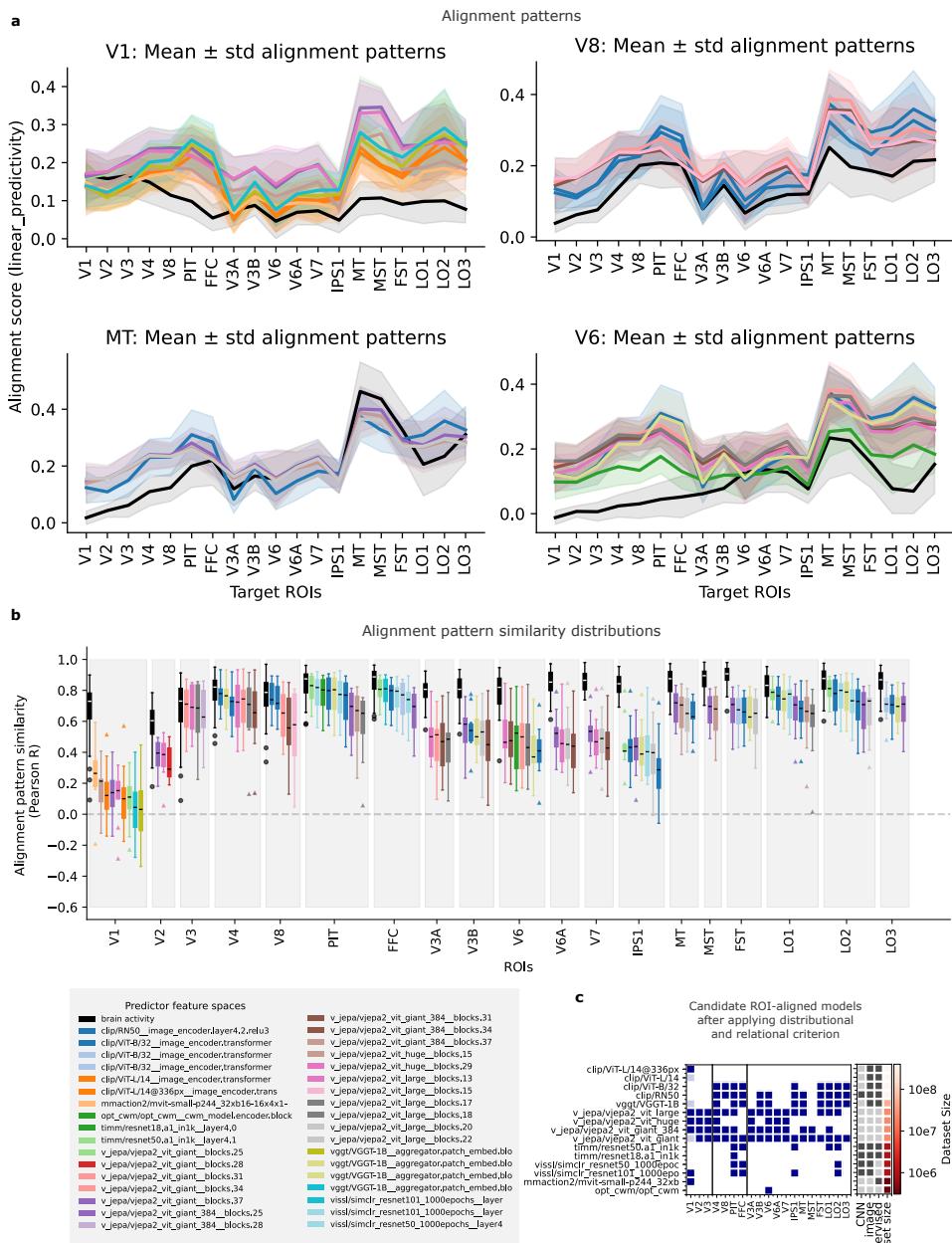


Figure S4.9: Alignment patterns and their similarities for ROIs and models, evaluated with LP. Same as figure 4 but with LP instead of RSA used as alignment measure.

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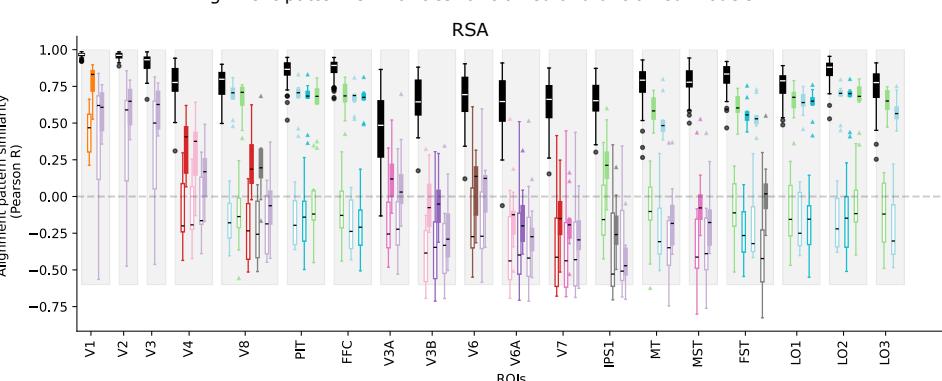
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a Alignment pattern similarities for trained and untrained models



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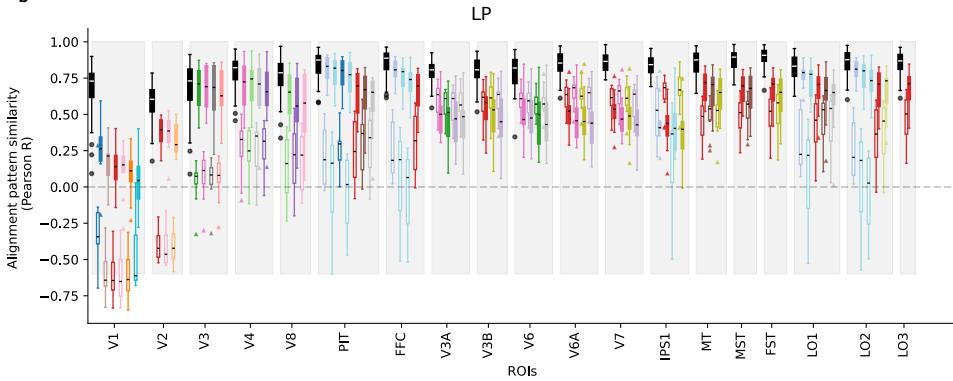
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RSA

LP

Predictor feature spaces



Predictor feature spaces



Figure S4.10: Alignment patterns and their similarities for trained and untrained models. a) RSA: Boxplots showing interquartile range of brain-brain APS (black) compared to model-brain APS for all models practically equivalent to the model with highest alignment to the region. Filled colorful boxes: trained models, white-filled boxes: untrained models. For model colors see legend. b) Same, but with LP as alignment measure.

