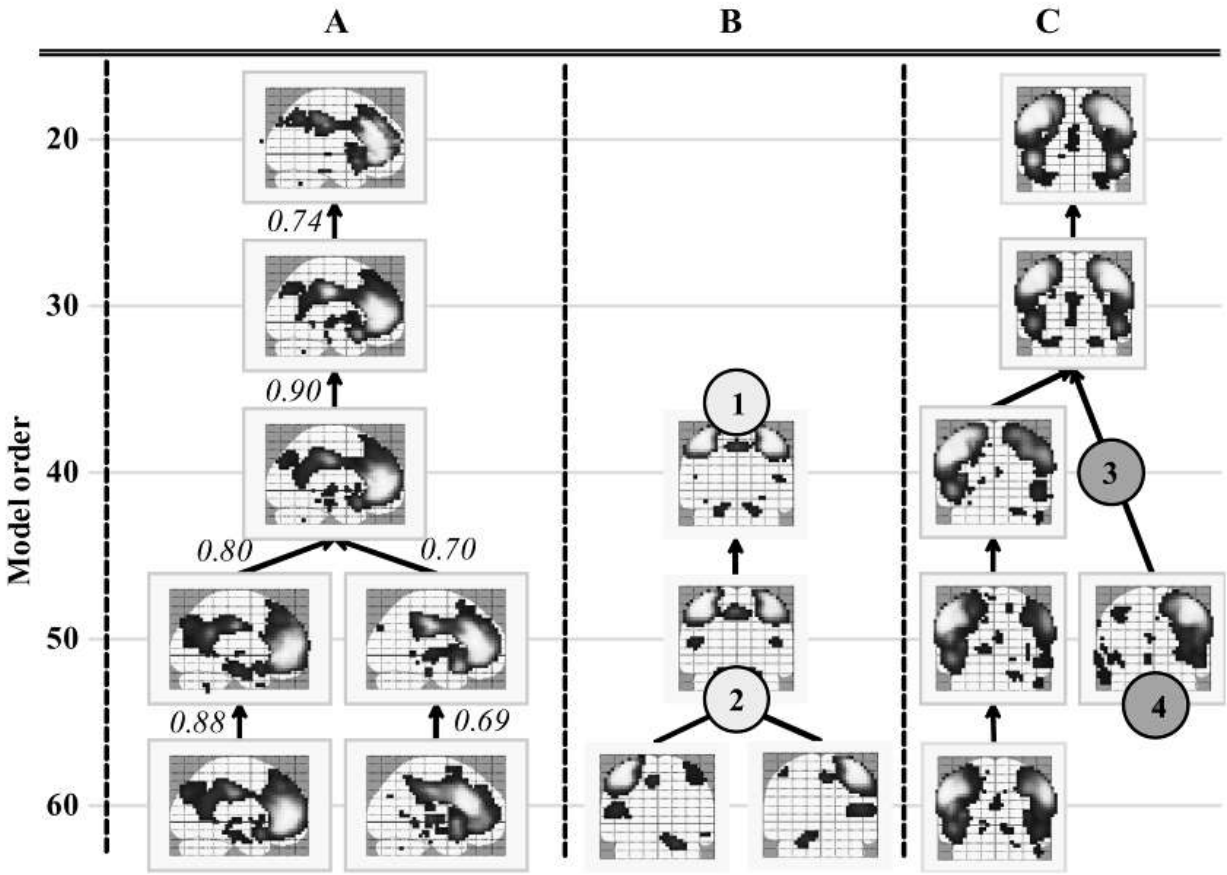
Concat-ICA supplementary results : multilevel model order analysis

- Here we present supplementary result of the submitted manuscript “A novel group ICA approach based on multi-scale individual component clustering: Application to fMRI resting-state data from a 310-subject cohort”.
- Method overview :
  - A total of 310 healthy young adults (152 women, 158 men) aged 18–57 years (27 ± 8 years, mean ± SD) participated in this study.
  - Spontaneous brain activity was monitored using BOLD-fMRI while the participants performed an 8-minute resting state condition. Prior to the fMRI session, high-resolution 3D T1-weighted structural MR brain images were acquired.
  - The fMRI data were corrected for slice timing differences and motion; normalized to the MNI stereotaxic space (4x4x4 mm^3 voxels); spatially smoothed (Gaussian 6 mm FWHM); regressed from time series for white matter, cerebrospinal fluid, and the six motion parameters; temporally band pass filtered (0.01 - 0,1Hz).
  - Using Concat-ICA, we performed a multilevel model analysis with five model orders (number of estimated components), ranging from 20 to 60 by a step of 10. The repetition factor was set to R=25, and we reported clusters of independent components which were detected in at least more than 50% of the repetitions.
  - We present a hierarchical representations of the results across different model orders as proposed by Abou-Elseoud et al. (2010).

Hierarchical representations of the results



Hierarchical representation of the multilevel order analysis. A Example of a component tree. Hierarchical representation of a frontal signal source. Weighted arrows indicate the inclusion index. B Descriptive indices of the trees: **"detection point" (1)** and **"branching point" (2).** C Lack of stability indices: **"missing link" (3)** and **"no child" (4).** Data are presented using a maximal intensity projection scheme in sagittal (A) and coronal orientations (B,C).

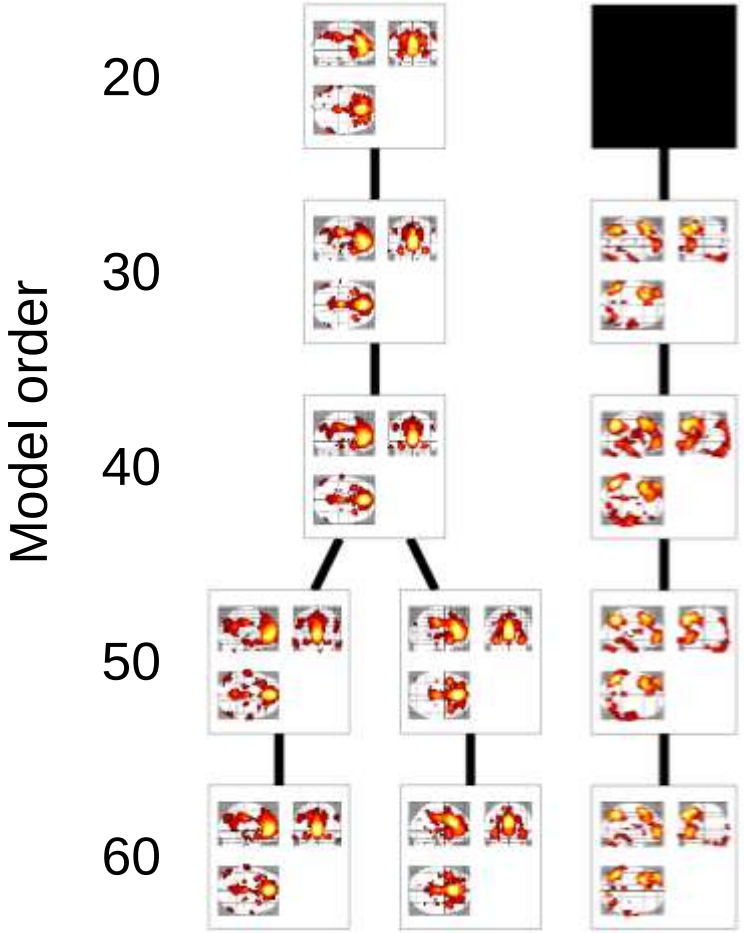
According to the hierarchical modeling, each component estimated at a defined model order (*i*) is spatially included in one component estimated at a lower model order (*j*). We defined an index (γ) to quantify the inclusion of two components between different model orders. This index equally mixed the spatial overlap and the spatial similarity between the significant voxels of the two components Z_i and Z_j, thresholded at $p > 0.95$ using the mixture model distribution (Beckmann and Smith 2004). Following equation computed the inclusion index between Z_i and Z_j :

$$\gamma(Z_i, Z_j) = 0.5 \frac{card(L)}{card(Z_i)} + 0.5 \frac{1}{card(L)} \sum_{l \in L} \left(\frac{Z_i(l) - \overline{Z_i}}{\sigma_{Z_i}} \right) \left(\frac{Z_j(l) - \overline{Z_j}}{\sigma_{Zj}} \right)$$

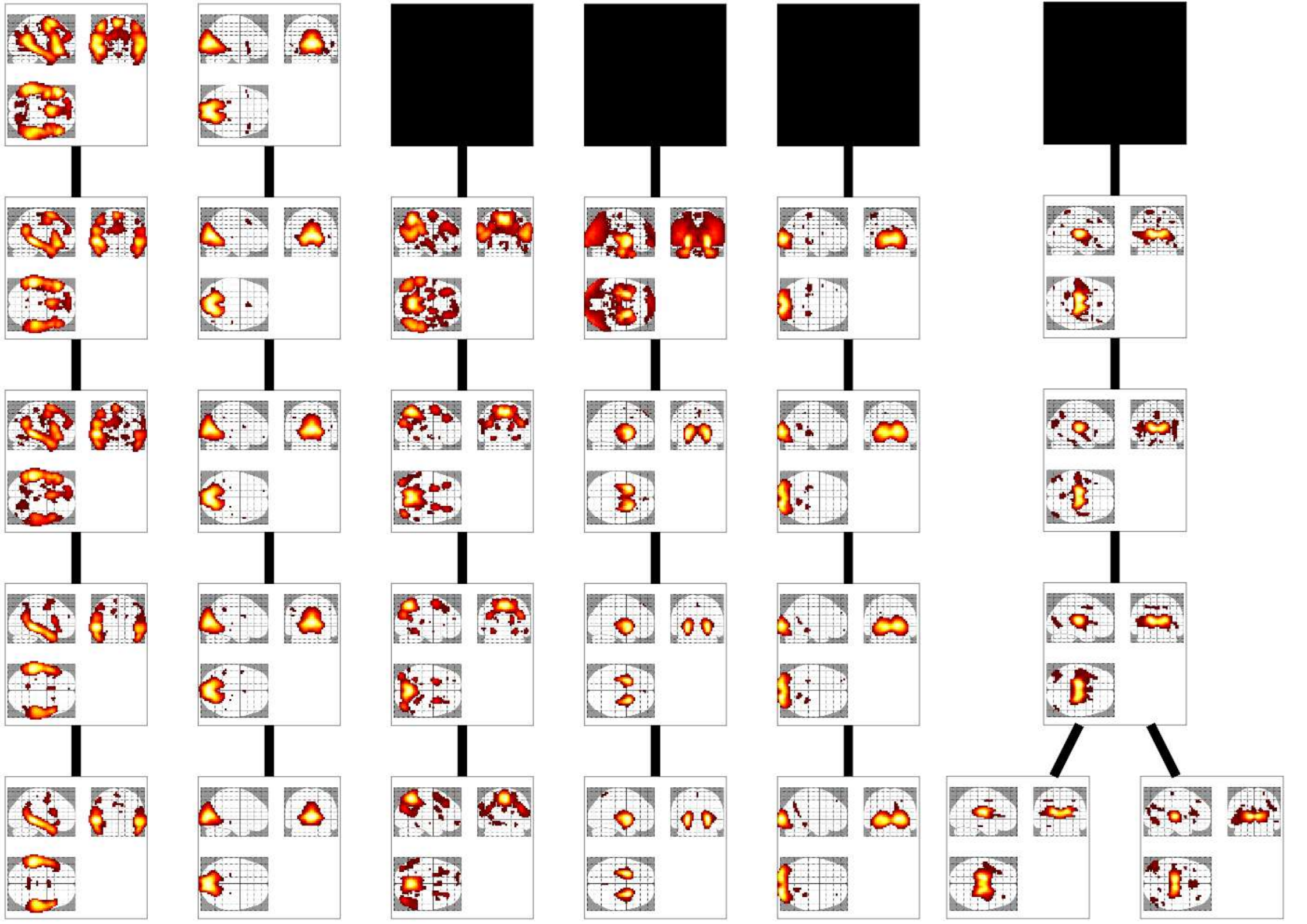
where $L = Z_i \cap Z_j$, $card(Z_i)$ is the number of significant voxels of the component Z_i. L is the intersection of the two components; and the average value of the significant voxels included in L for component Z_i and Z_j, respectively; σ_{Zi} and σ_{Zj} their standard deviation.

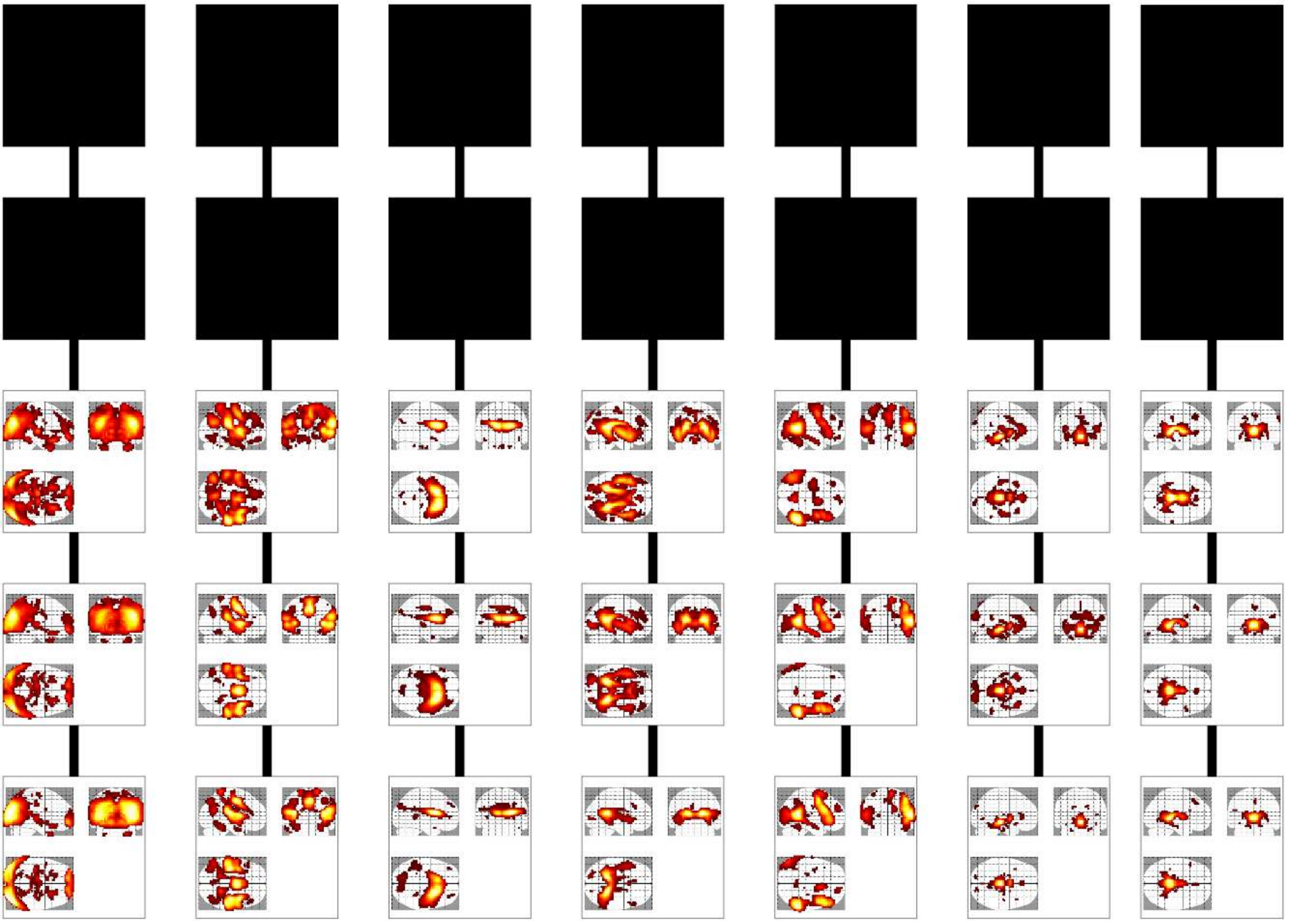
Well-formed trees

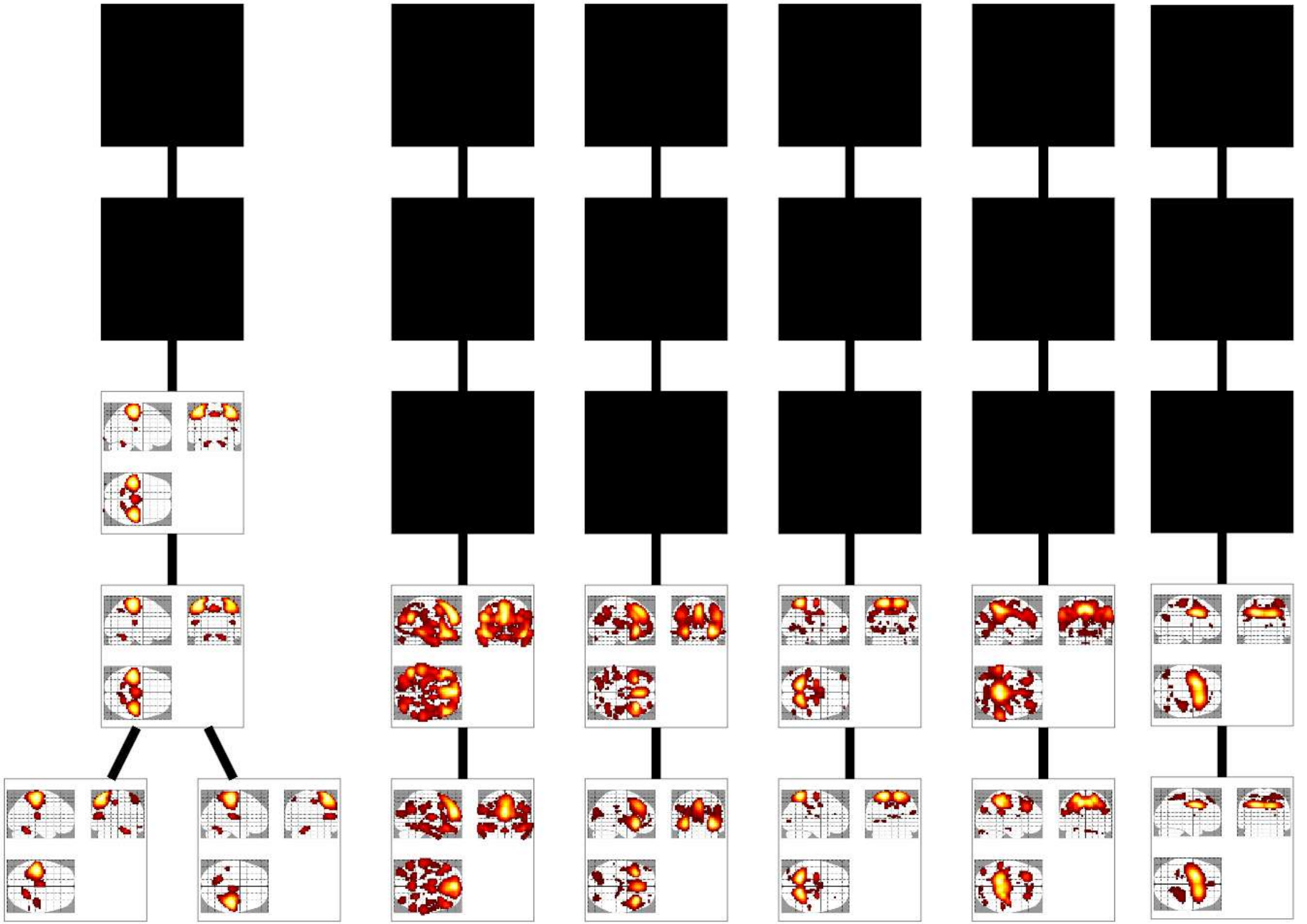
- A well formed tree does not include « missing link » or « no child »
- Examples :

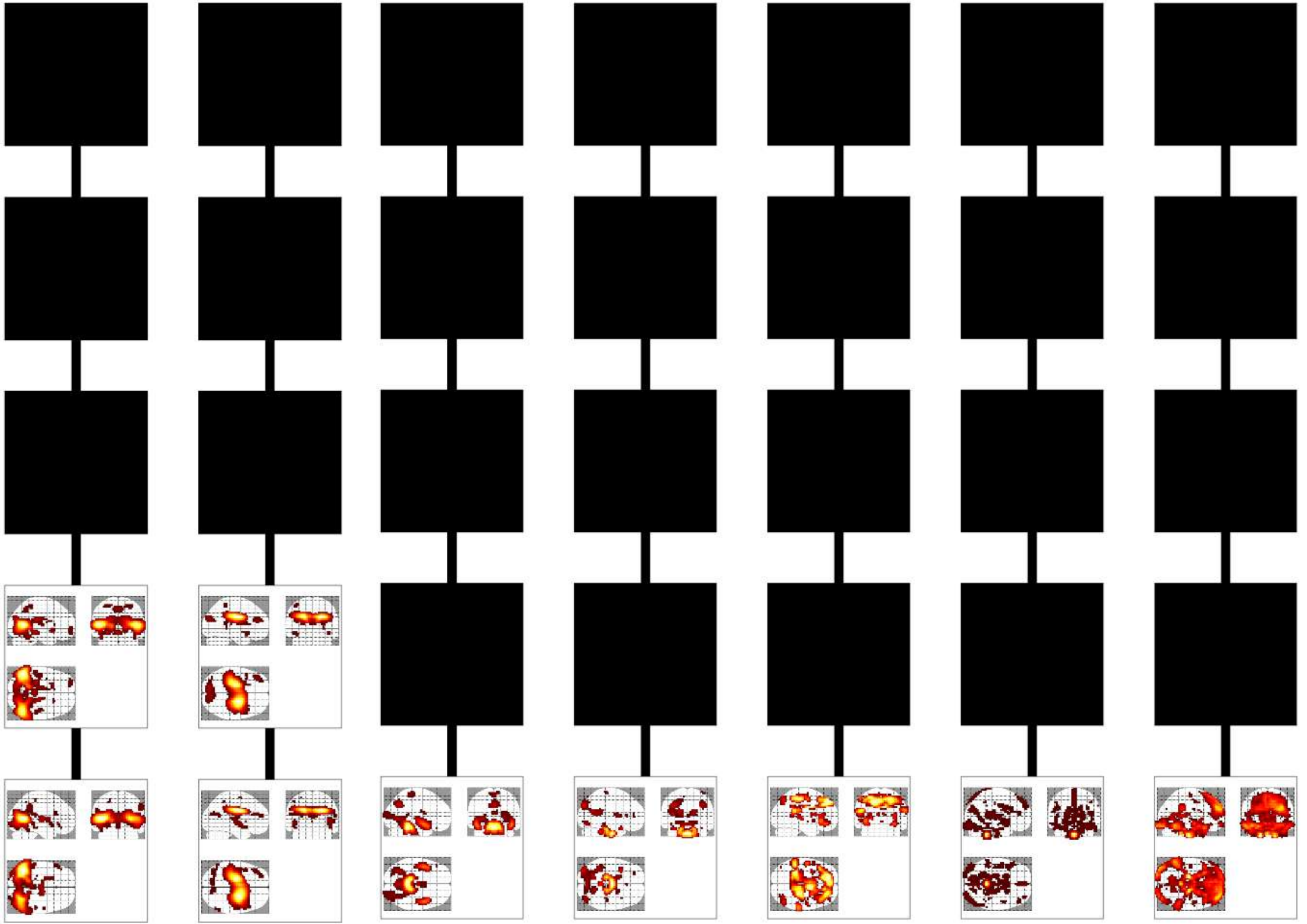


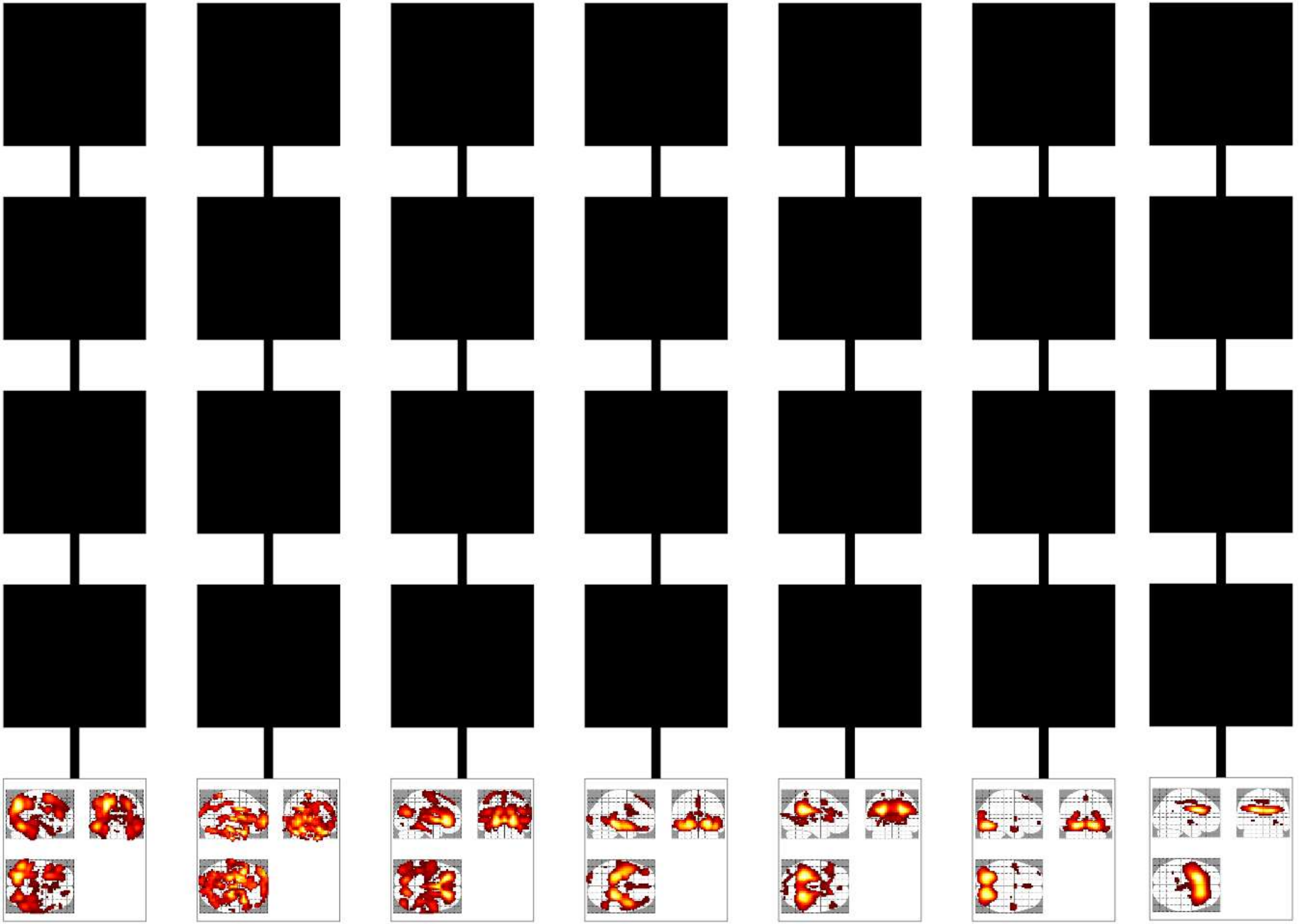
- Next slides shows the 28 well-formed trees observed with MICCA (45% of the trees)



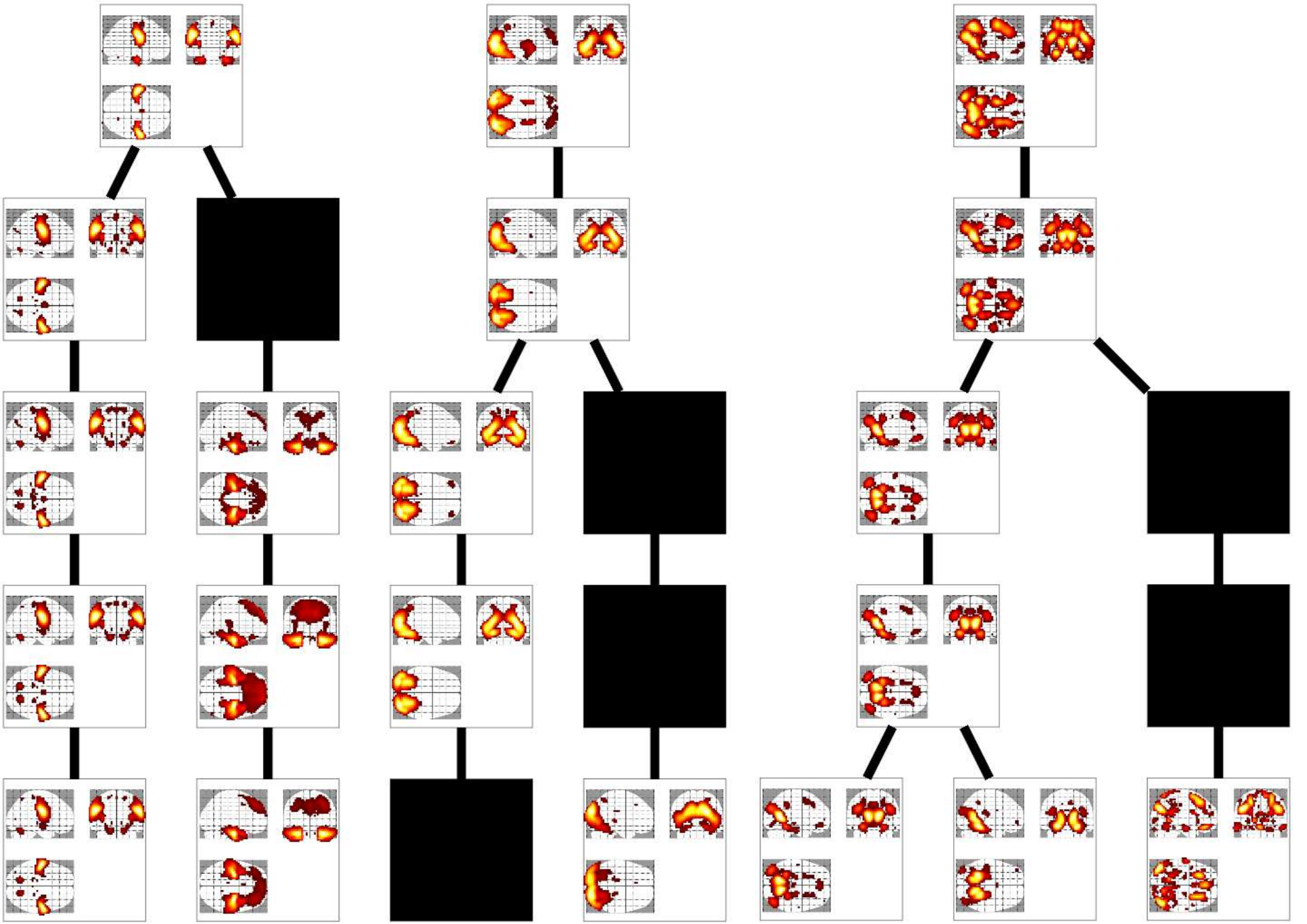


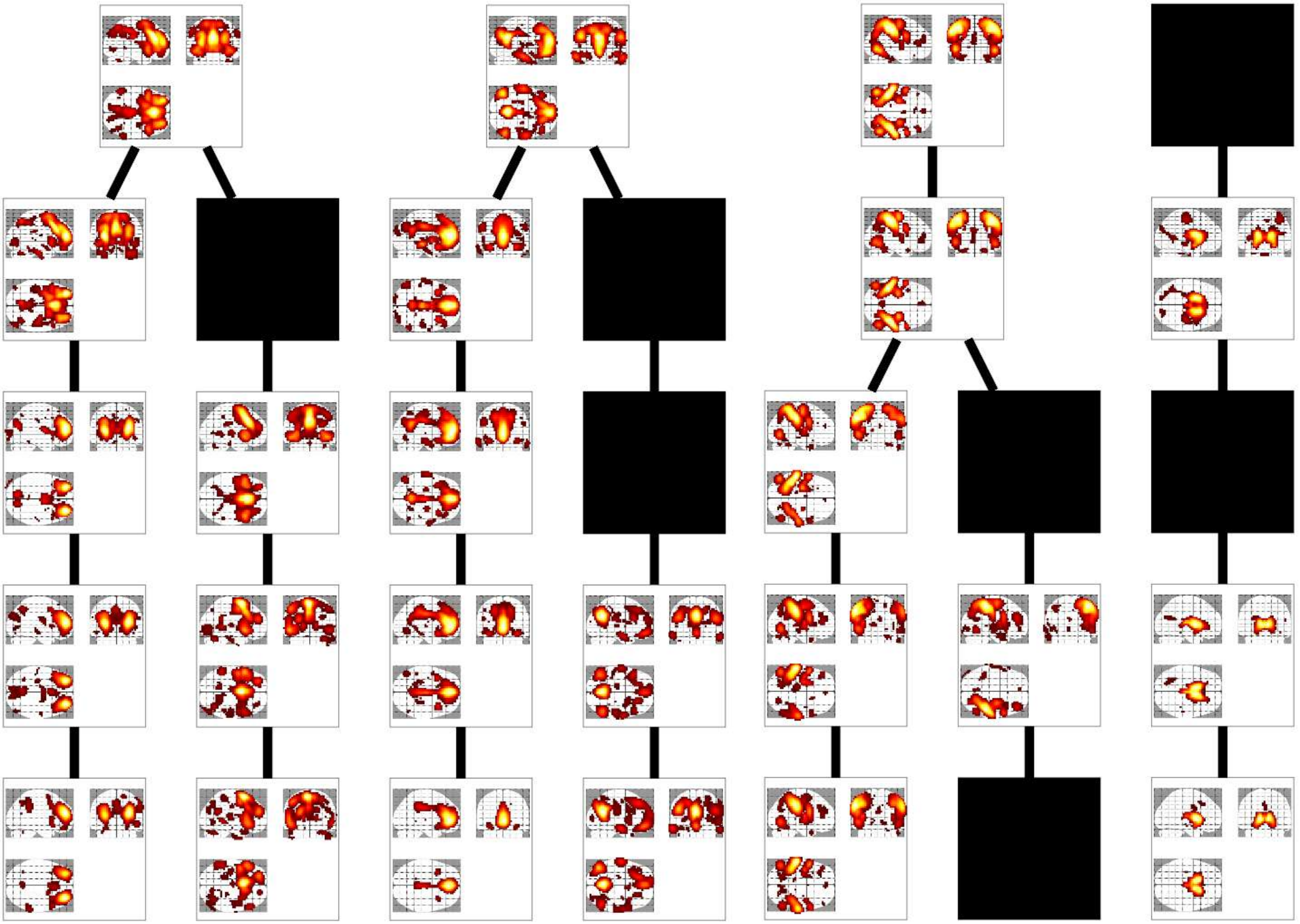


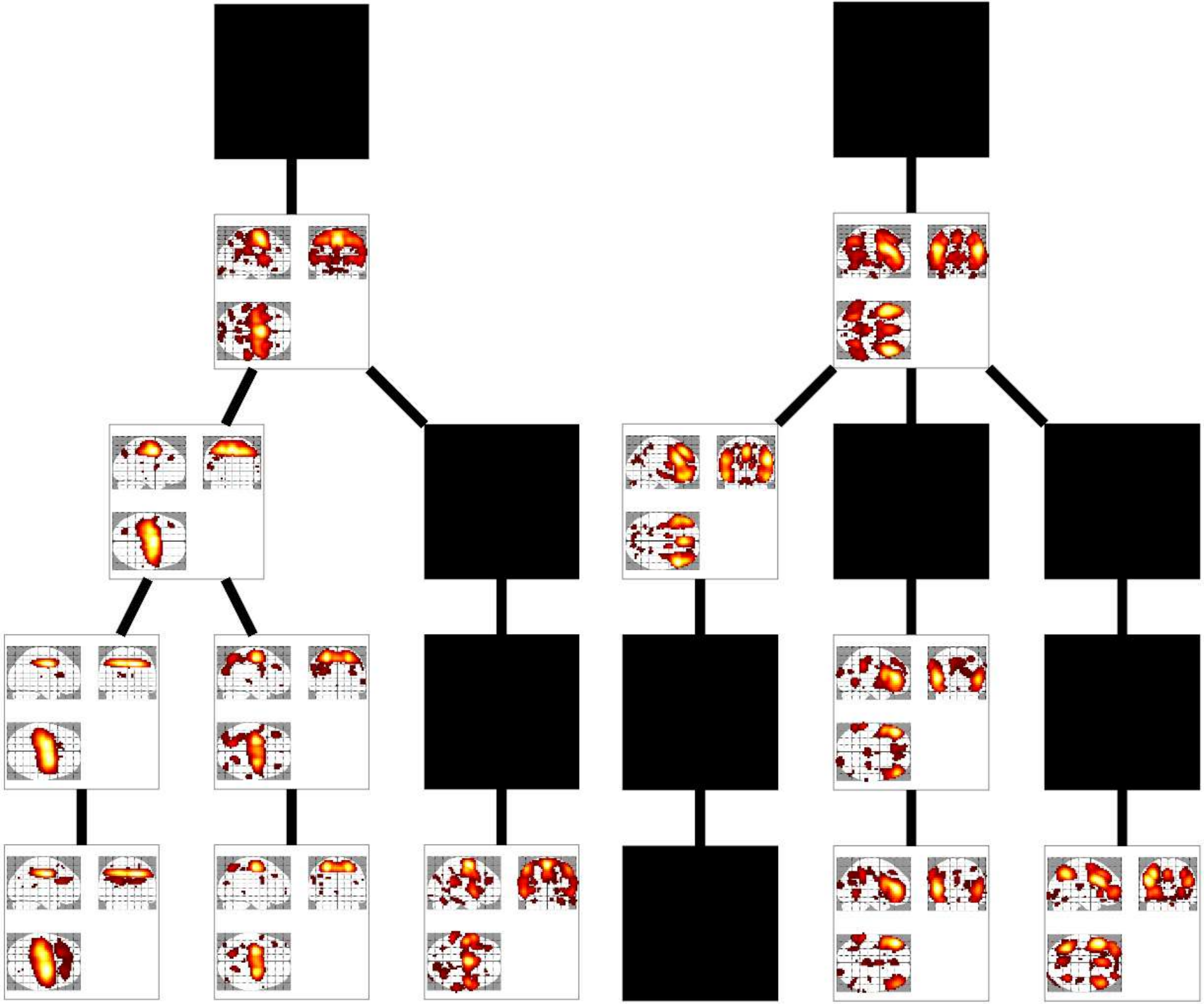


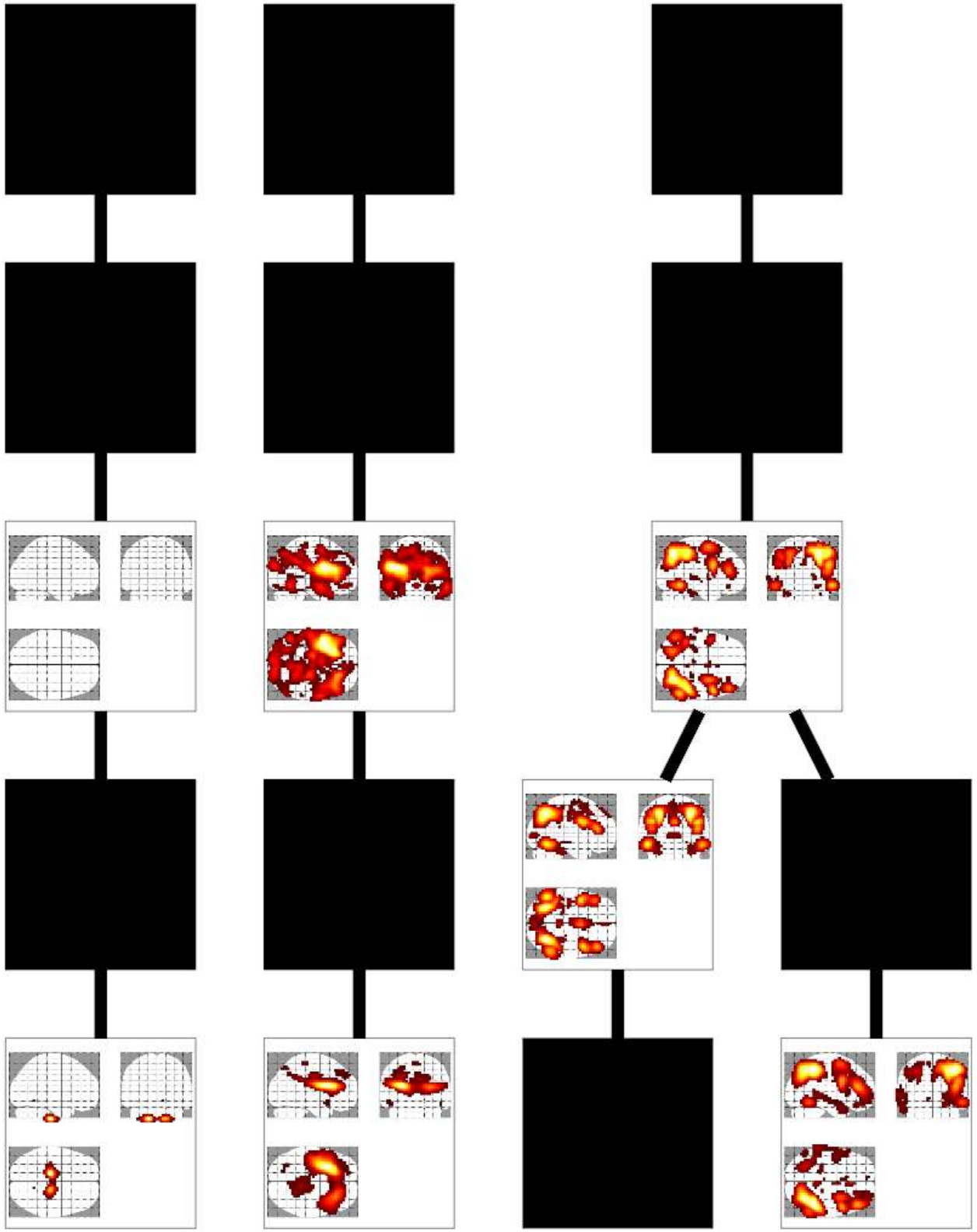


Trees including missing link









Other trees