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## Introduction & Source Data

• Human brain activity, as measured using resting-state functional (rsf)MRI, undergoes **changes** during neurodevelopment and aging [1–3].

• Despite solid evidence for age-related alterations, their **interpretation often remains unspecific** as non-invasive methods often cannot provide insights into underlying neurobiological processes.

• In related studies [4,5], we developed and validated a framework to identify potential neurobiological mechanisms contributing to **structural brain development**. Here, we explore this approach on the brain-functional level.

I. We establish **regional developmental trajectories** of two rsfMRI measures mapping **brain activity and connectivity** – **fALFF** (*fractional Amplitude of Low Frequency Fluctuations* [6]) and **GC** (*Global Correlation* between one and all other regions) – by normative modeling [7] of **Lifespan Human Connectome Project** data from 2445 individuals (5 – 90 years).

II. Using these trajectories, we construct “modeled” **brain maps** across the **lifespan**: (i) “**cross-sectional**” for a given year and (ii) “**longitudinal**” for the relative change between the cross-sectional maps of two given years in a sliding window approach.

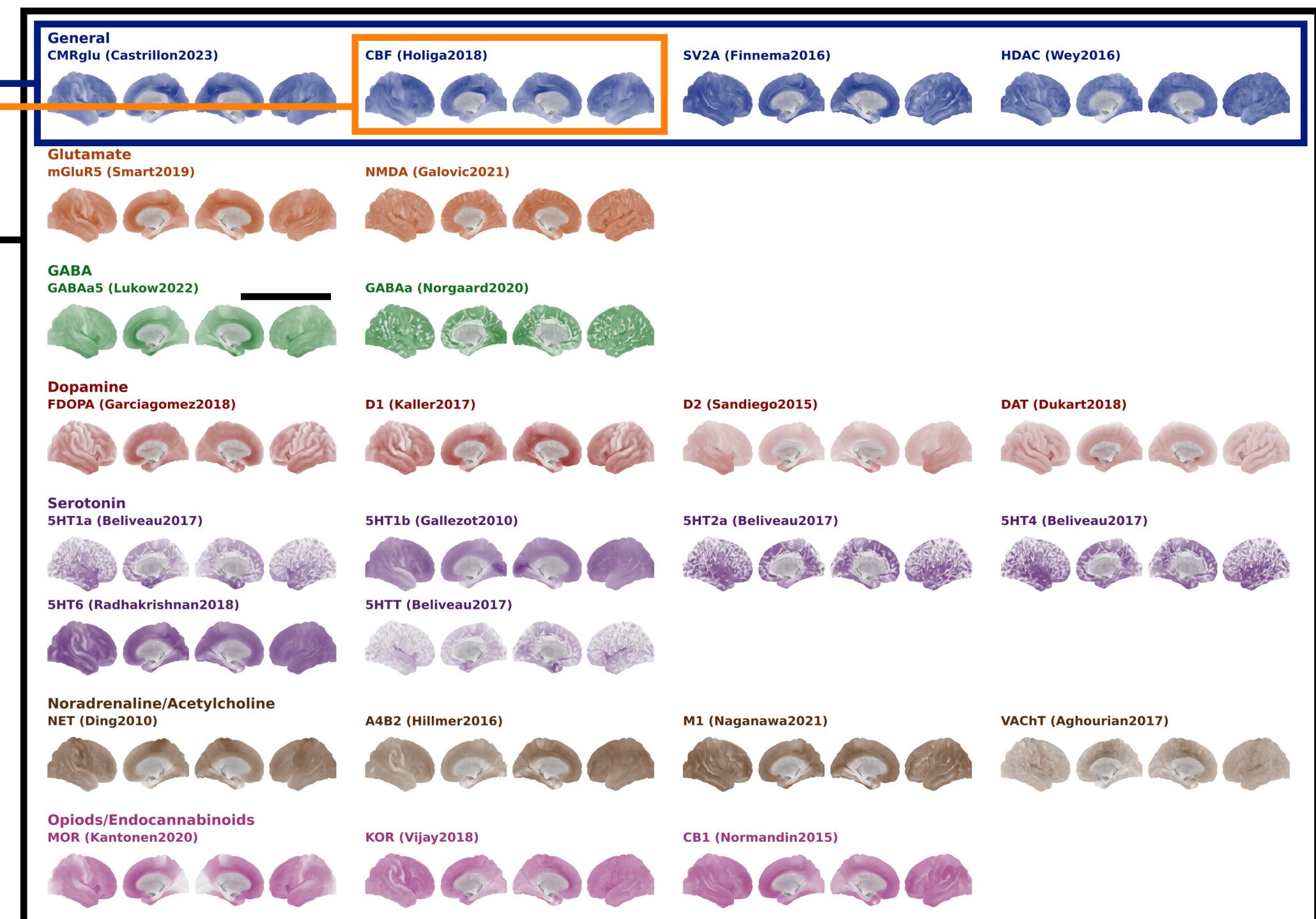
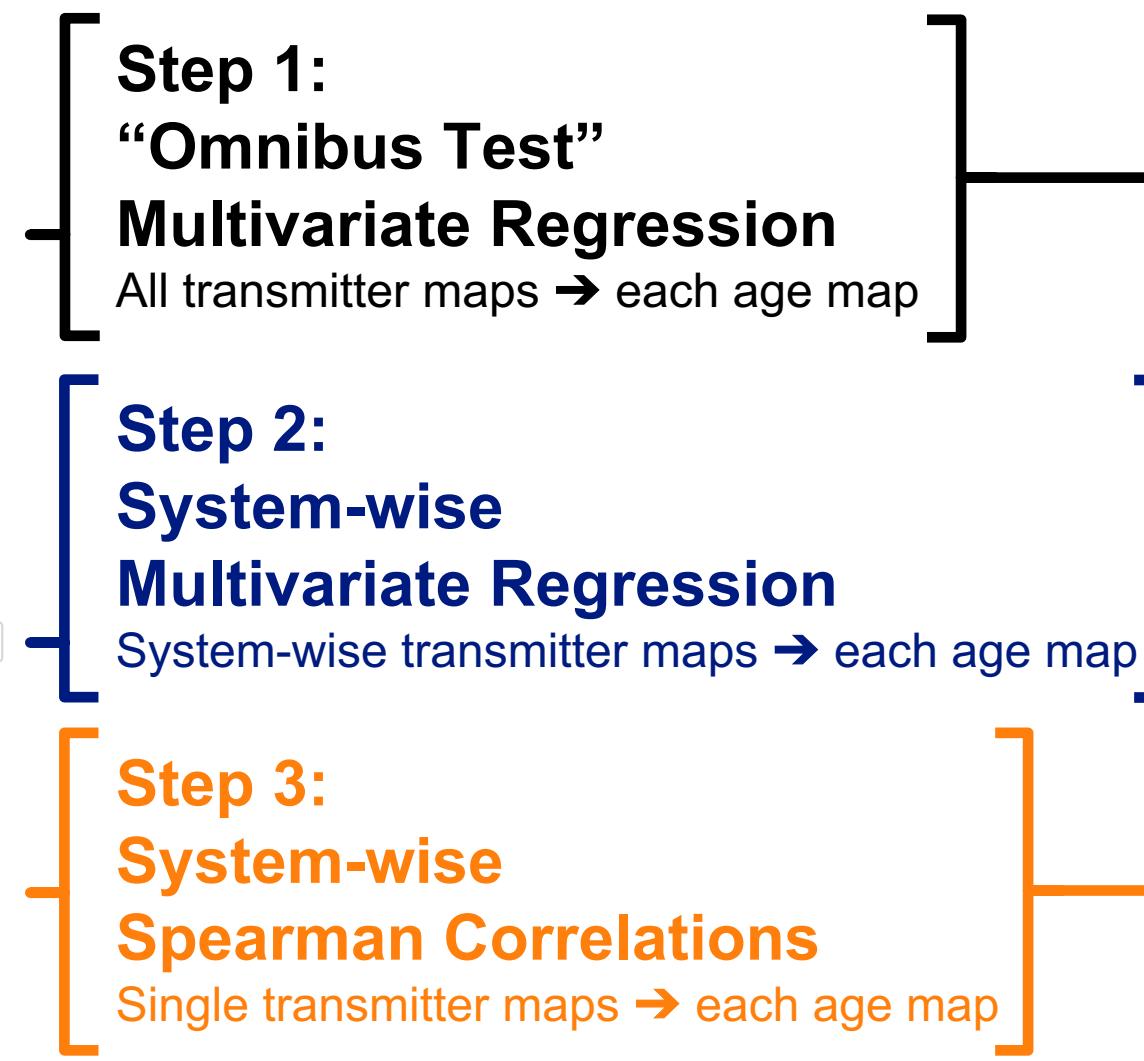
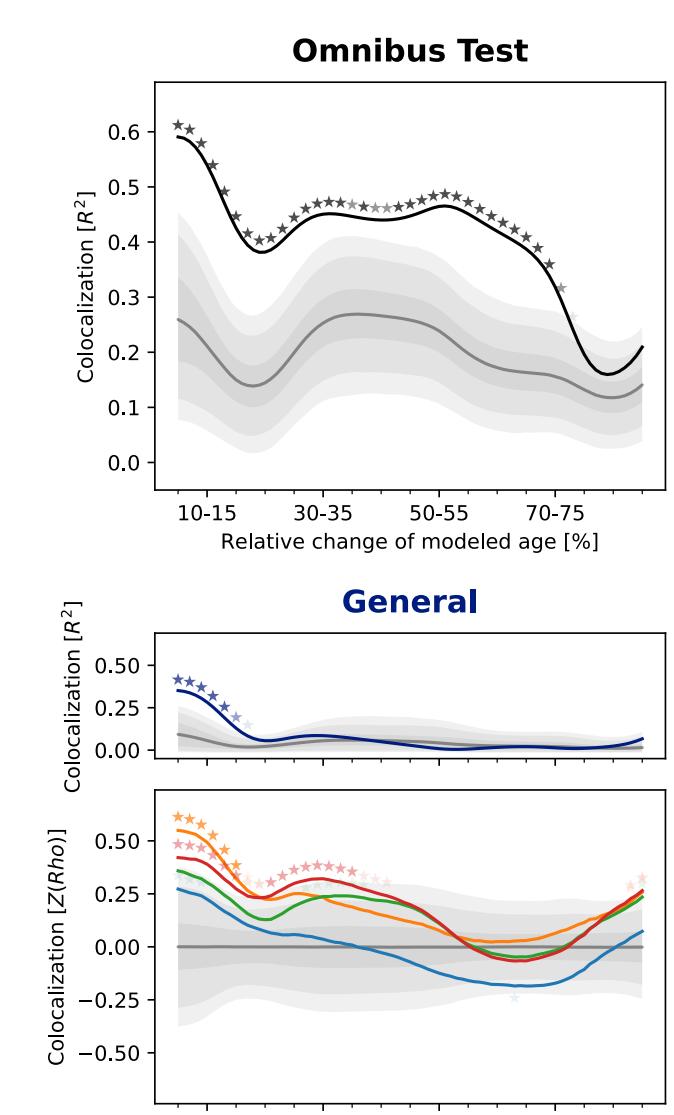
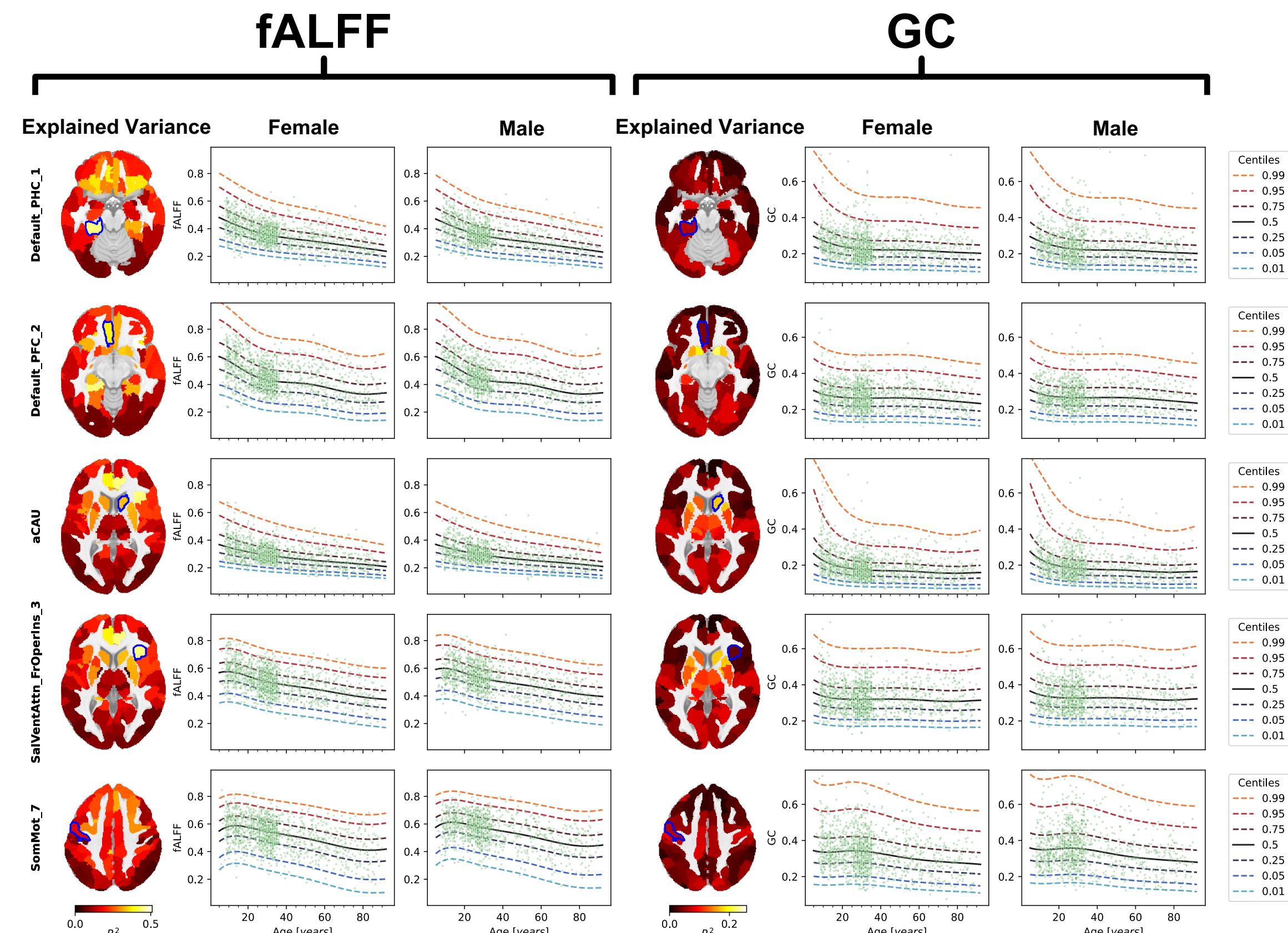
III. We hypothesize that these modeled **spatial rsfMRI change patterns** (i.e., stronger vs. weaker change in one vs. another brain region during a given age span) **reflect developmental changes in specific neurobiological systems** [4,8].

IV. We test this assumption using **spatial colocalization analyses** (Poster 2265) quantifying the degree to which the **spatial pattern of a modeled rsfMRI map** aligns with spatial patterns found in independent *in-vivo* **neurotransmitter maps** [4,8,9].

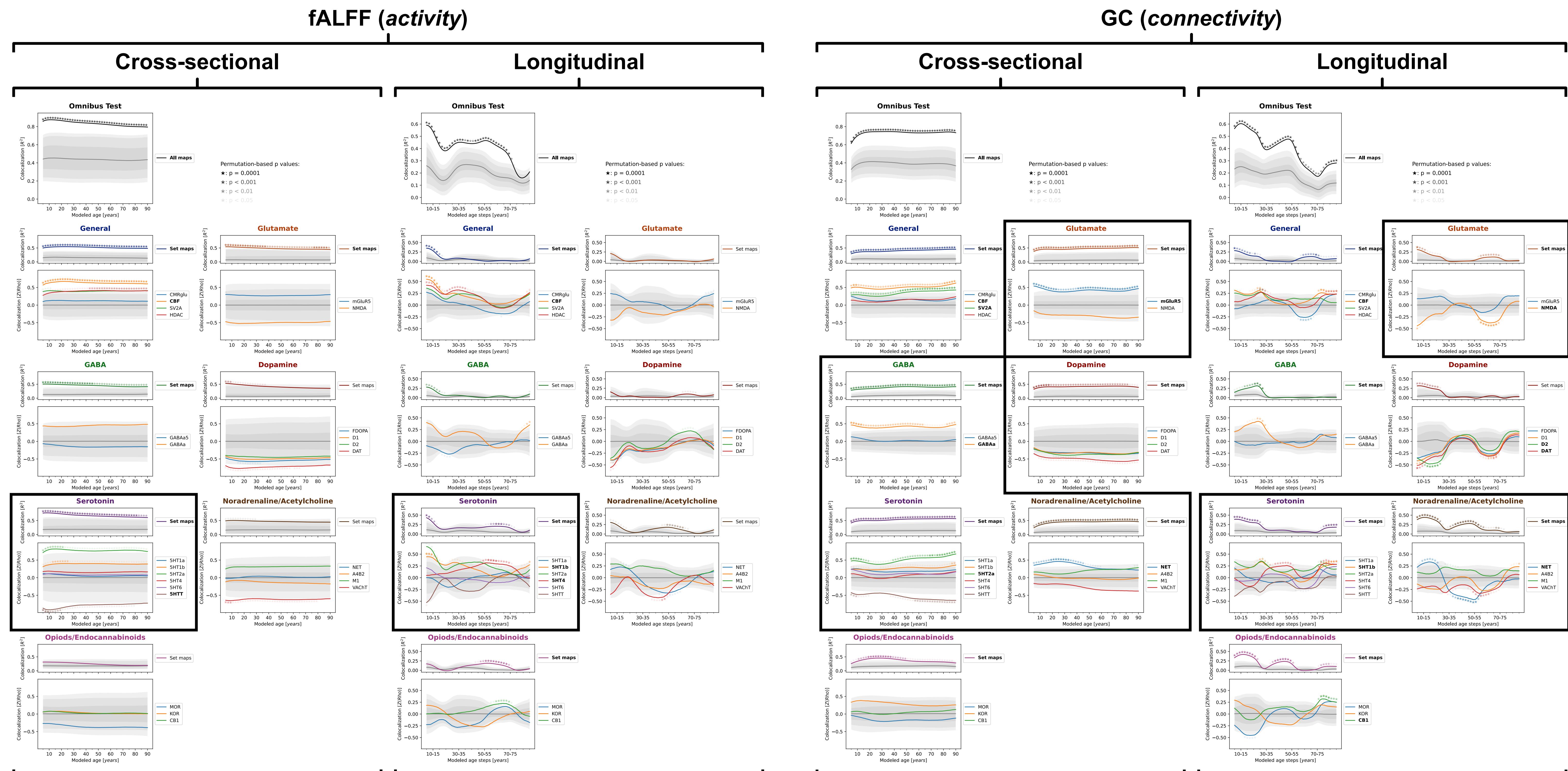
**Outlook:** Our results clearly require validation in independent longitudinal data. Tests in atypical developing cohorts will explore the approach’s clinical potential.

### Normative modeling of fALFF and GC development trajectories

Warped bayesian linear regression models fitted for each of 232 brain regions (Schaefer-200/Melbourne-S2) to predict fALFF/GC from age, while accounting for effects of sex, study site, and motion [7]. Data: Cross-sectional preprocessed data from 2445 HCP subjects (5 – 90 years). The 0.5th centile predictions were used as “modeled” cross-sectional MRI data in the following analyses. Relative change maps across 5 years (1-year steps) were used for (pseudo)longitudinal analyses.



## Results



The **fALFF distribution** across brain regions might mirror a **mixture of different neurotransmitter signals**, which may **not change relevantly** during the lifespan. The **serotonergic** system shows the **strongest effects at ~5–20 years**.

Up to ~60% (null: ~27%) of modeled lifespan changes of fALFF are **explained by neurotransmitter systems**. (Pseudo-) longitudinal effects are relatively sparse. The **serotonergic** system shows the **strongest effects at ~5–20 years**.

In line with the fALFF results, the **GC distribution** seems **stable across time**. However, several significant colocalization effects emerge for **glutamatergic, GABAergic, serotonergic**, and **noradrenergic** systems.

As for fALFF, up to ~60% (null: ~25%) of modeled GC changes are **explained**. **Cross-sectional and longitudinal** effects largely **converge**. **Noradrenergic** and **serotonergic** systems exhibit the **strongest effects** to up to 30 years.