

Colored figures

Franke & Gaser (2012): Longitudinal changes in individual *BrainAGE* in healthy aging, mild cognitive impairment, and Alzheimer's disease

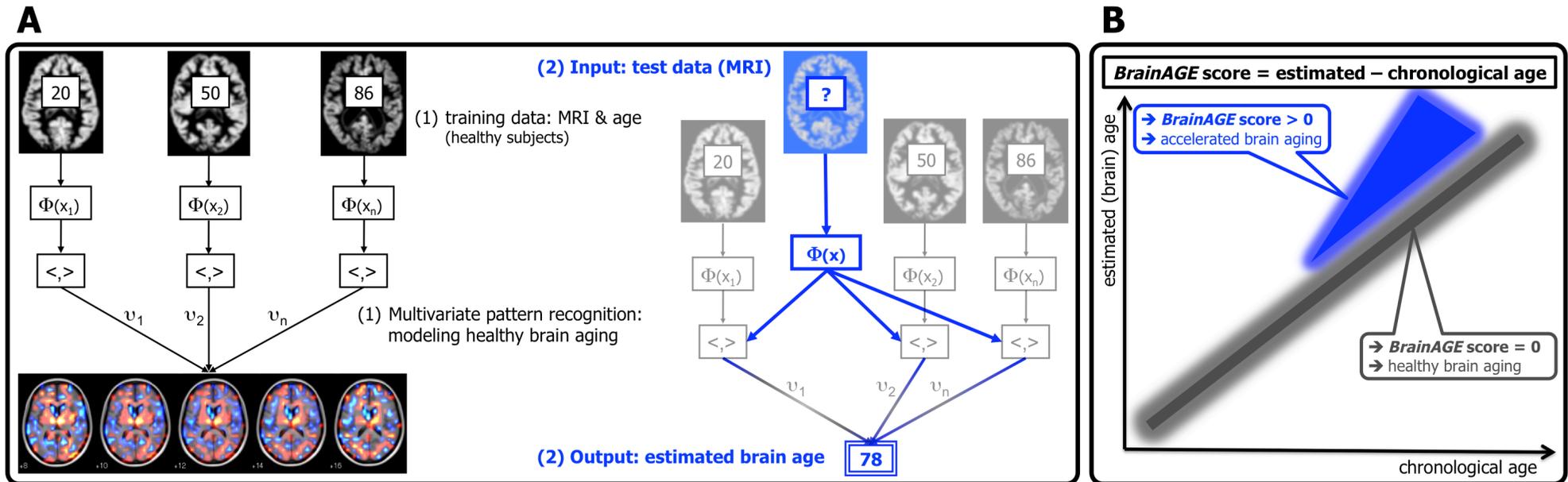


Figure 1: Depiction of the *BrainAGE* concept. **A:** The model of healthy brain aging is trained with the chronological age and preprocessed structural MRI data of a training sample (left; with an exemplary illustration of the most important voxel locations that were used by the age regression model). Subsequently, the individual brain ages of previously unseen test subjects are estimated, based on their MRI data (blue; picture modified from Schölkopf & Smola, 2002). **B:** The difference between the estimated and chronological age results in the *BrainAGE* score. Consequently, positive *BrainAGE* scores indicate accelerated brain aging (blue area; for more detailed information please refer to Franke et al., 2010)

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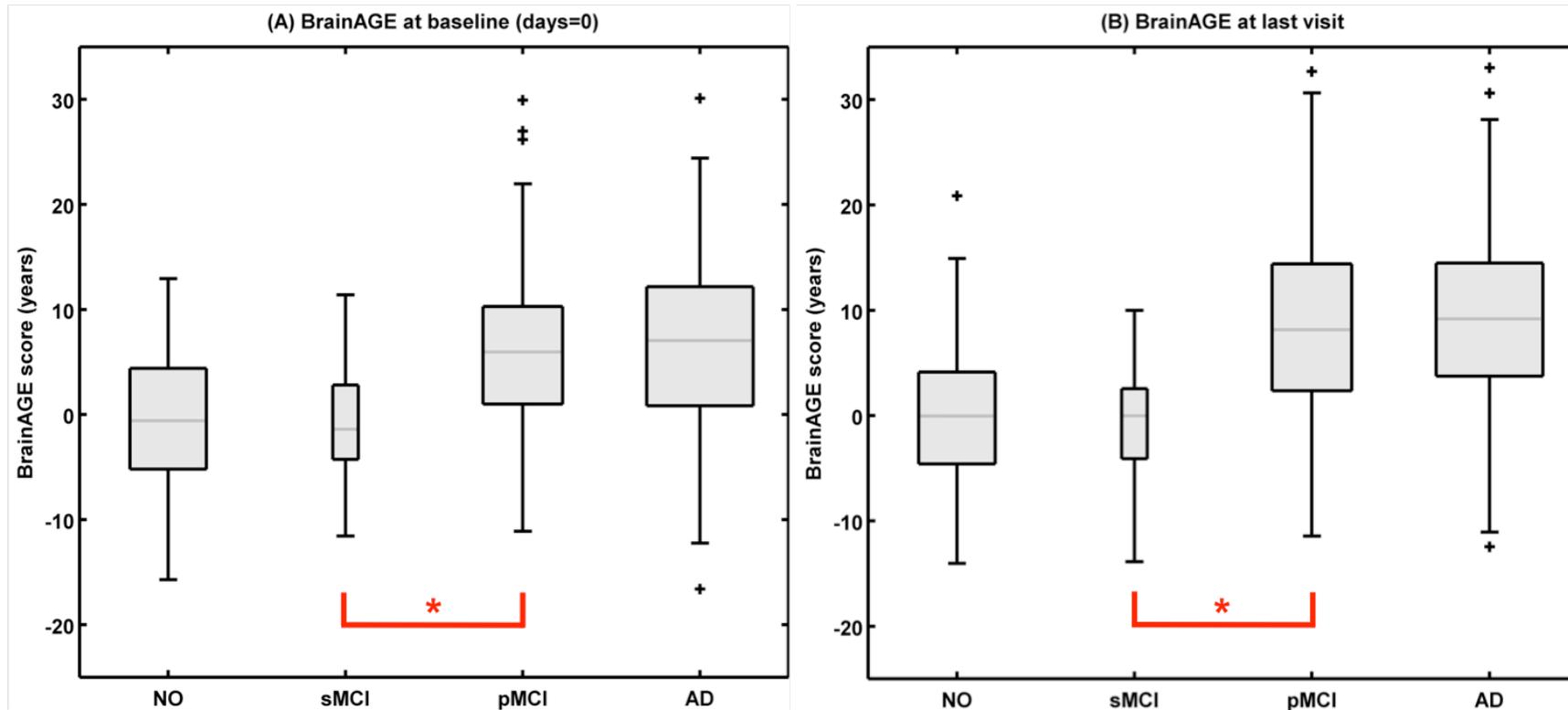


Figure 4: Box plots of (A) baseline *BrainAGE* scores and (B) *BrainAGE* scores of last MRI scans for all diagnostic groups. Post-hoc t-tests showed significant differences between NO/sMCI vs. pMCI/AD ($p < 0.05$; red lines) at both time measurements. The gray boxes contain the values between the 25th and 75th percentiles of the samples, including the median (dashed line). Lines extending above and below each box symbolize data within 1.5 times the interquartile range (outliers are displayed with a +). The width of the boxes depends on the sample size.

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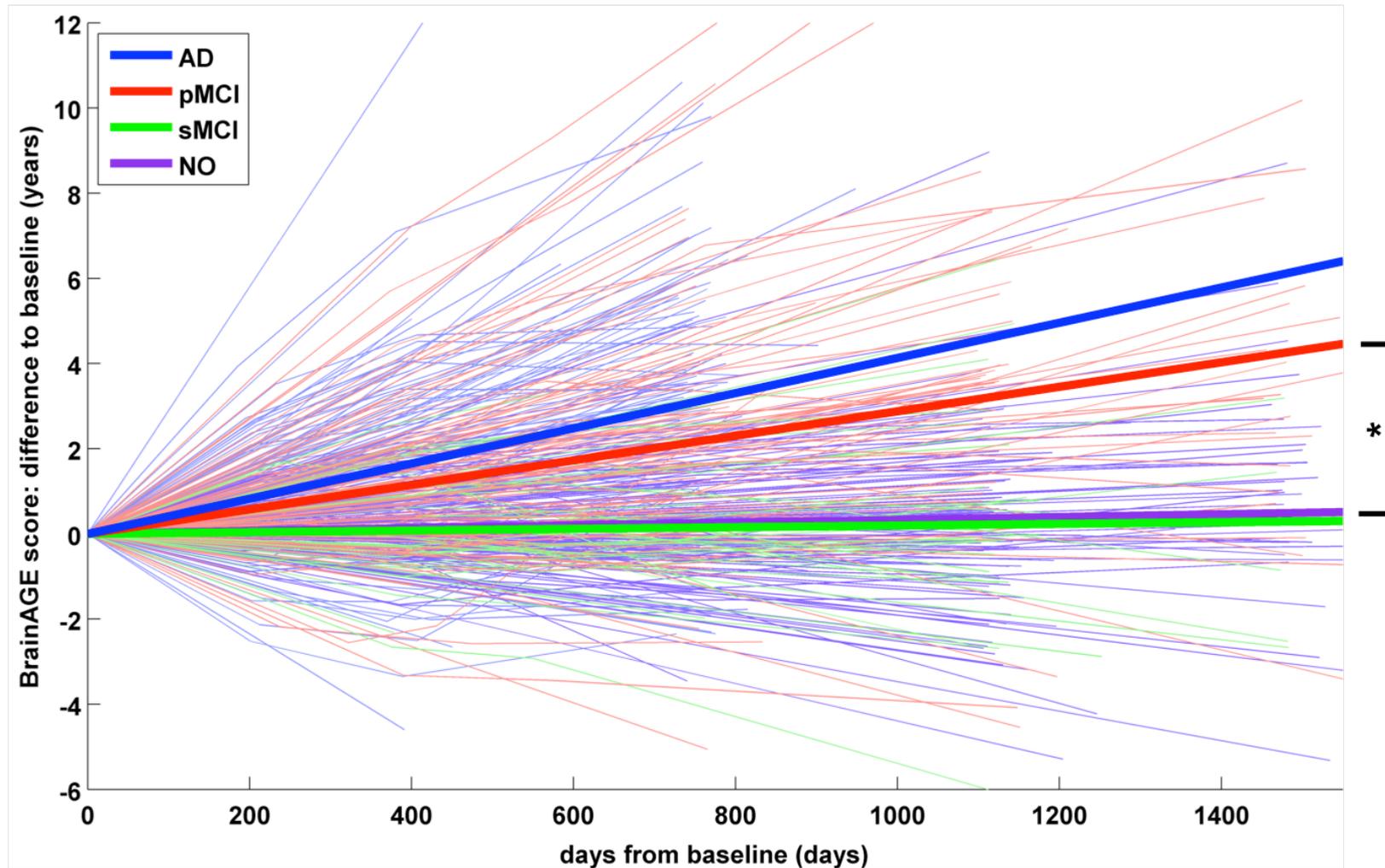


Figure 5: Longitudinal changes in *BrainAGE* scores for NO (purple), sMCI (green), pMCI (red), and AD (blue). Thin lines represent individual changes in *BrainAGE* over time; thick lines indicate estimated average changes for each group. Post-hoc t-tests showed significant differences in the longitudinal *BrainAGE* changes between NO/sMCI vs. pMCI/AD ($p < 0.05$; black lines).