Supporting Information: Bayesian moderation analyses

Methods

The moderation analyses described in sections 2.4.1 and 2.4.4 of the manuscript were conducted a second time but with a Bayesian approach using the "BayesFactor" package (version 0.9.12-4.2) in R. For the behavior data, the Bayes factors were calculated for 1) a "full model" consisting of same four predictors (depressive symptoms, PDS score, depressive symptoms × PDS interaction, and age) and 2) a "null model" which excludes the interaction term and thus consists of the three remaining predictors. The full model was divided by the null model to calculate the Bayes factor associated with the interaction term (depressive symptoms × PDS score).

For the amygdala connectivity data, the amygdala connectivity beta values were extracted from the mPFC region (see section 3.2.1) and averaged across voxels. Then a Bayes factor was calculated for 1) a "full model" consisting of same four predictors (depressive symptoms, PDS score, depressive symptoms × PDS interaction, and age) and 2) a "null model" which excludes the interaction term and thus consists of the three remaining predictors. The full model was divided by the null model to calculate the Bayes factor associated with the interaction term (valence bias × PDS score).

Results

The Bayesian analysis of the behavior data found moderate support for the hypothesis that puberty moderates the relationship between depression and valence bias ($BF_{10} = 5.59$, estimation error ± 0.004%) compared to the null hypothesis of no moderation.

The Bayesian analysis of the amygdala connectivity data found strong support for the hypothesis that puberty moderates the relationship between valence bias and amygdala-mPFC connectivity ($BF_{10} = 13.53$, estimation error ± 0.005%) compared to the null hypothesis of no moderation.