

1 **Title:** Development of subcortical volumes across adolescence in males and females: A
2 multisample study of longitudinal changes

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1 **Abstract**

2 The developmental patterns of subcortical brain volumes in males and females observed in
3 previous studies have been inconsistent. To help resolve these discrepancies, we examined
4 developmental trajectories using three independent longitudinal samples of participants in the
5 age-span of 8-22 years (total 216 participants and 467 scans). These datasets, including
6 *Pittsburgh* (PIT; University of Pittsburgh, USA), *NeuroCognitive Development* (NCD; University
7 of Oslo, Norway), and *Orygen Adolescent Development Study* (OADS; The University of
8 Melbourne, Australia), span three countries and were analyzed together and in parallel using
9 mixed-effects modeling with both generalized additive models and general linear models. For all
10 regions and across all samples, males were found to have significantly larger volumes as
11 compared to females, and significant sex differences were seen in age trajectories over time.
12 However, direct comparison of sample trajectories and sex differences identified within samples
13 were not consistent. The trajectories for the amygdala, putamen, and nucleus accumbens were
14 most consistent between the three samples. Our results suggest that even after using similar
15 preprocessing and analytic techniques, additional factors, such as image acquisition or sample
16 composition may contribute to some of the discrepancies in sex specific patterns in subcortical
17 brain changes across adolescence, and highlight region-specific variations in congruency of
18 developmental trajectories.

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22 **Keywords:** neurodevelopment; subcortical; adolescence; sex differences; replication;
23 longitudinal; Magnetic Resonance Imaging; amygdala; hippocampus

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2 **1. Introduction**

3 Developmental patterns of brain morphology, and sex differences in this structural
4 variation, exist due to both global and local maturational changes (Sowell, Thompson et al.
5 2004, Tamnes, Walhovd et al. 2013, Erus, Battapady et al. 2015, Giedd, Raznahan et al. 2015,
6 Narvacan, Treit et al. 2017). Determining when and how sex differences emerge in the
7 developing brain is essential to understanding differential risk for disease, especially
8 psychopathology (Kessler, McGonagle et al. 1993, Kessler, Berglund et al. 2005), as well as
9 life-long sex differences in various cognitive and behavioral traits (Choudhury, Blakemore et al.
10 2006, Rose and Rudolph 2006, Roalf, Gur et al. 2014, Gur and Gur 2016). For example, late
11 childhood and adolescence is a time period when many forms of psychopathology begin to
12 emerge and do so in a sex-specific fashion, with disproportionate increases in rates of anxiety
13 and depression seen in girls and a higher prevalence of externalizing behaviors and substance
14 use disorders in boys (Kessler, Berglund et al. 2005, Kuhn 2015). Given that structural and
15 functional abnormalities in subcortical regions have been associated with these various mental
16 health problems, it is thought that plausible sex differences in the development of subcortical
17 structures may be pertinent to explaining sex differences in onset, prevalence, and progression
18 of mental health disorders (Paus, Keshavan et al. 2008, Gogtay and Thompson 2010, Shaw,
19 Gogtay et al. 2010). As such, a number of sex differences have been reported in structural
20 magnetic resonance imaging (MRI) growth trajectories of subcortical structures. However,
21 developmental patterns observed in these structures have been inconsistent across studies,
22 and there has yet to be a consensus as to how these patterns differ between sexes (Sowell,
23 Trauner et al. 2002, Lenroot, Gogtay et al. 2007, Ostby, Tamnes et al. 2009, Dennison, Whittle
24 et al. 2013, Wierenga, Langen et al. 2014, Narvacan, Treit et al. 2017).

25 To date, studies have reported discrepant findings including growth versus reduction of
26 the thalamus and basal ganglia beginning in late childhood, as well as stability versus
27 continuing growth of the amygdala and hippocampus across adolescence (Giedd, Vaituzis et al.
28 1996, Sowell, Trauner et al. 2002, Ostby, Tamnes et al. 2009, Koolschijn and Crone 2013,

1 Wierenga, Langen et al. 2014). Similarly, reported sex differences in these trajectories remain
2 variable. From a study design perspective, it is believed that longitudinal study designs that are
3 able to better account for both within- and between- individual differences over time may help to
4 improve our understanding of cross-sectional findings that focus on mean group differences
5 between the sexes (Crone and Elzinga 2015). As such, longitudinal MRI studies using raw
6 volumes (uncorrected for whole brain size or other allometric scaling) consistently show larger
7 volumes in males as compared to females (i.e. main effects) (Dennison, Whittle et al. 2013,
8 Raznahan, Shaw et al. 2014, Wierenga, Langen et al. 2014, Narvacan, Treit et al. 2017).
9 However, findings are less clear in terms of sex differences in the trajectories (i.e. slopes) of
10 development seen across childhood and adolescence. Based on using raw volume estimates
11 (i.e. trajectories reported without including allometric scaling), some studies report sex
12 differences in neurodevelopmental trajectories of subcortical regions (Dennison, Whittle et al.
13 2013, Goddings, Mills et al. 2014, Raznahan, Shaw et al. 2014), whereas other studies find no
14 difference between the sexes (Wierenga, Langen et al. 2014, Narvacan, Treit et al. 2017).

15 These discrepant observations in studies of subcortical volume development and sex
16 differences in these patterns may be due to a number of factors, including cohort effects
17 inherent to the sample, variation in study design, image acquisition and preprocessing, and/or
18 statistical modeling approaches. In terms of image processing, dissimilarities have been
19 reported in the absolute volume estimates as well as in the reliability of subcortical brain
20 structures across different freely available automated segmentation software (Morey, Selgrade
21 et al. 2010, Makowski, Beland et al. 2017). In addition, software packages vary in their
22 methodology for processing longitudinal scans. For example, FreeSurfer's longitudinal pipeline
23 includes creating an unbiased within-subject template space to help reduce random variation
24 and improve the sensitivity of detecting changes over time (Reuter, Schmansky et al. 2012).
25 Recently, a longitudinal cortical thickness pipeline has also been developed as part of the ANTs
26 software (Tustison, Holbrook et al. Unpublished). To our knowledge, other commonly used
27 software packages for structural analysis (i.e. CIVET (Zijdenbos, Forghani et al. 2002), MAGeT

1 (Chakravarty, Steadman et al. 2013), and FSL (Zhang, Brady et al. 2001)) do not account for
2 within-subject variance in a similar fashion during the preprocessing stream. Beyond software,
3 differences in quality control (QC) procedures utilized across studies may also impact the
4 results (Ducharme, Albaugh et al. 2016).

5 From a statistical perspective, the inclusion of covariates and/or statistical model vary
6 widely by study and may impact results (Vijayakumar, Mills et al. Accepted). For example,
7 during statistical testing the inclusion of a 'global' or 'allometric' covariate to account for *between*
8 *subject* differences in body size or weight (Sanfilippo, Benedict et al. 2004) may directly influence
9 sex differences that are identified (Lenroot, Gogtay et al. 2007, Dennison, Whittle et al. 2013).
10 Moreover, despite sex differences in allometric variables (i.e. whole brain or intracranial
11 volume), recent findings suggest that the variability of anatomical volumes are not equal
12 between the sexes (males show larger variance expressed at both upper and lower extremities
13 of the distributions) (Wierenga, Sexton et al. 2017), allometric covariates follow non-linear
14 developmental patterns from childhood to adulthood (Mills, Goddings et al. 2016, Reardon,
15 Clasen et al. 2016), and regions including the thalamus, striatum, and pallidum show
16 hypoallometric scaling with whole brain size (i.e. volumes become proportionately smaller with
17 increasing head size) (Reardon, Clasen et al. 2016). Moreover, the inclusion of an allometric
18 term may be redundant when examining longitudinal change using hierarchical modeling, as
19 each subject receives its own intercept and slope (Crone and Elzinga 2015). Thus, the *between-*
20 *subject* variance due to individual differences in head size is captured at the individual level over
21 time; allowing for better characterization of changes in regional volume estimates over time.

22 Study results may vary based on the type of statistical analytic techniques employed.
23 Although longitudinal studies have typically used linear mixed effect modeling (LME) to describe
24 age-related changes, the model terms are diverse (Vijayakumar, Mills et al. Accepted). For
25 example, studies have differed in their modeling approach, including use of polynomial terms
26 (e.g. quadratic or cubic), model selection strategy (e.g. top-down or likelihood indices), testing
27 males and females separately and/or including sex as an interaction term, as well as regarding

1 the inclusion of other confounding factors (Ruigrok, Salimi-Khorshidi et al. 2014). Moreover,
2 while LME including polynomial terms remains a popular approach, polynomials are rather
3 restrictive, whereas other modeling techniques, such as general additive modeling (GAMM),
4 may allow for a more flexible fit of a curve to the data. Specifically, GAMM replaces the linear
5 slope parameters with 'smooth' functions to find the optimal functional form between the
6 predictor and response (Jones and Almond 1992). Given the existing discrepancies in the
7 existing literature and the vast array of methodology (including software, quality checking
8 procedures, and model terms) utilized between studies, there remains an important gap in our
9 knowledge regarding the reproducibility of possible sex differences in subcortical
10 neurodevelopmental trajectories across childhood and adolescence.

11 The goal of the current study was to utilize identical image processing and analysis
12 methods in three independent longitudinal neuroimaging samples to describe the development
13 of uncorrected subcortical volumes for males and females from late childhood into young
14 adulthood. This study is part of an international collaboration project intended to improve the
15 reliability and efficiency of neurodevelopmental research by simultaneously analyzing multiple
16 existing neuroimaging datasets (Mills, Goddings et al. 2016, Tamnes, Herting et al. 2017). By
17 keeping longitudinal preprocessing methods, quality control procedures, and statistical methods
18 constant across samples, we can assess and interpret the potential impact of sample and
19 acquisition differences on brain development patterns in males and females. Moreover, given
20 inherent study design differences between the longitudinal samples (e.g. age ranges and scan
21 follow-up), we explored age and age by sex relationships in each sample using both the more
22 flexible general additive modeling (GAMM) approach as well as the more common general
23 mixed-effects modeling (LME). Because LME is the most commonly used approach in
24 longitudinal MRI studies (Vijayakumar, Mills et al. Accepted), LME estimates in the current study
25 were included in order to help directly compare our results with those reported in previous
26 studies. Thus, we aimed to examine the consistency and reproducibility of neurodevelopmental

1 change for subcortical gray matter regions, including the thalamus, caudate, putamen, pallidum,
2 hippocampus, amygdala, and nucleus accumbens in males and females.

3 **2. Materials and Methods**

4 **2.1 Participants**

5 This study analyzed data from typically developing youth from three separate cohorts collected
6 utilizing longitudinal designs at three separate sites in independent research projects: *Pittsburgh*
7 (PIT; University of Pittsburgh, USA), *NeuroCognitive Development* (NCD; University of Oslo,
8 Norway), and *Orygen Adolescent Development Study* (OADS; The University of Melbourne,
9 Australia). Each project was approved by their respective local review board and informed
10 consent/assent was obtained from parents and children prior to data collection. In order to best
11 account for within-subject variance, only participants with ≥ 2 scans from each cohort were
12 included in analyses. Details regarding participant recruitment in each project have been
13 previously described (Yap, Allen et al. 2011, Tamnes, Walhovd et al. 2013, Herting, Gautam et
14 al. 2014). By study design, all projects enrolled typically developing children and adolescents at
15 baseline, although OADS over-sampled children at both high and low temperamental risk of
16 developing psychopathology. Only data passing QC procedures from typically developing youth
17 were included in the current study. Demographic information and sample distributions for each
18 sample are presented in Table 1 and Figure 1. For the PIT dataset, 126 participants were
19 recruited and scanned at baseline, with 20 not completing their follow-up visit, and 33 excluded
20 due to poor image quality of the MRI (see additional details of QC procedures in section 2.2).
21 For NCD, 111 participants were recruited and scanned at baseline; 26 were unable to complete
22 their follow-up visit, and 9 were excluded due to poor image quality. For OADS, 177 participants
23 completed a baseline visit, of which 45 did not complete any additional follow-up visits, 61 were
24 excluded due to psychiatric history or medical illness and 4 were excluded due to poor image
25 quality. The final samples thus included 73 participants from PIT, 76 from NCD, and 67 from
26 OADS. In total, the present study included 216 participants (110 females) and 467 scans
27 covering the age range of 8 to 22 years.

1 **2.2 Image Acquisition and Analysis**

2 T1-weighted anatomical scans were obtained at the three sites using different MRI scanners
3 and sequences (see Supplementary Material). At each site, a radiologist reviewed all scans for
4 incidental findings of gross abnormalities. Image processing, including whole brain
5 segmentation with automated labeling of different neuroanatomical structures, was performed
6 using the longitudinal pipeline of FreeSurfer 5.3 (<http://surfer.nmr.mgh.harvard.edu>; (Fischl,
7 Salat et al. 2002, Reuter, Schmansky et al. 2012). The longitudinal pipeline includes creating an
8 unbiased within-subject template space and image using inverse consistent registration. Skull
9 stripping, Talairach transform and atlas registration, and parcellations are initialized in the
10 common within-subject template, which increases reliability and statistical power. Similar
11 standard QC procedures were carried out between sites. QC details were as follows: 1) all raw
12 images were visually inspected for motion prior to processing, 2) post-processed images were
13 visually inspected by trained operators for accuracy of subcortical segmentation by the
14 longitudinal pipeline for each scan per participant, 3) images with inaccurate segmentation were
15 excluded (number of participants excluded during QC is outlined above in section 2.1). No
16 manual edits were made to subcortical regions of interests. Regions of interest for the present
17 study included the thalamus, caudate, putamen, pallidum, amygdala, hippocampus, and
18 nucleus accumbens for each hemisphere.

19 **2.3 Statistical Analyses**

20 Given previous findings highlighting hemispheric differences (Dennison, Whittle et al. 2013,
21 Herting, Gautam et al. 2014), we first examined if patterns of change differed by hemisphere by
22 plotting LOESS (locally weighted scatterplot smoothing) curves to each dataset. Overall,
23 trajectories were similar between hemispheres (see Supplementary Material SFigures 1-7), and
24 therefore left and right hemisphere volume estimates were averaged for all subsequent
25 analyses. Given that one of the primary aims of the study was to examine the distinct
26 developmental trajectories in males and females, and preliminary exploratory LOESS plots

1 confirmed the shape of developmental trajectories varied between males and females (see
2 Supplementary Material SFigures 1-7).

3 To more fully understand sex differences in subcortical volume changes from late
4 childhood and throughout adolescence, analyses were performed to examine age, sex, and age
5 by sex relationships both together across sites, as well as in each sample separately, using
6 mixed-effects modeling with both generalized additive models (GAMM) (mgcv package version
7 1.8-17) and general linear mixed effects modeling (LME) (R version 3.4.0; nlme package
8 version 3.1-131). Follow-up analyses were also conducted to examine age trajectories in each
9 sex separately, both based on the 3 samples as well as in each sample separately.

10 2.3.1 GAMM

11 Unlike parametric general linear modeling, GAMM does not require *a priori* knowledge of the
12 functional form for the data and is an extension of LME; rather GAMM replaces one or more of
13 the linear predictor terms with a 'smooth' function term. The non-linear smooth function
14 describes the best relationship between the covariate(s) and the outcome variable of interest.
15 For GAMM analyses on subcortical structure volume, the main predictor was age. GAMM can
16 be represented by the following formula:

$$G(y) = X^* \alpha + \sum_{j=1}^p f_j(x_j) + Zb + \varepsilon$$

17 where $G(y)$ is a monotonic differentiable link function, α is the vector of regression coefficients
18 for the fixed parameters; X^* is the fixed-effects matrix; f_j is the smooth function of the covariate
19 x_j ; Z is the random-effects model matrix; b is the vector of random-effects coefficients; and ε is
20 the residual error vector.

21 Using this approach, GAMM models were implemented to examine age, sex, as well as
22 an age*sex interaction to test a sex difference in the intercept (main effect of sex) as well as a
23 sex difference in the trajectory or slope of age (age*sex interaction), respectively; while also

1 controlling for sample at the level of intercept (main effect of sample) and slope (age*sample
2 term). Importantly, sex was coded as a factor (male=0, female=1), allowing for each term to
3 reflect the following: sex term reflected the difference in intercept in females as compared to
4 males; age term reflected the slope of age for males; age*sex term reflected the difference in
5 slope of females as compared to males. To better understand significant differences in age
6 trajectories between the sexes, GAMM estimates for age (controlling for sample) were also
7 implemented in each sample separately. Lastly, sample was converted to an ordered factor and
8 GAMM models were implemented to directly test significant differences in the slopes of age
9 between each sample for each region of interest. Thus, GAMM age, sex, and age*sex models
10 were updated to use the previous covariates of sample and sample*age as contrasting factors.
11 Sample was coded as a factor and two models were implemented to test sample differences:
12 one model included sample as a factor with OADS=1, NCD=2, and PIT=3 (in order to compare
13 OADS vs. NCD and OADS vs. PIT), and the second model included sample as a factor with
14 NCD=1, OADS=2, and PIT=3 (in order to compare NCD vs. PIT).

15 2.3.2 LME

16 LME estimates the fixed effect of measured variables on subcortical volume while including
17 within-person variation as nested random effects in the regression model. This is done to
18 account for individual subject effects and correlation of the data inherent to longitudinal analysis.
19 LME can be represented by the following formula for linear changes with age both between and
20 within participants:

$$Volume_{ij} = Intercept_{0i} + \alpha_{1i}(age)_{ij} + \varepsilon$$

21 where $Volume_{ij}$ represents the volume in an ROI at the j^{th} timepoint for the i^{th} participant, the
22 $intercept_{0i}$ represents the grand mean at the centered age (age 15), α_{1i} is the grand mean slope
23 of age (linear); and ε is the residual error and reflects within-person variance. All models also
24 included a random intercept for each participant. The linear model was then built upon to also

1 include quadratic and cubic fixed terms to assess linear versus more complex patterns of
2 change. The linear, quadratic, and cubic models were as follows:

3 1. *Linear model: Volume = Intercept + $\alpha(\text{age}) + \epsilon$*

4 2. *Quadratic model: Volume = Intercept + $\alpha(\text{age}) + \beta(\text{age}^2) + \epsilon$*

5 3. *Cubic model: Volume = Intercept + $\alpha(\text{age}) + \beta(\text{age}^2) + \gamma(\text{age}^3) + \epsilon$*

6 where α , β , and γ represent the effects of each fixed term. Likelihood ratio tests and Akaike
7 Information Criterion (AIC) were used to compare the models and to determine which had the
8 best fit. All models were tested against a null model that included only the intercept term, but not
9 the fixed effect of age. The model with the lowest AIC that was also significantly different from
10 the less complex model as determined by the likelihood ratio test was chosen as the best fit
11 model (e.g. linear had to have a lower AIC and be significantly different from null; quadratic had
12 to have a lower AIC and be significantly different from both the null and linear model).

13 Using LME, models of age were implemented on each sample separately to examine
14 sex differences by including a term for the main effect of sex as well as an age*sex interaction
15 to each model to test a sex difference in the intercept (main effect of sex) as well as a sex
16 difference in the trajectory or slope of age (age*sex interaction), respectively. In the cases
17 where polynomial LME best fits were different between males and females, sex difference were
18 only tested by using the highest polynomial fit. That is, if a linear best fit was detected for
19 females but a quadratic best fit for males, a quadratic fit was tested between sexes.

20 **3. Results**

21 **3.1 Description of Developmental Age Trajectories using GAMM**

22 GAMM estimates of developmental trajectories for volume for each region of interest in females
23 and males based on the three independent samples are presented in Figure 2. GAMM models
24 included age, sex, as well as an age*sex interaction to test a sex difference in the intercept
25 (main effect of sex) as well as a sex difference in the trajectory or slope of age (age*sex

1 interaction), while covarying for sample (sample and age*sample). A significant sex difference
2 was detected for the smoothed slope of age for all seven regions of interest (Table 2). To better
3 understand these differences, we examined age trajectories in each sex separately, while again
4 covarying for sample. These results are presented in Table 3, and we below describe these
5 developmental trajectories for each subcortical structure in females and males.

6 3.1.1 Thalamus

7 Overall, females showed smaller thalamus volumes as compared to males across the entire age
8 range of 8 to 22 years. Moreover, both males and females showed a nonlinear change with age,
9 with decreases seen during mid-adolescence and into adulthood; however, when tested
10 separately, the slope for age was only significant in males, and not in females.

11 3.1.2 Pallidum

12 Age trajectories for each sex displayed greater divergence in pallidum volumes from ages 8 to
13 22 years, with males showing larger volumes as compared to females beginning in early
14 adolescence thru young adulthood. However, when each sex was examined separately, age
15 trajectories for the pallidum did not reach statistical significance in either females or males
16 alone.

17 3.1.3 Caudate

18 Males and females displayed similar volumes during late childhood and early adolescence,
19 whereas females had smaller volumes compared to males by young adulthood. When each sex
20 was examined separately, the sex difference detected in young adulthood was a result of
21 females showing a decrease in caudate volumes across adolescence, with no significant
22 change seen in volumes with age in males.

23 3.1.4 Putamen

24 Similar to the caudate, sex differences in the putamen volumes also emerged with age, with
25 greater sex differences seen in later adolescence and young adulthood. When examined

1 separately, putamen volume showed a nonlinear decrease with age in females, whereas
2 changes in volumes did not reach significance in males.

3 3.1.5 Nucleus Accumbens

4 Nucleus accumbens volumes were similar in males and females from late childhood to mid-
5 adolescence, with sex differences emerging during late adolescence and young adulthood.
6 Examining the sexes separately revealed a significant decrease in nucleus accumbens volumes
7 for females, with no changes in volume in males from ages 8 to 22 years.

8 3.1.6 Hippocampus

9 Females showed smaller hippocampal volumes by 10 years of age compared to males.
10 Moreover, females and males both showed significant nonlinear patterns of hippocampal growth
11 with age, with an emergent divergence between the sexes across adolescence and into young
12 adulthood. These nonlinear changes with age reached significant in males and females when
13 examined separately.

14 3.1.7 Amygdala

15 Females showed smaller amygdala volumes at age 8 years compared to males, with greater
16 separation in volumes seen between the sexes with age. Again, these nonlinear changes with
17 age reached significant in males and females when examined separately.

18 **3.2. Testing Between Sample Differences**

19 Spaghetti plots of GAMM estimates of developmental trajectories for volume for each region of
20 interest in females and males for each of the three independent samples are presented in
21 Figures 3-5. To directly test sample differences, previous GAMM models were updated to
22 change the covariates of sample and sample*age as contrasting factors (sample: OADS=1,
23 NCD=2, PIT=3). This allows for directly comparing the main effect of sample as well as if the
24 samples have significantly different trajectories over age. GAMM estimates for each of these
25 smooth terms are presented in Table 4 and described below.

1 3.2.1 Thalamus

2 The main effect of sample was not significant. However, the OADS and NCD samples showed
3 significant sample differences in growth trajectories for the thalamus, whereas trajectories were
4 not significantly different between PIT and OADS or NCD for this region.

5 3.2.2 Pallidum

6 A main effect of sample was seen with OADS having significantly smaller volumes compared to
7 NCD and PIT at baseline. Sample differences were also seen in age trajectories, with significant
8 differences noted between each of the three samples (OADS vs. PIT, OADS vs. NCD, and PIT
9 vs. NCD).

10 3.2.3 Caudate

11 A main effect of sample was seen with PIT having significantly smaller volumes compared to
12 NCD and OADS. Significant sample differences were seen in age trajectories between OADS
13 and NCD as well as OADS and PIT samples, whereas trajectories were not significantly
14 different between PIT and NCD.

15 3.2.4 Putamen

16 A main effect of sample was seen with OADS having significantly larger volumes compared to
17 NCD and PIT. However, the samples did not have significantly different age trajectories.

18 3.2.5 Nucleus Accumbens

19 A main effect of sample was detected reflecting the largest volumes seen in NCD, followed by
20 PIT, and OADS (all p 's <0.05). However, the samples did not have significantly different age
21 trajectories.

22 3.2.6 Hippocampus

23 A main effect of sample included OADS having larger hippocampal volumes as compared to
24 NCD and PIT. In addition, OADS and PIT samples showed significant sample differences in

1 growth trajectories for the hippocampus, whereas trajectories were not significantly different
2 between OADS and NCD or PIT and NCD.

3 3.2.7 Amygdala

4 A main effect of sample was seen with PIT having significantly larger volumes compared to
5 NCD, but no significant difference detected between PIT vs. OADS or NCD vs. OADS. The
6 samples did not significantly differ for age trajectories for the amygdala.

7 **3.3 Testing of Developmental Models using LME**

8 Linear, quadratic, and cubic LME were used to determine best fit models for females and males
9 of each sample. The highest-order polynomial model for each brain region is summarized in
10 Table 5 (for AIC comparisons, see Supplementary Tables 1-7). LME best fits were also different
11 between samples in both sexes for most ROIs, except for the caudate and nucleus accumbens.
12 For the caudate, both males and females in each sample showed similar trajectories with age
13 (PIT: linear, NCD: quadratic, and OADS: linear). For the nucleus accumbens, no significant
14 change was found in all samples, except for OADS females, which showed a linear decrease
15 with age. Overall, LME best fit models per sample were largely in agreement with the GAMM
16 trajectories; the exception to this are highlighted in Supplementary Table 8 and include the
17 pallidum for NCD females (LME=cubic, GAMM=n.s.), the hippocampus for PIT females
18 (LME=cubic, GAMM=n.s.), the amygdala for PIT females (LME=quadratic, GAMM=n.s.) and the
19 hippocampus for NCD males (LME=n.s., GAMM=nonlinear). Full model details for LME results
20 when testing sex, age, and age*sex using linear and polynomial LME best fit models are
21 presented in Supplementary Tables 10-16. Using LME, a few models that were identified as
22 significant using GAMM did not reach significance using best fit models including the pallidum
23 and putamen in the OADS sample and the putamen in the NCD sample (as shown in
24 Supplementary Table 17).

25 **4. Discussion**

1 This is the first study to examine longitudinal subcortical neurodevelopmental trajectories
2 in males and females using a multisample approach spanning ages 8 to 22 years. The current
3 study is an extension from an on-going international collaboration project aiming to improve the
4 understanding, reliability, and efficiency of neurodevelopmental research by simultaneously
5 analyzing multiple existing longitudinal neuroimaging datasets (Mills, Goddings et al. 2016,
6 Tamnes, Herting et al. 2017). By utilizing the identical longitudinal preprocessing pipeline, QC
7 procedures, and statistical methods across samples, we aimed to shed light on the potential
8 impact of sample and acquisition differences on our ability to detect sex differences in
9 subcortical developmental patterns. While sex differences in patterns of subcortical
10 development across adolescence were identified using all three datasets, divergent results were
11 also seen for both within-sex and between-sex differences when comparing estimates from
12 each of the independent datasets. Below we describe the findings using all samples as well as
13 the differences detected between samples, as well as highlight the additional factors that may
14 continue to contribute to mixed findings in our understanding of sex differences in subcortical
15 neurodevelopment.

16 **4.1 Patterns of Age Related Changes in Males and Females**

17 GAMM estimates highlight an overall sex difference in patterns of development of subcortical
18 volumes based on data from three independent samples (Figure 2). Significant non-linear
19 changes were seen with age in the thalamus, curvilinear growth of the pallidum and amygdala,
20 and decreases in the caudate, putamen, and nucleus accumbens. The average trajectories from
21 our longitudinal datasets are largely in agreement with previous research that sensory, motor,
22 and cognitive related subcortical regions, such as the caudate and the thalamus, undergo
23 reduction into young adulthood (Lenroot, Gogtay et al. 2007, Raznahan, Shaw et al. 2014), as
24 well as increases in amygdala volumes (Goddings, Mills et al. 2014).

25 Estimated sex differences across all participants confirmed previous findings of overall
26 smaller volumes in females compared to males in all subcortical regions examined in the

1 present study. In addition, significant sex differences were detected for changes with age for all
2 regions of interest (Table 2). Of these results, replication across all three independent samples
3 was relatively poor, as assessed by statistical results comparing age trajectory GAMM
4 estimates. In fact, when directly testing between sample differences in age trajectories, only the
5 putamen, nucleus accumbens, and amygdala showed no significant differences in trajectories of
6 age development between the samples (Table 4). These findings may suggest greater
7 generalizability of the sex differences in curvilinear amygdala growth across childhood and
8 adolescence, with males showing significantly steeper increases compared to females. In
9 addition, across samples, females displayed decreases in nucleus accumbens and putamen
10 volumes, whereas males showed no change (nucleus accumbens) or less change (putamen)
11 with age from 8 to 22 years.

12 **4.2 LME versus GAMM Modeling**

13 LME is perhaps the most commonly used statistical approaches to determining both between
14 and within-person changes in longitudinal neuroimaging studies (Vijayakumar, Mills et al.
15 Accepted). At the outset of the study, it was assumed that using LME might therefore allow for a
16 more direct comparison of our results and previous studies. However, previous studies have
17 also shown that the shape of growth trajectories can vary when examining each sex separately
18 (Goddings, Mills et al. 2014). When using LME, this creates a challenge because in the case
19 where the shape of the trajectory may differ between groups, putting both males and females in
20 the same model may incorrectly assume similar shapes in growth in both sexes. For these
21 reasons, GAMM may allow for a more flexible fit, given that it does not assume the curve to the
22 data at the time of fitting the model. For these reasons, we chose to examine each sex
23 separately as well as together using both LME and GAMM. Overall, strong similarities were
24 seen in the ability for GAMM and LME modeling strategies to detect significant age-related
25 changes in each sex separately across the three independent samples. However, when testing
26 significant differences in changes in volumes with age between the sexes, GAMM identified
27 changes in the pallidum for NCD and OADS and the putamen for NCD as significantly different

1 between males and females, whereas LME models had p 's > 0.05. Thus, GAMM models may be
2 able to help reframe and bring additional clarity in understanding group differences in patterns of
3 neurodevelopment, especially when there are presumed sex differences in the shape of
4 trajectories in males versus females.

5 **4.3 Sample Consistencies and Differences**

6 Despite our best efforts to minimize between sample effects by utilizing similar
7 preprocessing and analytic techniques, both within-sex and between-sex trajectories of
8 neurodevelopment were nevertheless significantly different between samples. This may suggest
9 that factors such as population differences, sampling strategy, scanning protocols, as well as
10 age-range and statistical power may influence best model fits in longitudinal studies of
11 subcortical development. Because studies often differ in their age-ranges, scan intervals, and
12 sample size, the conclusion that a particular region shows a linear, quadratic, or even cubic
13 developmental pattern will not necessarily generalize to another study. For example, the current
14 LME results show both linear and quadratic best fits for caudate volumes in males and females,
15 and in contrast the putamen showed linear and cubic fits in females, but linear and quadratic for
16 males. Similarly, previous single-sample longitudinal studies have also reported linear
17 decreases in caudate and putamen volumes in both sexes (7-24 years; $n=223$ scans from 147
18 individuals; (Wierenga, Langen et al. 2014)); but also no change for caudate and quadratic for
19 putamen volumes from 5 to 27 years ($n=175$ scans from 84 individuals; (Narvacan, Treit et al.
20 2017)) or quadratic for females and cubic for males from 3 to 26 years ($n=829$ scans from 387
21 individuals (Lenroot, Gogtay et al. 2007)). This poses a challenge for the field, especially given
22 that we are rarely interested in exact ages, but rather periods of development across the life
23 span. Furthermore, while GAMM models may provide greater precision in the description of
24 volumetric change by moving away from more traditional polynomial assumptions in
25 neurodevelopmental growth trajectories, significant differences were also found in the current
26 study when using these models to examine developmental changes in subcortical volumes with
27 age across the included samples. Given how sensitive these analyses can be to sample

1 differences, it may be more useful as a field to focus on patterns of change (i.e. periods of
2 relative stability/change and direction of change, as opposed to using model terms) when trying
3 to understand overall developmental patterns, as well as providing access to statistical code in
4 order to allow for directly testing prediction accuracy of previously published models on new
5 datasets.

6 Besides inherent study population and sample differences, power is likely an issue when
7 examining each sample separately (N's ranging from 67-76 per study versus N=216 together).
8 Interestingly, despite being able to better account for within-subject variability, these longitudinal
9 findings are in agreement with recent reports that sample composition can alter age
10 associations in large cross-sectional study designs (LeWinn, Sheridan et al. 2017).
11 Furthermore, when examining sex differences in each sample separately (Supplementary Table
12 9), OADS was also found to show significant sex differences for each region of interest,
13 whereas the other two samples were more variable. The ability for OADS to detect similar sex
14 differences as seen with the larger combined sample may in fact be due to better within-subject
15 estimates due to three waves of data collection as compared to the two waves design used for
16 NCD and PIT.

17 Although using a commonly employed longitudinal preprocessing pipeline stream, the
18 degree to which automated segmentation programs may contribute to the seen sample
19 differences remains a concern. Given that manual tracing requires availability of multiple highly
20 trained raters without intra- and inter-rater drift over time, manual tracing becomes exceeding
21 time intensive for even medium scaled longitudinal studies that span multiple years, such as
22 those included here (PIT=146, NCD=152, and OADS=169 scans). For these same reasons,
23 poor segmentations are often excluded from the analyses rather than performing manual edits
24 to the FreeSurfer subcortical volume segmentation (e.g. aseg) (as done in the current study).
25 Thus, large scaled studies often implement automated software and in the current study we
26 implemented the FreeSurfer longitudinal pipeline given that it was specifically created to better
27 capture within-subject changes over time in the subcortical regions examined (as shown by

1 intraclass correlation coefficients ranging from .90 for the left amygdala to .99 for the right
2 caudate and putamen; note that nucleus accumbens volumes were not included in this report)
3 (Reuter, Schmansky et al. 2012). While to our knowledge, no study has been published
4 comparing the longitudinal pipeline estimates with manual tracing, cross-sectional studies have
5 found that automated software tend to overestimate subcortical volumes as compare to manual
6 tracings (Schoemaker, Buss et al. 2016, Makowski, Beland et al. 2017). Moreover, for
7 longitudinal studies if an over estimation in volumes consistently occurs at both the between-
8 and within-subject levels, relative differences are likely to still be meaningful (Chepkoech,
9 Walhovd et al. 2016). However, variation in volume estimates between scanners types and
10 acquisition parameters is likely more problematic, especially if this interacts with age. In this
11 regard, cross-sectional studies have reported the pallidum to have poor reliability out of
12 subcortical volume measurements using FreeSurfer, with volume estimates for this region
13 impacted by MP-RAGE acquisition parameters, such as isotropic versus anisotropic voxel size
14 (Wonderlick, Ziegler et al. 2009). Furthermore, low reliability of pallidum volumes, specifically,
15 have been attributed to the T1-weighted contrast profile of the pallidum which is less distinct
16 from its surrounding white matter as compared to other subcortical regions such as the
17 thalamus or caudate (Fischl, Salat et al. 2002, Wonderlick, Ziegler et al. 2009). With dedication
18 to automated software continuing to improve (e.g. FreeSurfer 6.0 was released mid-way through
19 the current project), future studies will benefit from reductions in such potential software
20 confounds.

21 **4.4 Limitations**

22 Recent studies document the impact of motion on structural measures (Reuter, Tisdall et al.
23 2015, Alexander-Bloch, Clasen et al. 2016, Ducharme, Albaugh et al. 2016), and this likely
24 represents an especially important confound for developmental studies. We therefore conducted
25 detailed QC of all raw and processed images and excluded participants with excessive motion.
26 Nonetheless, future studies could benefit from employing standardized and well-documented
27 QC procedures (Backhausen, Herting et al. 2016), and/or methods for tracking in-scanner

1 motion, automated QC assessment, and motion correction procedures (further discussed in
2 (Vijayakumar, Mills et al. Accepted)). Previous studies suggest that within-subject changes in
3 puberty (both physical and hormonal) are important factors for amygdala growth in male and
4 female adolescents (Goddings, Mills et al. 2014, Herting, Gautam et al. 2014); with very similar
5 curvilinear amygdala growth patterns seen as reported here when raw volumes were estimated
6 based on Tanner stage in males and females separately (Goddings, Mills et al. 2014). Puberty
7 has also been found to relate to nucleus accumbens volumes (Goddings, Mills et al. 2014),
8 although the trajectories do not mirror the patterns of volumetric change identified in the current
9 study. Unfortunately, pubertal metrics were not consistent across the three cohorts; making it
10 impossible for us to investigate how puberty may contribute to differences in amygdala and
11 nucleus accumbens trajectories in males and females in the current study. Thus, future
12 research is warranted to examine the contributions of hormones to sex differences in the
13 neurodevelopmental trajectories of the amygdala and nucleus accumbens. In addition,
14 FreeSurfer 6.0 was released mid-way through the current project, after the preprocessing for the
15 current study was complete. Replication studies are always warranted, and should consider also
16 examining the potential impact of the longitudinal processing stream of FreeSurfer 5.3 versus
17 FreeSurfer 6.0, especially given the efforts of this new version on estimating the putamen.

18 **5. Conclusions**

19 Across all participants from the three independent samples, sex differences in age trajectories
20 of volumetric development for the thalamus, pallidum, caudate, putamen, nucleus accumbens,
21 hippocampus, and amygdala were apparent. Using a multisite approach with consistent
22 longitudinal preprocessing (software and quality checking) and statistical analyses,
23 generalizable patterns were found for age changes across adolescence in the amygdala,
24 putamen, and nucleus accumbens. However, conspicuous sample differences were seen for the
25 thalamus, pallidum, caudate, and hippocampus; perhaps a cautionary limitation when
26 attempting to generalize subcortical findings from these regions of interests in longitudinal
27 samples with different age ranges. Efforts aimed at improving our ability to replicate trajectories

1 in typical development, such as the current study, are ultimately necessary in order to be able to
2 further focus our inquiry on the factors influencing sex differences and individual differences in
3 subcortical growth; including genetic, and/or environmental effects that may contribute to the
4 observed differences at the group and individual-level. Furthermore, improving our ability to
5 assess the 'age residual' of within-subject changes in deep gray matter structures is crucial in
6 our ability to understand risk and resilience for psychopathology during development.

7

8

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Figure 1. Age and sex distributions for each sample.

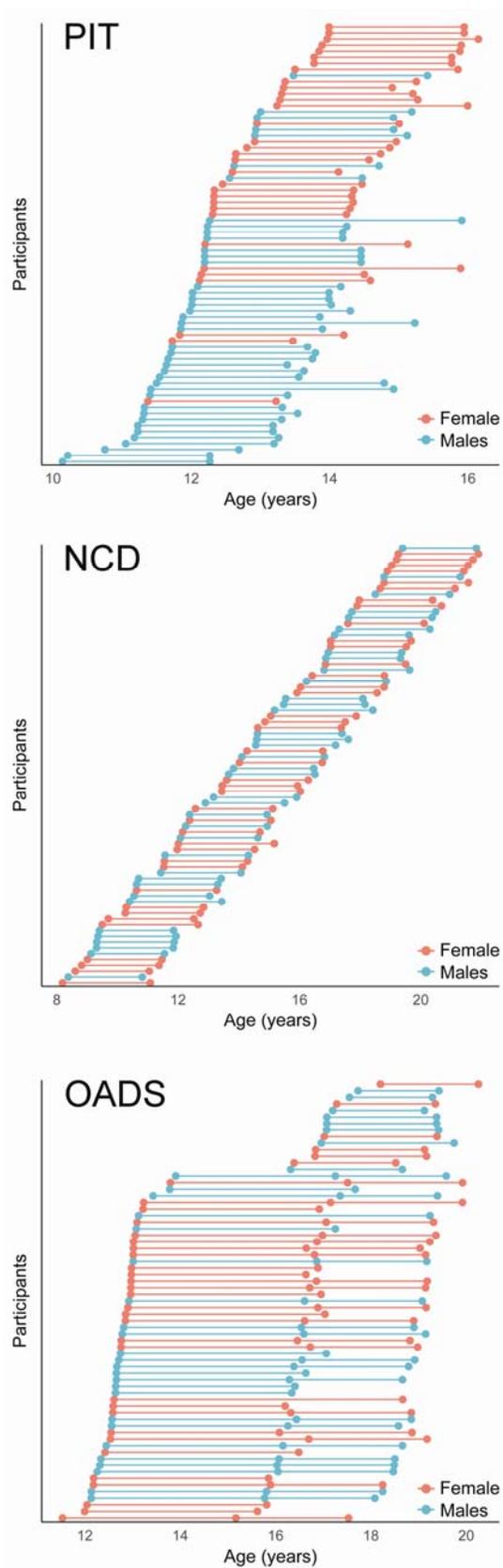


Figure 2. Sex differences in the developmental age trajectories for subcortical volumes based on three independent samples.

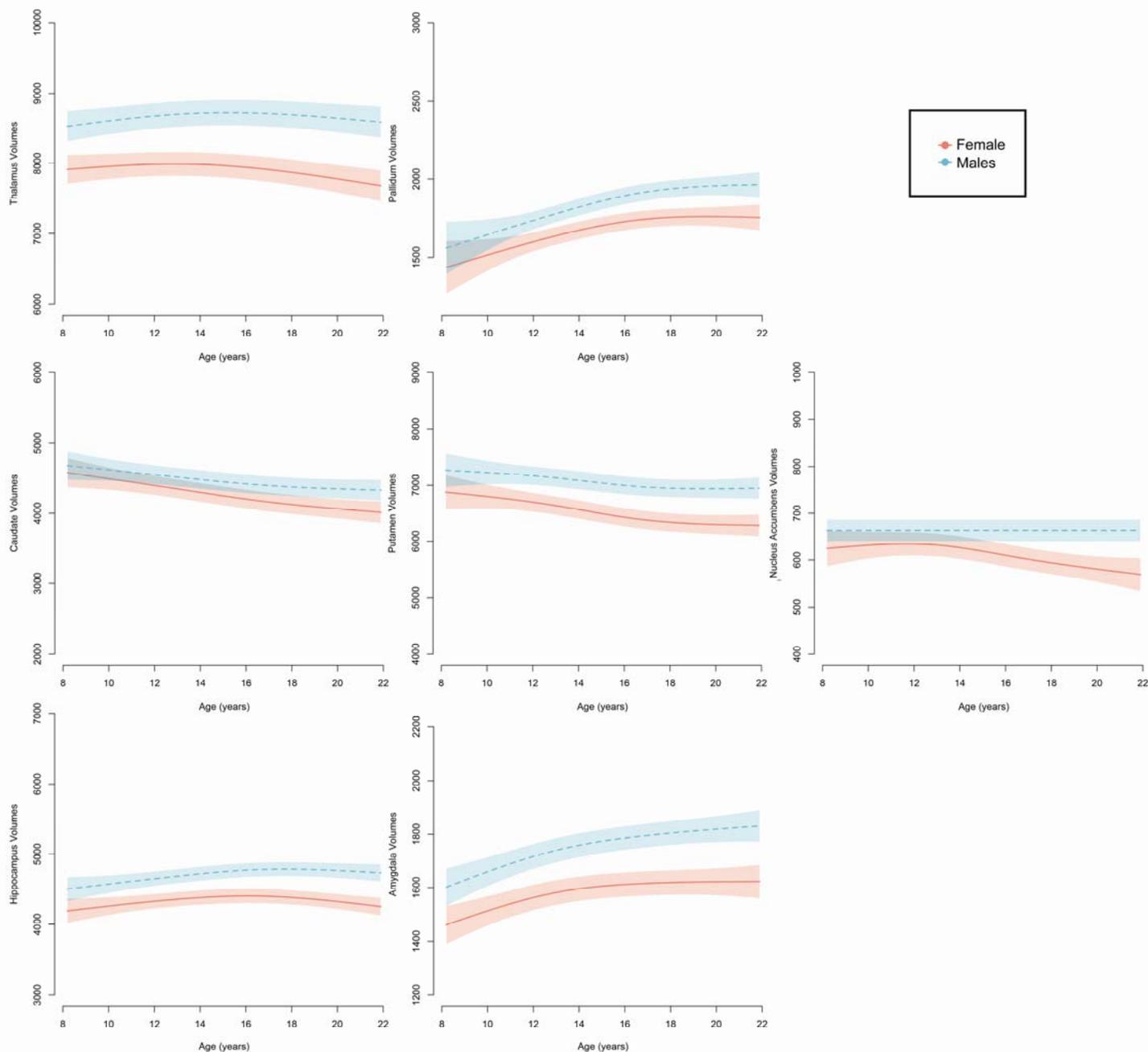


Figure 3. Developmental age trajectories for the thalamus and pallidum. a) Females and b) males are plotted separately. Individual datapoints are shown, connected for each participant, in the appropriate sample color. The bolded colored lines represent the GAMM fitting for each sample with 95% confidence intervals. c) Representation of GAMM fits (with 95% confidence intervals) for each sex per sample plotted together, p-values represent sex differences per sample.

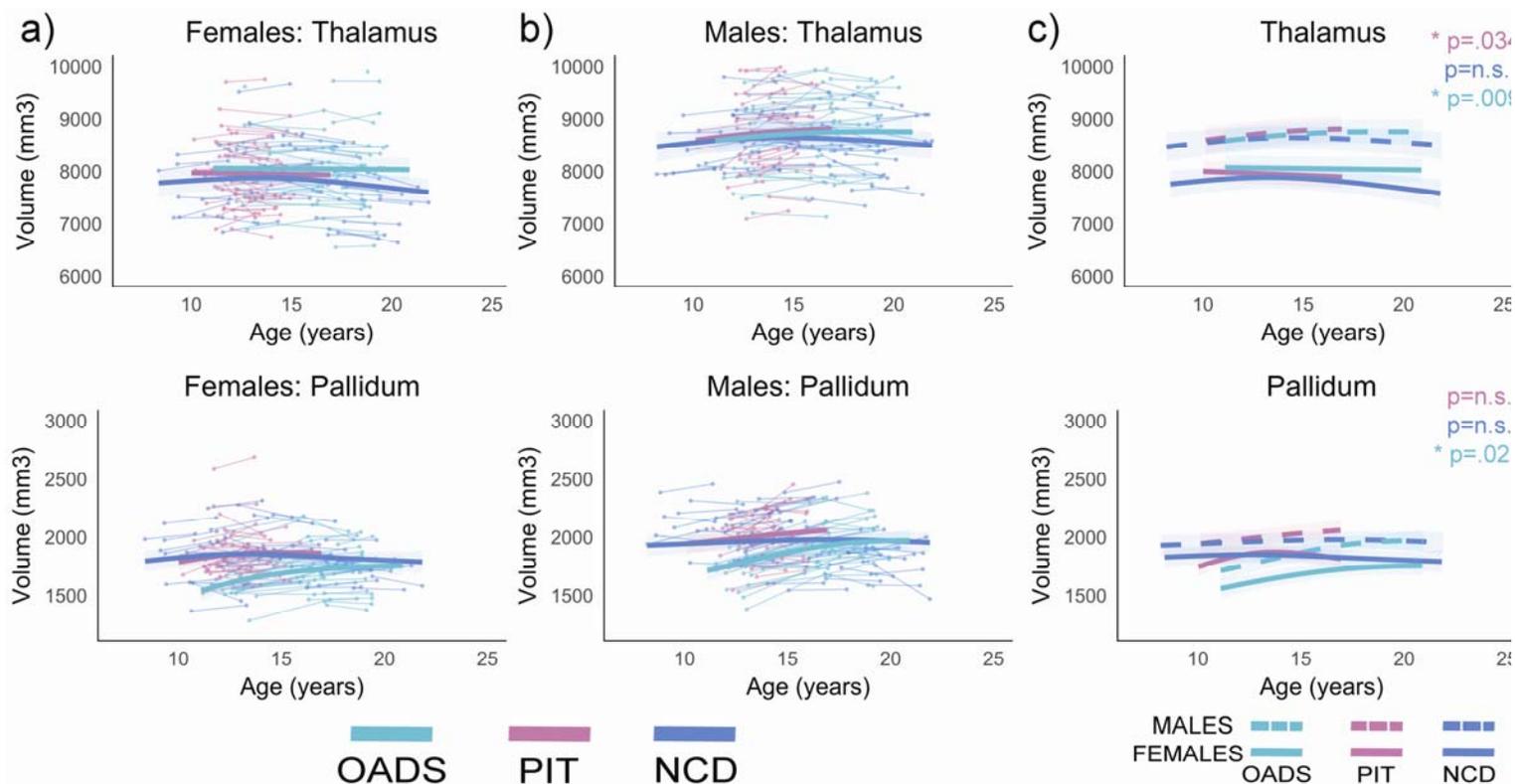


Figure 4. Developmental age trajectories for the caudate, putamen, and nucleus accumbens. a) Females and b) males are plotted separately. Individual datapoints are shown, connected for each participant, in the appropriate sample color. The bolded colored lines represent the GAMM fitting for each sample with 95% confidence intervals. c) Representation of GAMM fits (with 95% confidence intervals) for each sex per sample plotted together; p-values represent sex differences per sample.

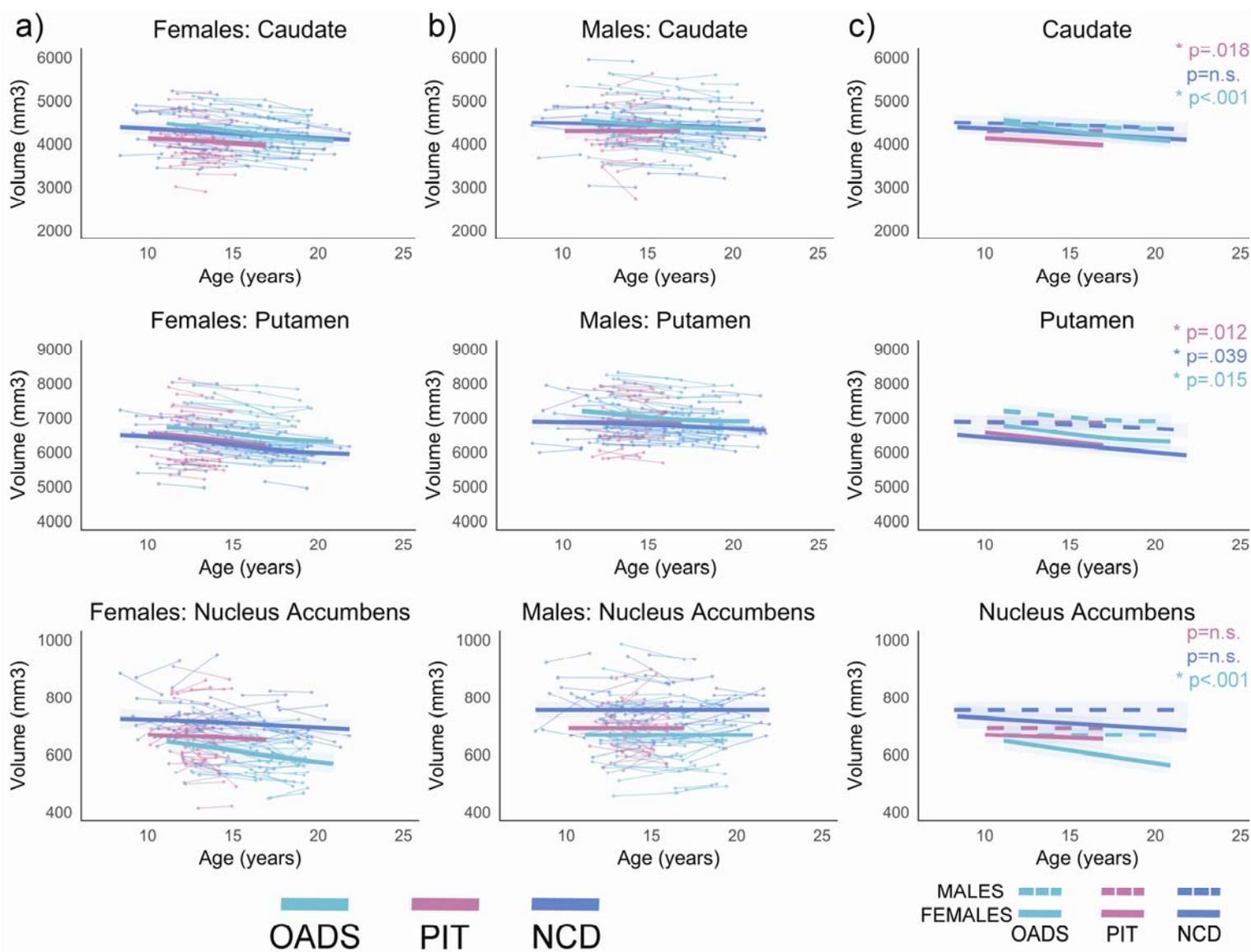


Figure 5. Developmental age trajectories for the hippocampus and amygdala. a) Females and b) males are plotted separately. Individual datapoints are shown, connected for each participant, in the appropriate sample color. The bolded colored lines represent the GAMM fitting for each sample with 95% confidence intervals. c) Representation of GAMM fits (with 95% confidence intervals) for each sex per sample plotted together; p-values represent sex differences per sample.

