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Reporting Summary

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Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed	
☐	☒	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒	A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒	The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☐	☒	A description of all covariates tested
☐	☒	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒	A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☐	☒	For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☐	☒	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☐	☒	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☐	☒	Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	No software was used.
Data analysis	MATLAB 2016b (https://de.mathworks.com/products/matlab.html), SPM12 r7219 (https://www.fil.ion.ucl.ac.uk/spm/software/), hMRI toolbox for SPM (https://github.molgen.mpg.de/VBQ-toolbox-group/hMRI-Toolbox-public), CAT12 toolbox for SPM r1318 (http://www.neuro.uni-jena.de/cat/), Sandwich Estimator Toolbox for SPM r2.0.0 (http://www.nisox.org/Software/SwE/)

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

Whole-brain results are available for inspection online on Neurovault (https://neurovault.org/collections/YAHZLJRW/). Data for this specific paper has been uploaded to the Cambridge Data Repository (https://doi.org/10.17863/CAM.12959) and password protected. Our participants did not give informed consent for their measures to be made publicly available, and it is possible that they could be identified from this data set. Access to the data supporting the analyses presented in this paper will be made available to researchers with a reasonable request to openNSPN@medschl.cam.ac.uk or the corresponding authors [G.Z., T.U.H.].

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	Imaging sample size of 300 was determined by NSPN consortium before onset of the study as a power analysis of the then (2012) available developmental studies.
Data exclusions	Available image data was visually quality checked by experts during processing and final image data underwent movement artifact removal using using R2* during-scan motion criteria with excluding 10% of worst cases. Moreover a covariance-based statistical outlier check was applied before entering analysis. Severe artifacts and outliers were excluded and motion proxy was entered as covariate during analysis. Exclusion criteria were established during the study.
Replication	We perfomed a validation study using a region-based summary statistic approach to reproduce the main finding of developmental effects and affected rates of change of growth with higher expression of psychiatric traits. Summary statistics here refers to calculating intercept and slope for each ROI and individual and modelling those in a second level model with age, sex, ses and traits as predictors. We were able to confirm the same pattern of results as presented in voxel-based Sandwich estimator analysis. Difference in terms of statistical effect sizes and spatial specificity due to different level of aggregation (voxel- vs. ROI based analysis) were observed but expected.
Randomization	Since the NSPN is an observational desgin, no randomization of subgroups was applicable. We include measures of socioeconomical disadvantage during all analysis as covariate to account for unknown confounding effects of related variable during sampling.
Blinding	Blinding was not relevant to our study since an observational design was used and not an experimental design.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☐	☒ Human research participants
☒	☐ Clinical data

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☐	☒ MRI-based neuroimaging

Human research participants

Policy information about studies involving human research participants

Population characteristics	The NSPN study used an accelerated longitudinal design to investigate psychiatric traits and brain maturation during adolescence and early adulthood. Subjects were sampled in six age bins 14-15y, 16-17y, 18-19y, 20-21y, and 22-24y, with roughly balanced numbers (overall age mean (std) 19.45 (2.85) years). Each age bin was balanced for sex and ethnicity (relative to the local population). From the 2406 participants that took part in the study and which filled out socio-demographic information and questionnaires at least once, 318 healthy subjects (~60 subjects per age bin) participated in the MRI arm (after screening out subjects with self-reported pervasive neurological, developmental or psychiatric disorders). More details can be found in Kiddle, B. et al. Cohort profile: The NSPN 2400 Cohort: a developmental sample supporting the Wellcome Trust NeuroScience in Psychiatry Network. Int. J. Epidemiol. (2017). doi:10.1093/ije/dyx117
Recruitment	Participants were recruited in London and Cambridgeshire from schools, colleges, primary care services and through advertisement. Self-selection bias is likely to operate in at two ways. First, the sample may not be fully representative of the underlying population, in that participants for the scanning study were recruited out of those that returned self-report questionnaires, these were in turn recruited from those that returned and 'expression of interest' form, who were recruited from the target population. Each stage is likely to leave behind more young people who are less planful and/or too stressed and/or too busy to participate in studies. Second, participants were recruited in parallel in the five age bins. The age bins were

balanced with respect to sex and ethnicity, but were not equally easy to fill. Trained research assistants telephoned participants who consented to be contacted and directly asked them to participate in order to fill the age-sex bins that were harder to fill. For example males of age 20 were recuited less readily than females of age 16. Although we do not have direct evidence for this, it could be that ease of recruitment may be correlated with impulsivity, or its neurological correlates, or impulsivity may interact with age to influence recruitment. Such recruitment effects may explain why longitudinal and cross-sectional results may not always concur, so that say young people having their second scan at age 18 differ from the ones recruited to have their first scan at age 18.

Ethics oversight: Ethics were approved by the Cambridge Central Research Ethics Committee (12/EE/0250).

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Magnetic resonance imaging

Experimental design

Design type: accelerated longitudinal observational design

Design specifications: repeated-measures MRI design with 1-3 scans per subject

Behavioral performance measures: To assess self-reported features along obsessive-compulsive and impulsivity spectra, we used well established questionnaires that were handed out to the participants over the course of the study along with baseline MRI acquisitions and follow-ups with up to 3 observations available per person. In particular, we had two measures to assess obsessive-compulsive features, namely the revised Obsessive-Compulsive Inventory (OCI-R) and Padua Inventory (PI-WSUR). For measuring general impulsivity, we used the Barratt Impulsiveness Scale (BIS).

Acquisition

Imaging type(s): multi-echo FLASH Multiparameter Mapping Protocol (longitudinal and transverse relaxation rates R1 and R2*, proton density PD, and magnetization transfer MT) (Weiskopf et al., 2013)

Field strength: 3T

Sequence & imaging parameters: Three different multi-echo FLASH scans were acquired with predominant T1-, PD-, and MT-weighting by appropriate choice of the repetition time (TR) and the flip angle α: TR/α = 18.7 ms/20◦ for the T1w scan and 23.7 ms/6◦ for the PDw and the MTw scans. MT-weighting was achieved by applying an off-resonance Gaussian-shaped RF pulse (4ms duration, 220◦ nominal flip angle, 2 kHz frequency offset from water resonance) prior to the excitation. Multiple gradient echoes were acquired with alternating readout polarity at six equidistant echo times (TE) between 2.2 and 14.7ms for the T1w and MTw acquisi- tions and at 8 equidistant TE between 2.2 ms and 19.7 ms for the PDw acquisition. Other acquisition parameters were: 1 mm isotropic resolution, 176 sagittal partitions, field of view (FOV) = 256 × 240 mm, matrix = 256 × 240 ×176, parallel imaging using GRAPPA factor 2 in phase-encoding (PE) direction, 6/8 partial Fourier in partition direction, non-selective RF excitation, read- out bandwidth BW = 425 Hz/pixel, RF spoiling phase increment = 50◦ , total acquisition time ~19 min. More details can be found in multi-site validation study supporting the reported study. Weiskopf, N., Suckling, J., Williams, G., Correia, M. M., Inkster, B., Tait, R., et al. (2013). Quantitative multi-parameter mapping of R1, PD(*), MT, and R2(*) at 3T: a multi-center validation. Frontiers in Neuroscience, 7, 95. http://doi.org/10.3389/fnins.2013.00095

Area of acquisition: whole-brain MPM acquisition

Diffusion MRI ☐ Used ☒ Not used

Preprocessing

Preprocessing software: MT images were generated based on muli-echo FLASH MPM protocol and hMRI toolbox for SPM (https://github.molgen.mpg.de/VBQ-toolbox-group/hMRI-Toolbox-public). Custom made code based on SPM and CAT toolbox functions is provided along with the manuscript.

First, we performed symmetric diffeomorphic registration.
Second, we applied SPM12's Computational Anatomy Toolbox (CAT, r1318, Structural Imaging Group, http://dbm.neuro.uni-jena.de/cat12/) segmentation to each subject's midpoint image.
Third, nonlinear template generation and image registration to MNI space was performed using the individual midpoint GM and WM tissue maps and diffeomorphic registration using SPM's geodesic shooting .
Fourth, normalized MT maps were smoothed using previously established tissue-weighted-smoothing with a Gaussian kernel of 6 mm full width at half maximum (FWHM) for subcortical and cortical regions, respectively.
Fifth, maps were carefully checked manually before and after longitudinal registration by an expert. Additionally, the obtained normalized and smoothed MT data (in MNI space) was quality checked using statistical covariance-based sample inhomogeneity measures (as implemented in the CAT toolbox) to exclude subjects with extremal overall deviation of quantitative values due to acquisition or processing artefacts.
Finally, we used above within- and between subjects diffeomorphic registration to obtain normalized (gray and white matter) tissue segment maps in the MNI template space for VBM analysis. We accounted for existing differences and ongoing changes of local tissue volumes under applied registrations using both within- and between-subjects modulation. Obtained modulated normalised tissue segments were smoothed using Gaussian filter with 6 mm full width

at half maximum (FWHM).

Normalization: diffeomorphic registration using geodesic shooting toolbox for SPM (Ashburner & Friston, 2011).

Normalization template: study wise template was generated using geodesic shooting toolbox for SPM

Noise and artifact removal: CAT12 toolbox uses non-local means filtering to reduce local noise levels before segmentation. Since smoothing was applied SNR is improved substantially after accounting for normalization errors. Artifacts were detected manually in terms of visual inspection of movement artifacts and unexpected processing errors were excluded.

Volume censoring: Covariance-based homogeneity checking (CAT toolbox) removing outliers with >2 std in search volume for VBM.

Statistical modeling & inference

Model type and settings: In this study, we performed modelling of the image data using a state-of-the-art analysis method recently introduced as the longitudinal Sandwich Estimator (SwE), http://warwick.ac.uk/tenichols/SwE, SPM toolbox). Using this so-called marginal model one describes individual i's data as $y_i = X_i*\beta + \varepsilon_i*$, i.e. based on only fixed effects design matrix X_i. The randomness is treated as nuisance and modelled by marginal error terms ε_i* with mean 0 and positive semi-definite covariance V_i. Marginal models do not require specification of random-effects and allow unbiased population-average inference and predictions about brain change in certain sub-groups or in relation to covariates.

Effect(s) tested: We tested for positive effects of time/visit, and mean age of individual on MT and according negative effects indicative of shrinkage of volume. We tested for effects of sex and the interactions of those demographic covariates. Moreover we tested for the key hypothesis that higher expression for psychiatric traits were related to impaired growth of MT over visits/time and main effects of traits at baseline.

Specify type of analysis: ☐ Whole brain ☐ ROI-based ☒ Both

Anatomical location(s): Demographic effects were analyzed on whole-brain voxel-based level since myelination trajectories have not been explored longitudinally before. For trait dimension we focussed a voxel-based analysis on a wholebrain level requested during reviews.

Statistic type for inference (See Eklund et al. 2016): if not stated otherwise in the manuscript all main findings are based on voxel-wise inference

Correction: FDR, cluster FWE, TFCE

Models & analysis

n/a	Involved in the study
☒	☐ Functional and/or effective connectivity
☒	☐ Graph analysis
☐	☒ Multivariate modeling or predictive analysis

Multivariate modeling and predictive analysis: item-level pca was performed to operationalize the compulsivity dimension