Probing the overarching continuum theory: Data-driven phenotypic clustering of children with ASD or ADHD Deserno, M.K.^{1,3*}, Bathelt, J.1*, Groenman, A.P.1, Geurts, H.M.^{1,2} ¹ Dutch Autism & ADHD Research Centre (d'Arc), Department of Psychology, University of ² Dr. Leo Kannerhuis, Amsterdam, The Netherlands ³ Max Planck Institute for Human Development, Berlin *these authors contributed equally to this work Corresponding Author. Deserno, M.K., Max Planck Institute for Human Development, Berlin, Germany. Email: marie.deserno@gmail.com Conflict of Interest. None. **Financial Support.** This work was supported by an Innovational research incentives scheme VICI from the Netherlands Organization for Scientific Research (NWO, VICI Grant No. 453-16-006) awarded to HMG, a Rubicon fellowship from NWO (No. 019.191SG.005) awarded to MKD, and an Amsterdam Brain & Cognition (ABC) Talent Grant awarded to HMG and JB. Word Count. 4657 **Running Head.** ASD and ADHD – an overarching continuum?

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The clinical validity of the distinction between ADHD and ASD is a longstanding discussion. Recent advances in the realm of data-driven analytic techniques now enable us to formally investigate theories aiming to explain the frequent co-occurrence of these neurodevelopmental conditions. In this study, we probe different theoretical positions by means of a pre-registered integrative approach of novel classification, subgrouping and taxometric techniques in a representative sample (N=434) and replicate the results in an independent sample (N=219) of children (ADHD, ASD, and typically developing) aged 7 to 14 years. First, Random Forest Classification could predict diagnostic groups based on questionnaire data with limited accuracy - suggesting some remaining overlap in behavioural symptoms between them. Second, community detection identified four distinct groups, but none of them showed a symptom profile clearly related to either ADHD or ASD in neither the original sample nor the replication sample. Third, taxometric analyses showed evidence for a categorical distinction between ASD and typically developing children, a dimensional characterization of the difference between ADHD and typically developing children and mixed results for the distinction between the diagnostic groups. We present a novel framework of cutting-edge statistical techniques which represent recent advances in both the models and the data used for research in psychiatric nosology. Our results suggest that that ASD and ADHD cannot be unambiguously characterised as either two separate clinical entities or opposite ends of a spectrum and highlight the need to study ADHD and ASD traits in tandem.

The prevalent co-occurrence of Autism Spectrum Disorder (ASD) and Attention-Deficit Hyperactivity Disorder (ADHD) reflects a pressing problem for diagnosis and treatment in child psychiatry (Melegari et al., 2015; Rommelse, Franke, Geurts, Hartman, & Buitelaar, 2010; Simonoff et al., 2008). The two diagnostic categories share etiological factors, overlapping characteristics (e.g., symptoms of inattention and impulsivity; Ronald, Larsson, Anckarsäter & Lichtenstein, 2014) and are both associated with Generalized Anxiety Disorder (GAD), Obsessive-Compulsive Disorder (OCD) and Major Depression (MD; Mulligan et al., 2009; Rommelse et al., 2010). Common practices of small sample size studies and case control models, however, have stalled progress in the pursuit of a better understanding of the discriminant properties between these two neurodevelopmental conditions. Here, we employ a data-driven clustering approach to investigate whether these neurodevelopmental conditions comprise of subtypes that cross clinical boundaries in a large cohort of atypically and typically developing children, and cross-validate our results subsequently. A growing body of literature concerned with the diagnostic validity of consensusdriven methods (Insel et al., 2010), such as the International Disease Classification [ICD] (World Health Organisation, 2018) and the Diagnostic and Statistical Manual of Mental Disorders [DSM] (American Psychiatric Association, 2013), alludes to an unresolved issue: the intensive search of discriminatory biomarkers for psychiatric conditions, so far, did not result in traceable pathogenic pathways that enable precision medicine and person-centred support. Rather, as both ASD and ADHD remain behaviourally diagnosed conditions, about 30-60% of autistic individuals meet diagnostic criteria for ADHD (Carlsson et al., 2013) and about 21-40% of individuals with ADHD meet criteria for an ASD diagnosis (Antshel, Zhang-James, Wagner, Ledesma, & Faraone, 2016; Grzadzinski, Dick, Lord & Bishop, 2016; Rommelse et al., 2010; Ames & White, 2011). With its recent changes, the DSM-5

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acknowledges this frequent co-occurrence with revised criteria to explicitly allow for combined diagnosis of ADHD and ASD. Recent work, however, even hypothesizes that these two conditions should not be conceptualized as distinct disorders but rather as manifestations of one overarching disorder with a similar aetiology (Van der Meer et al., 2012). The hypothesis underlying this theory considers ASD to be a manifestation of the most severe subtype on one end of the overarching continuum, while mild ADHD would be located on the other end of this hypothesized continuum. If this hypothesis holds, its theoretical implication would be that ASD cannot exist without ADHD. One would, therefore, expect the categorical classification of individuals as either ASD or ADHD-cases to be difficult since there is a sliding scale between the symptoms rather than two distinct clinical entities. In a parallel line of reasoning, it is often suggested that symptoms related to attention may stem from inhibitory atypicalities when it comes to ADHD, but social atypicalities in the case of ASD phenotypes (Visser, Rommelse, Greven, Buitelaar, 2016; Ingram, Takahashi & Miles, 2008). Also, several studies have shown disorder-specific effects for the exact same psychiatric drugs, such as different normalisation effects in ADHD and ASD of brain dysfunction through serotonin reuptake inhibitors (Chantiluke et al., 2015), while others report shared dysfunction in ADHD and ASD, such as reduced activation in the right PFC indicating shared inhibitory dysfunction (Xiao et al., 2012). The underlying explanation would then be that similar symptoms could have different underlying causes instead of a common cause (Happé & Ronald, 2008; James, Dubey, Smith, Ropar & Tunney, 2016). In the current study, we investigated if behavioural characteristics are sufficient to classify children into diagnostic categories of ADHD and ASD. In a first step, using taxometric analyses, we tested whether the classification performance may arise because of an underlying continuum. Alternatively, the overlap may arise from subgroups within each diagnostic category that

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share behavioural features. In a second step we, therefore, investigated this alternative hypothesis using a data-driven clustering approach to identify potential subgroups.

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Methods

Participants

The current analysis was based on data obtained from the Child Mind Institute Biobank database (https://childmind.org, date of access: February 21st, 2019). The initial sample consisted of 475 children (ADHD: 249, ASD: 90, TD: 136) between 7 and 13 years of age. This sample is part of a larger cohort of the Healthy Brain Network Biobank based on a communityreferred recruitment model of children with developmental psychopathology (Alexander et al., 2017). One participant in the ASD group and 8 participants in the TD group were removed because of missing questionnaire data or missing diagnostic information. Diagnostic classifications were based on extensive clinicians-administered assessments, including the Autism Diagnostic Observation Schedule (ADOS) for suspected autism (Alexander et al., 2017). For the current analyses we used structured questionnaire data from the selfadministered assessment protocol entered through the online patient portal (Alexander et al., 2017). Questionnaire measures may show extreme responses that are not related to the content of the questionnaire that arise due to unintended, extreme, fake, or random responses. We, therefore, calculated the Mahalanobis distance to detect and remove these respondents (Zijlstra, van der Ark, & Sijtsma, 2011). According to this measure, 32 participants were identified as multivariate outliers and were removed from the analysis (Mahalanobis distance > 14.07; 18 ADHD, 21 ASD, 2 TD). The final sample consisted of 434 children (231 ADHD, 77 ASD, 126 TD). There were no significant differences in age between the diagnostic groups, but there was a disproportionate number of boys in the ADHD and ASD groups (see Table 1) consistent with the greater prevalence of these diagnoses in males (Loomes, Hull & Mandy,

2017). A third of the children in the ADHD group had an additional diagnosis. The most common were Oppositional Defiant Disorder (n=72 [29.38%]), Autism Spectrum Disorder (n=39 [15.92%]), Specific Learning Disorder with Impairment in Reading (n=34 [13.88%]), Language Disorder (n=33 [13.47%]), Generalized Anxiety Disorder (n=23 [9.39%]), and other less frequent diagnoses (e.g. Enuresis, Specific Phobias, Separation Anxiety; n<20 [≦5%]¹. Around a fifth of children in the ASD group had an additional diagnosis. The most common diagnoses were ADHD-Combined Type (n=36 [14.69%]), ADHD-Inattentive Type (n=13 [5.31%]), and other less frequent diagnoses (e.g., Oppositional Defiant Disorder, Specific Learning Impairment, Generalized Anxiety Disorder; n<10 [≦5%]).

Table 1 Comparison of demographic information between the diagnostic groups.

	ADHD	ASD	TD	Statistics		
N	249	89	128			
Male [%]	186 [42]	65 [12]	68 [58]	$\chi^2 = 86.06*,$	$\chi^2=36.48*$	$\chi^2=0.79*,$
				<i>p</i> <0.001	<i>p</i> <0.001	<i>p</i> =0.373
				ADHD vs ASD	ADHD vs TD	ASD vs TD
Age	9.39±0.109	9.26±0.188	9.41±0.137	t(131)=0.58,	t(273)=-0.12,	t(173)=-0.63,
[mean+±SE]				p=0.566	p=0.908	<i>p</i> =0.527

^{*} Compared to equal split

Pre-registration

The analysis steps (see also Figure 1) and expected results were preregistered before accessing the data. The preregistration can be accessed online (https://aspredicted.org/ya7wr.pdf).

Analysis code

The code for the analyses is available via the Open Science Framework

159 (https://osf.io/vkwma/?view_only=1e66771d9b8c4f1dab7af35918345432).

¹ Please note that multiple comorbid diagnoses were possible, i.e. the percentages are not additive.

[INSERT FIGURE 1 ABOUT HERE]

Figure 1 Overview of the analysis steps. First, item scores were summarized within questionnaire scales to obtain individual profiles. Then, the profiles were used to predict the diagnostic labels using random forest classification. The proximity matrix generated by the random forest classification was used to detect subtypes. In addition, the questionnaire scales that best distinguished the diagnostic groups were used for taxometric analysis to determine if a categorical or a dimensional account provided a better fit to the data.

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Materials

The Strengths and Weaknesses of ADHD-symptoms and Normal-behaviors ratings Scale 171 (SWAN; Swanson et al., 2001) is a questionnaire with 18 items that assesses potential 172 strengths and weaknesses related to ADHD symptoms on a single parent-rated scale. It uses 173 items from the Swanson Nolan And Pelham IV (SNAP IV; Swanson, 2003). The SNAP-IV 174 teacher and parent rating scale is often used to assess ADHD symptoms, but the SWAN 175 rephrases the symptoms into strength-based statements making them follow a normal 176 distribution instead of a skewed distribution (Alexander, Salum, Swanson, & Milham, 2019). 177 For example, "Often does not seem to listen when spoken to directly" from the SNAP IV is 178 reworded to "Listens when spoken to directly". The SWAN items are grouped into the 179 Hyperactivity/Impulsivity (HY) and the Inattention (IN) subscale. A validation study of the 180 SWAN indicated high internal consistent (Cronbach's alpha=0.95) and adequate test-retest 181 reliability (r=0.66; Lakes, Swanson, & Riggs, 2012). 182 183 The Social Responsiveness Scale (SRS; Constantino & Todd, 2003) is a 65-item scale that is 184 designed to obtain parents- or teacher-ratings of autistic symptomatology as observed in naturalistic social settings. The SRS-assessed symptoms are combined into five subscales: 185 186 Social Awareness (AWR), Social Cognition (COG), Social Communication (COM), Social 187 Motivation (MOT), and Restricted Interests and Repetitive Behaviours (RRB). Also, the

assessment scale suggests combining these scales into two symptom comparison subscales: the DSM Social communication & interaction subscale and the DSM RBB. We did not include the latter DSM subscale since it is only based on the RRB subscale and, therefore, redundant in the here employed analyses. Validation studies have shown that the SRS has good psychometric properties (3-month test-retest reliability: 0.88, inter-rated reliability: 0.8, correlation with the Autism Diagnostic Interview Revised (ADI-R) score: 0.7; Constantino, Przybeck, Friesen & Todd, 2000, Constantino & Todd, 2003). Of note to the current investigation is that although the SRS was originally designed to produce continuously distributed scores, recent results indicated a bimodal distribution within affected and unaffected family members of children with ASD (Constantino, Zhang, Frazier, Abbacchi & Law, 2010; Virkud, Todd, Abbacchi, Zhang, & Constantino, 2009).

Replication sample. The independent replication sample consisted of 219 children (73 female, ADHD: 87 [39.73%], ASD: 69 [31.51%], TD: 63 [28.77%]) between 8 and 12 years (mean: 10.11, SE: 0.092). For the purpose of replication, we focus solely on the SWAN and SRS data.

Random Forest Classification

First, we applied random forest classification (RFC) to investigate if the selected questionnaire scales can be used to classify participants into diagnostic groups (ADHD, ASD, TD). For multi-class classification, the diagnostic groups were recoded according to a one-versus-all coding scheme, e.g., ADHD vs ASD and TD. The RFC model was trained in a random subsample of 75% of the participants and 25% of the data were held-out for the final validation. To identify the optimal tree depth (i.e., the more splits the more detailed information is explained), bootstrap cross-validation with 10 random resamples was

employed. Synthetic minority oversampling (SMOTE) was used to account for class imbalance in the subsets (Chawla, Bowyer, Hall, & Kegelmeyer, 2002) and the area under the receiver-operating characteristic curve (AUROC) averaged across all classes was used to tune the model. These procedures were implemented in R v3.5.2 using the randomForest v4.6 (Liaw & Wiener, 2002) and caret v.6.0 (Kuhn, 2018) packages. In order to work with the best performing classification approach, we evaluated and compared the classification performance of alternative machine learning approaches (11-/12-regularised support vector classification, ridge regression) and cross-validation strategies (k-fold, stratified shuffle split). The machine learning approach presented in the main analysis showed better or equivalent performance as these alternatives (the detailed results are included in the Supplementary Materials). As an adjunct to the random forest classification, we employed an additional method that uses dimensional factors to discriminate between classes. In contrast to the random forest classification that splits participants according to scores on a scale, this approach can assign weights to individuals scales. For instance, ADHD and ASD may share features of executive function difficulties, but this characteristic may be more important, i.e. has a higher weight, for the discrimination of ADHD versus CMP compared to ASD versus CMP. Partial least squares (PLS) analysis creates linear combinations of input variables, in this case questionnaire scales, that are aligned with outcome variables, here one-hot encoded diagnostic labels. An extension of the PLS approach has been developed for classification problems that also incorporates regularisation for better discrimination (Le Cao, Boitard, & Besse, 2011). The current analysis used the implementation in the mixOmics package v6.7.2 in R (Rohart, Gautier, Singh & Le Cao, 2017). The full analysis code is available online (https://osf.io/vkwma/).

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As a second step, we then employed a community detection approach to investigate the possibility of subtypes across the ADHD-ASD spectrum based on the clinically sensitive questionnaire scales from the RFC in step one. Community detection is an optimization clustering method to detect communities, or subgroups, of nodes (e.g., people), within networks. In the current analysis, the network is based on the RFC proximity matrix which represents the proximity of each participant to all other participants in the sample according to the RFC solution. The proximity indicates how often two participants were assigned to the same leaf node across decision trees in the random forest that aimed to predict the diagnostic label using splits on the questionnaire ratings. The advantage of applying the community detection to the proximity matrix is that the subgroups are necessarily relevant to the diagnostic categorisation (Feczko et al., 2018), whereas grouping based on e.g. the correlation of questionnaire scales may be influenced by other characteristics such as variance of the scale. Here, the Louvain algorithm was used for community detection (Blondel, Guillaume, Lambiotte, & Lefebvre, 2008) followed by a fine-tuning step using the Keringhan-Lin algorithm (Kernighan & Lin, 1970). Due to randomness in the initial assignment of nodes to communities, the algorithm may produce slightly different results at different instantiations. In order to reach a stable assignment, the algorithm was run 50 times to construct an agreement matrix, which was then used to obtain a consensus community partition (Lancichinetti & Fortunato, 2012). We repeated this procedure for multiple resolutions (varying y between 0.1 and 5.0; Reichardt & Bornholdt, 2006). We selected the solution that provided the best separation and internal consistency of groups (maximal modularity index) while providing the highest agreement across different resolutions (maximal normalized mutual information between successive values of γ). This solution was indicated at resolution

 γ =0.2. To estimate the reliability of the clustering at this resolution, we repeated the clustering with a randomly selected subset of 80% of the data and compared the results to clustering with the full dataset across 100 repetitions (Tibshirani & Walter, 2005). The results indicated very high stability of the clustering (mutual information: 0.93, 95%-CI: 0.90-98). Both the random forest classification and community detection analyses were repeated in the independent replication sample.

Taxometric Analysis

Because the community clustering solution suggested a dimensional distribution of groups and scores, we conducted an additional exploratory analysis, which was not part of the preregistration. In subsequent steps we carried out taxometric analysis to assess if a dimensional or categorical account provided a better fit to the questionnaire data including either the diagnostic information or the clustering information. Prior to taxometric analysis, we assessed the suitability of the data (Ruscio, Ruscio, & Carney, 2011). Tables with the corresponding *a priori* parameters can be found in the Supplementary Materials. A solution with the three most important indicator variables as determined by the random forest classification (SWAN HY, SRS RRB, SRS AWR) is presented in the main text below. The solution with three indicators is shown, because three indicators are the recommended minimum for taxometric analysis (Ruscio, Ruscio, & Carney, 2011). Solutions with two and four indicators variables can be found in the Supplementary Materials. As recommended in an authoritative review (Ruscio, Ruscio, & Carney, 2011), we used a combination of fit indices for taxometric analysis that are implemented in the RTaxometrics package v2.3 (Ruscio & Wang, 2017). For two indicators, the Mean Above Minus Below A Cut (MAMBAC) and Maximum Slope

(MAXSLOPE) procedure were employed. For three or more indicators, MAMBAC, the maximum eigenvalue (MAXEIG), and the Latent Mode (L-Mode) procedure were used. The consensus result across the procedures is presented in the main text, i.e. the mean comparison curve fit index (CCFI). The comparative curve fit index (CCFI) can be used to investigate if a latent construct is dimensional (CCFI < 0.4) or categorical (>0.6; Ruscio, Ruscio & Carney, 2011) through comparison to simulated data in parallel analysis. Results for each separate procedure can be found in the Supplementary Materials.

297 Statistical analysis

Group-wise comparisons were based on Welch-corrected t-tests that account for differences in variance between the groups. Bonferroni correction was used to account for multiple comparisons and corrected p-values are reported in the main text.

Results

Diagnostic groups show different profiles on questionnaires of social

304 communication and ADHD symptoms

The diagnostic groups showed different profiles of scores on the SRS and SWAN questionnaires (analysis of variance (ANOVA) – group: F(2, 3017)=801.8, p<0.001; group x scale: F(12, 3016)=10.7, p<0.001). While both diagnostic groups showed higher scores compared to the TD group across all questionnaire scales (see Table 2 & Figure 2), the ASD group scored higher on the SRS compared to the ADHD group. In contrast, there was no significant difference between the ADHD and ASD group for any of the SWAN subscales. Highly similar results were obtained in the replication sample (see Figure S1).

Table 2 Comparison of questionnaire profiles between the ADHD, ASD, and TD groups. Significant differences are shown in bold print.

	AD	HD	A	SD	T	D	AD	HD vs T	Γ D	AS	SD vs T	D	AD	HD vs A	SD
	mean	SE	mean	SE	mean	SE	t	df	d	t	df	d	t	df	d
AWR	0.17	0.056	0.83	0.084	-0.81	0.073	-10.66	266.04	-1.18	-14.76	173.93	-2.12	-6.55	149.33	-0.83
COG	0.10	0.058	0.97	0.093	-0.78	0.057	-10.80	329.26	-1.14	-16.04	132.32	-2.40	-7.92	140.95	-1.02
COM	0.13	0.056	1.00	0.087	-0.85	0.055	-12.45	328.52	-1.32	-18.00	136.23	-2.68	-8.40	145.44	-1.08
MOT	0.04	0.060	0.85	0.117	-0.60	0.063	-7.42	313.71	-0.79	-10.92	120.30	-1.66	-6.15	118.33	-0.84
RRB	0.11	0.059	1.02	0.091	-0.82	0.044	-12.51	354.97	-1.28	-18.17	112.51	-2.78	-8.40	146.28	-1.08
HY	0.44	0.040	0.35	0.087	-1.02	0.086	-15.40	181.81	-1.81	-11.21	188.34	-1.58	0.98	111.12	0.14
IN	0.39	0.044	0.49	0.081	-1.02	0.082	-15.17	198.00	-1.76	-13.11	190.97	-1.85	-1.05	124.55	-0.14

Abbreviations: d – Cohen's d, df – degrees of freedom, SE – standard error, AWR – Social Awareness, COG – Social Cognition, COM – Social Communication, MOT – Social Motivation, RRB – Restricted Interests and Repetitive Behaviours, HY – Hyperactivity/Impulsivity, IN – Inattention.

Random Forest Classification can predict diagnostic groups based on questionnaire data with some accuracy

Our results indicated that the optimal classification accuracy was achieved at a tree-depth of two, i.e. two questionnaire scales were sufficient to discriminate the groups. Cross-validation supported that a tree depth of two was optimal for classification. At this depth, the accuracy of the model for the training set was 87% (CI= 83.03-90.44, κ = 0.79, McNemar's p-value=4.6e⁻⁸) and 72% for the test set² (CI=62.76-80.17%, κ =0.56, McNemar's p-value=0.037; f1-score: 0.72, precision: 0.77, recall: 0.79). Sensitivity and specificity of the model indicated that diagnostic groups could be distinguished (see **Table 3**, ADHD: 0.67/0.84; ASD: 0.68/0.78; TD: 0.83/0.96 [sensitivity/specificity]). The most important scales for classification were SWAN HY (variable important as indicated by the percentage of trees that used the variable to split for classification: 100%) and SRS RRB (77.27%), followed by SRS AWR (63.37%), SRS COG (62.65%), SRS COM (57.20%), SRS IN (29.17), and

 $^{^2}$ Classification using sPLS-DA led to similar accuracy: 72% accuracy in the validation dataset, 73.87% when comorbid cases were excluded. The details of the full analysis are presented in the Supplementary Materials.

SRS MOT (0.00%). The accuracy of the classification model was similar when applied to the independent replication sample (overall accuracy: 76%, ADHD: 0.69/0.84, ASD: 0.68/0.94, TD: 0.94/0.85 [sensitivity/specificity]).

When excluding comorbid cases (ASD with a secondary diagnosis of ADHD or vice versa), the random forest classification reached an accuracy of 94.41% (n=340, CI: 91.41-96.61%) in the training set and 71.17% (n=111, CI: 61.81-79.37%; f1-score: 0.787, precision: 0.787, recall: 0.787) in the held-out test set. The specificity and sensitivity were acceptable for all classes (sensitivity/specificity, ADHD: 0.77/0.74; ASD: 0.63/0.82; TD: 0.65/0.98). Without the cases with a dual diagnosis the SRS RRB seemed less important. The most important scales for classification were SRS HY (100%) followed by SRS COM (76.59%), SRS AWR (72.65%), SRS COG (71.68%), SRS RRB (58.53%), SWAN IN (42.47%), and SRS MOT (0.00%).

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Table 3 Confusion matrix for the test data. Rows indicate the predicted (Pred.) diagnostic group, columns indicate the actual diagnostic group (Reference [Ref.]).

Pred.			
Ref.	ADHD	ASD	TD
ADHD	41	6	2
ASD	17	13	3
TD	3	0	26

Community detection identifies subgroups that cross diagnostic boundaries

The community solution consisted of five groups with four large groups (see Figure 2, C1: n=141 [31.26%], C2: n=86 [19.7%], C4: n=85 [18.85%], C5: n=136 [31.16%]) and one small group³ (C3: n=3 [0.67%]). The community detection algorithm converged at a stable solution that showed a good separation between the identified groups (Q=0.92). The four

 $^{^3}$ Please note that we do not include this group (C3) in between-group comparisons since there are only three people in that group.

large groups showed different profiles of questionnaire scores (ANOVA: group – F(2, 3108)=738.01, p<0.001; group x scale: F(18, 3109)=63.49, p<0.001, see Figure 2 & Table 4). One group (C2: low symptoms) scored around 1 standard deviation (SD) below the other groups across all questionnaire scales and mostly contained children without a diagnosis (TD: 79 [85.11 %], ADHD: 5 [10.64 %], ASD: 2 [4.26%], comparison of proportions to the whole sample: $\chi^2 = 288.10$, p < 0.001). A second group (C5: high symptoms) had scores around 1 SD above the mean and consisted of two thirds of children with ADHD and one third children with ASD (TD: 3 [2.92%], ADHD: 92 [67.15%], ASD: 41 [29.93%], $\chi^2 = 226.05$, $\rho < 0.001$). The other groups had contrasting symptom profiles. One group (C1: SWAN↑) showed low symptoms on the SRS scales, but high symptoms on the SWAN scales and consisted mostly of children with ADHD (TD: 15 [10.64%], ADHD: 120 [81.11%], ASD: 6 [5.26%]). Another group (C4: SRS ↑) showed elevated symptoms on the SRS scales with lower ratings on the SWAN scales and consisted to equal proportion of children from all diagnostic categories (TD: 29 [34.12%], ADHD: 27 [31.76%], ASD: 29 [34.12%]). The different groups were associated with differences in demographics and comorbid profiles: children in the cluster with higher SRS scores (C4) were slightly older compared to the rest of the sample, there were more females in the cluster with low symptoms (C2) and more males in the cluster with high symptoms (C5). The other clusters did not deviate in sex ratio or age from the rest of the sample (see Table 5). Furthermore, the cluster with low symptoms (C2) and the cluster with relatively high SWAN scores (C1) contained fewer cases with a dual diagnosis of ASD and ADHD than would be expected given the proportion observed across the whole sample (see Table 5). In contrast, the cluster with high symptoms (C5) and the cluster with high SRS scores (C4) contained more ADHD-ASD comorbid cases

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than expected (see Table 5).

[INSERT FIGURE 2 ABOUT HERE]

Figure 2 Profiles of diagnostic groups and groups identified through community clustering. **A)** The proximity between participants according to the random forest classification is shown in Force Atlas layout (Jacomy, Venturini, Heymann, & Bastian, 2014) either coloured according to the diagnostic group (top) or according to the groups identified through community detection (bottom). The smaller plots show the proximity matrix ordered according to either diagnostic or community detection labels. The figure illustrates the separation and overlap of the diagnostic groups as seen by the RFC algorithm. **B)** Profiles of the groups according to diagnosis (left) or community detection (right). The lower part of the figure shows the effect size of comparisons between the group. The circular plots in the right figure indicate the relative proportion of diagnoses within the groups identified through community detection. The error bars indicate one standard error around the mean. Abbreviations: AWR – Social Awareness, COG – Social Cognition, COM – Social Communication, MOT – Social Motivation, RRB – Restricted Interests and Repetitive Behaviours, HY – Hyperactivity/Impulsivity, IN – Inattention.

Table 4 Comparison of questionnaire profiles between the community clustering-defined groups. Significant differences are shown in bold print. Abbreviations: d – Cohen's d, df – degrees of freedom, SE – standard error, AWR – Social Awareness, COG – Social Cognition, COM – Social Communication, MOT – Social Motivation, RRB – Restricted Interests and Repetitive Behaviours, HY – Hyperactivity/Impulsivity, IN – Inattention.

	C1 (SWAN†)		C2 (low symp)		C4 (SRS†)		C5 (high symp)		
	mean	SE	mean	SE	mean	SE	mean	SE	
AWR	-1.11	0.068	-0.15	0.055	-1.11	0.068	0.80	0.069	
COG	-1.03	0.053	-0.33	0.055	-1.03	0.053	0.81	0.070	
COM	-1.07	0.052	-0.35	0.047	-1.07	0.052	0.90	0.067	
MOT	-0.81	0.067	-0.38	0.053	-0.8	0.067	0.68	0.083	
RRB	-1.08	0.018	-0.53	0.033	-1.08	0.018	1.09	0.055	
HY	-1.43	0.098	0.34	0.039	-1.43	0.098	0.84	0.040	
IN	-1.32	0.098	0.22	0.055	-1.32	0.098	0.68	0.055	
		C1 vs C2	2		C1 vs C	4	(C1 vs C5	
	t	df	d	t	df	d	t	df	d
AWR	-10.92	183.37	-1.50	-10.43	150.88	-1.61	-19.73	209.51	-2.66
COG	-9.19	216.36	-1.22	-11.94	126.56	-1.84	-20.97	219.31	-2.74
COM	-10.24	199.40	-1.38	-11.40	124.77	-1.76	-23.08	219.76	-3.02
MOT	-4.95	182.05	-0.68	-8.89	137.81	-1.37	-13.87	219.97	-1.83
RRB	-14.67	207.41	-1.84	-14.35	90.62	-2.21	-37.63	163.19	-4.67
HY	-16.74	111.86	-2.46	-9.18	118.14	-1.41	-21.41	113.89	-3.15
IN	-13.78	138.47	-1.97	-9.51	161.87	-1.46	-17.86	138.46	-2.56
		C2 vs C4	1	(C2 vs C	5	(C4 vs C5	
	t	df	d	t	df	d	t	df	d
AWR	-2.56	137.27	-0.37	-10.90	259.47	-1.32	-5.64	163.70	-0.79
COG	-5.72	134.73	-0.82	-12.74	258.47	-1.54	-3.90	161.51	-0.55
COM	-5.26	119.82	-0.77	-15.23	241.72	-1.84	-5.39	155.32	-0.76
MOT	-5.93	122.75	-0.86	-10.72	230.38	-1.30	-2.34	170.97	-0.33
RRB	-8.15	105.72	-1.21	-25.47	220.97	-3.09	-7.78	143.59	-1.11
HY	13.23	193.68	1.80	-9.07	274.15	-1.09	-21.47	196.52	-2.93
IN	3.66	162.57	0.51	-5.93	274.88	-0.71	-8.45	162.18	-1.19

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Table 5 Comparison of demographic information between the clusters. For the statistical analysis, groups were compared to the frequencies observed across the whole sample regarding sex and comorbidity, and to the rest of the sample regarding age.

	C1 (SWAN↑)	C2 (low sym)	C4 (SRS↑)	C5 (high sym)
N	141	86	85	136
Male [%]	110 [78.72%]	45~[52.33%]	60 [70.59%]	113 [83.09%]
Stat.	$\chi^2 = 2.05, p = 0.152$	$\chi^2 = 19.55, p < 0.001$	$\chi^2 = 0.34, p = 0.559$	$\chi^2 = 6.55, p = 0.011$
Age [mean \pm SE]	$9.34{\pm}0.144$	$9.47{\pm}0.161$	9.72 ± 0.186	9.22±0.133
Stat.	t(254.21) = -0.44	t(139.96) = 0.5	t(120.23) = 1.98	t(272.61) = -1.54
	p = 0.659	p = 0.617	p = 0.05	p = 0.124
n comor. [%]	8 [5.67%]	0 [0.00%]	24 [28.24%]	60 [44.12%]
Stat.	$\chi^2 = 19.66, p < 0.001$	$1 \chi^2 = 22.64, p < 0.001$	$\chi^2 = 2.82, p = 0.093$	$\chi^2 = 44.66$, p<0.001

Taxometric Analyses

Given these results, we next tested whether based on such discriminatory measures (SRS and SWAN) taxometric analyses would yield clear evidence in favour of either a dimensional or a categorical account of the differences between the diagnostic groups. The comparative curve fit index (CCFI) can be used to investigate if a latent construct is dimensional (CCFI < 0.4) or categorical (>0.6; Ruscio, Ruscio & Carney, 2011) through comparison to simulated data in parallel analysis. Across different measures of curve fit, we found support for a dimensional distribution when including the typical and both atypical groups (mean=0.36), and when including the ADHD and TD groups (mean=0.35). The ASD-TD comparison was consistent with a categorical account (mean=0.76). There was no strong support for either a categorical or a dimensional account for the comparison between ADHD and ASD (mean=0.49, all based on 3 indicators; see Supplementary Materials for similar results obtained with 2 or 4 indicators). To test if the results were influenced by edge cases, we conducted a further taxometric analysis that only included cases that were assigned to one of the major clusters in the consensus community clustering analysis. Taxometric analysis indicated that all groups identified through community clustering were more compatible with a dimensional than a categorical account (see Table 6).

Table 6 Comparative curve fit index (CCFI) using three indicators for comparisons of the community clustering defined groups. CCFI values <0.4 indicate a dimensional distribution, CCFI >0.6 are more compatible with a categorical account.

	l-mode	mambac	maxeig	mean
C1 vs $C2$	0.37	0.33	0.34	0.35
C1 vs $C4$	0.37	0.33	0.35	0.35
C1 vs C5	0.33	0.35	0.37	0.35
C2 vs $C4$	0.33	0.35	0.39	0.36
C2 vs $C5$	0.36	0.31	0.34	0.34
C4 vs C5	0.37	0.34	0.36	0.36

Discussion

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By adopting multiple analytical routes to subtyping, we investigate subgroups within a large cohort of typically and atypically developing children that either (a) represent a taxometric difference between ADHD and ASD or (b) indicate an underlying condition with ADHD and ASD as opposite ends of a dimension. Our results suggest that neither a categorical nor a dimensional characterization of the indicators used in this study (standard symptom scales) to define ADHD and ASD is more sensible than the other. In other words, the autistic and ADHD related behavioural traits as assessed in the current sample cannot, unambiguously, be characterized as either two separate clinical entities or as two opposite ends of a spectrum. In contrast, we show that the difference between ADHD children and typical children in the current sample is *dimensional*, while the difference between ASD children and typical children can best be characterized as categorical. Whereas our results do not support recent literature arguing for an underlying dimension that explains the frequent overlap of the two conditions, they do highlight the importance of studying ASD and ADHD in tandem, as has been suggested by many developmental researchers before (e.g., Rommelse et al., 2011; Van der Meer, 2012; Johnson, Gliga, Jones, & Charman, 2015; Geurts et al., 2004). The classification algorithm we applied was able to classify the diagnostic groups to some extent, but never reaches particularly high accuracy in distinguishing them. Moreover, we find that even with community detection techniques - focused on making detected groups most distinct - results

do not show separate groups of ADHD vs. ASD, but suggesting that the behavioural symptom scales are not sufficient to fully distinguish the diagnostic group. This is in line with current clinical practice in which clinicians are trained to not only base their diagnosis on these type of proxy reports of behavioural symptoms but take additional factors into account.

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Essentially, the current study underlines the potential of studying risk factors in relation to both, ADHD and ASD symptoms. First, our community detection and taxometric results suggests that ADHD and ASD cannot, unambiguously, be characterized as two separate clinical entities or as two opposite ends of a spectrum based on behavioural traits. However, although the definitions of ADHD and ASD are based on behavioural traits, they are associated with a wide range of atypicalities in other areas such as neurobiology and genetics. Taking these into account could lead to more clear-cut results concerning the distinction between ADHD and ASD. Nevertheless, as all identified clusters contain some combination of ADHD and ASD diagnoses, clinically, our results imply that screening for ADHD in ASD is imperative. Theoretically, our results underline taking a dimensional approach that could advance knowledge about genetical, brain, cognitive, and behavioral underpinnings of symptomatology. Dimensional analyses, however, are only useful when it can be demonstrated that the association of predictors with dimensional scores are constant throughout the relevant dimensional severity range (Kessler, 2002). In order to draw strong clinical policy-related conclusions such dimensionality first needs to be justified by demonstrating the absence of non-linear effects outside the clinical range that cause predictors to be significant for dimensional scores (Kessler, 2002). Moreover, we show that a completely dimensional view might be adequate for the relation between typical developing children and ADHD children but does not do just to the complexity of the relationship between ADHD and ASD. Given the dimensional characterization that our results suggest regarding ADHD, the clinician will still need external criteria, such as impairment or

suffering, to determine cut points on such dimensional measures that indicate the existence of impaired functioning.

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Second, this study is methodologically a first in the developmental literature. It is the first to adopt a multiverse approach with replication of cutting-edge subtyping and taxometric procedures to shed new light on one of the oldest psychometric issues in the field of atypical development research, the question of whether mental disorders should be thought of as discrete categories or as continua. In their review of psychometric modelling approaches, Borsboom and colleagues (2016) note that the psychometric work related to this issue has not been able to put forward a systematic methodological procedure to investigate the kind vs. continua question. The authors suggest that this might be due to the limited range of hypotheses tested by common approaches as these procedures do not test the exhaustive hypotheses space of latent structures, but treat the potential answer as binary: evidence in favor of categorical distinction is treated as evidence against the hypothesis of a dimensional structure leaving no room for other (hybrid) possibilities, such as some alternative factor mixture models or network models do. We here proposed a combined framework of analytic steps that cover a wider hypothesis space from different methodological angles avoiding the abovementioned issue. However, even with such systematic methodological procedure, we were unable to yield clear results regarding the question whether ADHD and ASD lie along an underlying continuum.

Third, previous autism research has suggested a taxon higher up the proposed gradient scale than DSM classification suggests, i.e. a 'highly severe' ASD subgroup (Frazier et al., 2014). We find that our taxometric results are ambiguous when performed comparing the ASD children with the ADHD children, instead of in all three groups. This ambiguity may be explained by the presence of a such a specific ASD subgroup. Also, the fact that the diagnostic procedure used in this sample was contingent on a clinician's suspicion of ASD (see

Alexander et al., 2017) might explain the 70/30 division of ADHD/ASD diagnoses in the high symptom subgroup we identified. Nevertheless, our taxometric analysis underlines the dimensional account of ADHD symptoms in typical children.

Limitations

Despite several strong points of this study, including pre-registration, cutting-edge statistical techniques, a large sample size, and replication in an independent sample, several limitations should be considered when interpreting our results. First, it should be stressed that our analyses are based on validated ASD and ADHD symptom scales reflecting a wide range of behaviors and symptoms. Naturally, however, this focus does not cover all potential tributaries to ASD and ADHD phenotypes, such as neuropathological and genetic factors (Rutter, 2013). Also, the SRS scale used in the current study mainly covers the ASD social domains, with only a few indicators of repetitive and restrictive behaviors and no assessment of the sensory sensitivities that often go along with ASD. The literature, however, suggests significant clinical difference between ADHD and ASD samples on this specific domain: reports of repetitive behaviours in ADHD are less frequent than reports of communicative and social difficulties (Nijmeijer et al., 2008). Another large epidemiological study reports that repetitive and restrictive behaviors explain a substantial part of the co-occurrence of ASD and ADHD traits (Polderman, Hoekstra, Posthuma & Larsson, 2014). Future studies should, therefore, include extensive assessments of the whole range of symptoms.

Additionally, it should be noted that a taxometric approach to unveiling the latent structure of psychological conditions is not uncontroversial in psychometrics (Lubke & Miller, 2015; Borsboom et al., 2016). We here explicitly accommodate all recent advances and recommendations by adopting taxometric procedures based on simulation (Ruscio et al. 2017) to deal with exceptions in its core assumptions (i.e. the assumption that categorical

structures produce peaked covariance functions might not be true under certain conditions; Molenaar, Dolan & Verhelst, 2010). Our results are, furthermore, based on (i) a large sample to make sure sampling fluctuation has less impact (Lubke & Neale, 2008) and (ii) symptom scales with varying endorsement probabilities of their items (Lubke & Miller, 2015). Although we combine different symptom scales with different response formats for our taxometric analyses, we chose to only include the combined, continuous subscales of the SRS to make sure the response range taps into the gradual differences of scale (Hay, Bennett, Levy, Sergeant & Swanson, 2007).

Third, current research on ADHD and ASD is highly skewed towards childhood, including this study. There are strong indications that the co-occurrence between ADHD and ASD is dependent on age (for review see Hartman 2016). For example, genetic research (Stergiakouli et al., 2017) indicates that although the biological etiology of the symptoms is dependent on similar biological pathways that the influences of these pathways ADHD co-varies throughout development. Therefore, longitudinal research is warranted.

Conclusion

In conclusion, this study supports those voices in the literature that are doubting the categorical differences between the consensus-based sets of ADHD symptoms and ASD symptoms, however we also cannot, unambiguously state that ADHD and ASD should be characterized as two opposite ends of a spectrum or as two separate clinical entities. In the long run, the statistical developments might result in a non-binary answer to the kind vs. continua question in psychiatry based on a novel way of conceptualizing non-linear transitions between different psychiatric conditions that follow from the complex interplay of their symptoms and the individual environment. For now, it is unambiguous that ADHD and ASD traits need to be studied in tandem.

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