A causal Bayesian network model for early diagnosis of autism

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***Abstract* — The aetiology of the condition autism spectrum disorder is suspected to derive from multiple dependent and independent factors, and as such lends itself well to analysis and diagnosis by Bayesian networks. In this project, a state-of-the-art network using Bayesian artificial intelligence and probabilistic reasoning is built for the purpose of aiding accurate early diagnosis of autism spectrum disorder, incorporating some of the growing new body of knowledge.**

Keywords — ASD; Autism spectrum disorder; diagnostic model; medical idioms; causal Bayesian network, AI tool; CNV; copy number variation; de novo mutation; diagnosis mitigation.

I. INTRODUCTION

Autism spectrum disorder (ASD) is a subcategory of pervasive developmental disorder (PDD), characterised by a range of symptoms and comorbidities (NHS, 2022a) (NAS, 2022a) (Hayes, et al., 2018). Severity varies widely, with capabilities able to evolve over time in diametrically opposite directions, but common to all is the altered impact on the lives of sufferers and their families. Confirmed diagnosis requires psychiatric/psychological assessment by trained professionals using recognised standard custom graded questionnaires. Despite considerable advances in elucidation of the neurobiology of ASD that span genetic factors and markers (Timothy, et al., 2013) (Toma, 2020) to radiomics (Sen, et al., 2018), its method of diagnosis has barely changed since it was devised some five decades ago.

Basic and applied research in the last two decades keeps accumulating increasing evidence that the aetiology of ASD conforms to the so-called "multiple-hit theory", i.e. clinical conditions that arise when genetically susceptible individuals are further exposed to certain environmental insults.

ASD incidence has progressively increased to almost epidemic proportions in the last few decades (Lord, et al., 2018). Early positive diagnosis can lead to early intervention leading to better outcomes for sufferers and parents, while negative diagnosis enables further assessment and identification of alternative or no condition. The World Health Organization (WHO) puts the current worldwide base rate at 100 per 10,000 population or 1 ASD person per every 100 people (WHO, March 2022), although reliable global base rates are elusive in the literature due to lack of accurate statistics from low and middle-income countries. Numerous artificial intelligence (AI) methods have been proposed in recent years for diagnosing ASD, however many lack clarity and reproducibility when given different realistic scenarios of risk factors. Bayesian networks offer many advantages over traditional AI that make their use in modelling and hence diagnosing ASD a preferably choice. They have been described as direct representations of the world that model the "... top-down (semantic) and bottom-up (perceptual) combination of evidence ..." (Pearl, 2011). The model built in this research project follows these principles to offer a more accurate and reliable diagnostic tool.

II. LITERATURE REVIEW

A. Autism in General

Although the earliest formalised study and publication on ASD by Grunya Efimovna Sukhareva was in 1925 (Wolff, 1996) (Posar & Visconti, 2017), it wasn't until the 1960s that data on population incidence/base rates began to appear in the literature. In the early 1970s reported base rates (per 10,000 children aged 8 to 14) were typically on the order of 4.1 in the UK (Lotter, 1966), 4.3 in Denmark (Brask, 1972), and 0.7 in the USA (Treffert, 1970). Current rates are 78.1 to 100 in UK (WPR, 2022) (NAS, 2022a) (Brugha, et al., 2012), 73.8 in Denmark (WPR, 2022), and 80.9 to 222 in USA (WPR, 2022) (Zablotsky, et al., 2015), and Christensen et al. (2016) cited for children aged up to 8 years. Though bitterly contested, it is agreed by a significant proportion of leading public health experts, epidemiologists, toxicologists, general medicine practitioners, and researchers that the steady increase in ASD base rates is *not all accounted for* by increased awareness, increased screening, and diagnostic expansion (Windham, et al., 2006) (Gilbert, et al., 2010) (Landrigan, et al., 2012) (Eriksson, et al., 2012) (Lyall, et al., 2017) (Rogers, 2019).

Autism occurred prior to its formal identification and diagnosis – accounts and chronicles of characteristics that can only be described as autism exist in the literature from after late renaissance, of individuals from Isaac Newton (physicist, 1642–1727) (Westfall, 1983), Wolfgang Mozart (composer, 1756–1791) (Suchet, 2016), to Paul Dirac (physicist, 1902-1984) (Farmelo, 2010), and others. Genome-sequencing based methods have already identified about 65 genes in ASD risk with strong genetic evidence (Sanders, et al., 2015) (Krishnan, et al., 2016). A higher number of genes are suspected (Willsey, et al., 2013) (Ronemus, et al., 2014).

The role of environmental factors, pollutants, and toxicants can no longer be denied in the light and volume of recent research. Among the top toxicants incriminated are aluminium adjuvants (Schofield, 2016) (Dorea, 2020) (Boretti, 2021), endocrine disruptors (Larsson, et al., 2009) (Ejaredar, et al., 2015), mercury (Palmer et al., 2006) (Ida-Eto, et al., 2013), and particularly a number of *in utero* exposures (Bal-Price, 2012) (Hay-Schmidt, et al., 2017) (McCrae, et al., 2018) (Buhrer, et al., 2021). Environmental factors would account for most of the exponential increase in ASD prevalence in recent years, as genetics alone cannot theoretically and empirically give rise to steep, near-epidermic base rates without ***epigenetic*** factors influencing gene expression population-wide, as well as in individual de novo mutations and in copy number variation (CNV).

Early theories on the causes of ASD, now discredited, include Bruno Bettelheim's '*homicidal mothers*' theory (Bettelheim, 1967) and Kanner's original theory of '*refrigerator mothers*' (Kanner, 1943 and 1951), both theories typical in the manner of psychiatrists. Current accepted theories of ASD neurophysiology are treated at length under section V "Discussion". The seminal work in current theories labelled "*the biomedical model*" is the 1964 book publication titled '*Infantile Autism: The Syndrome and Its Implications for a Neural Theory of Behavior*' by Bernard Rimland (Rimland, 1964). Among recent notable popular literature is Stephen Silberman's '*NeuroTribes: The Legacy of Autism and the Future of Neurodiversity*' (Silberman, 2015) which won a number of awards including the 2015 award for the Baillie Gifford Prize for Non-Fiction (formerly the Samuel Johnson Prize), and is listed among "best books of 2015" by The Economist magazine, Financial Times newspaper, The Guardian newspaper, and The New York Times Book Review. While its premise that ASD is not recent but historic divides opinion, its advocacy of accepting neurodiversity is not in contest.

B. Diagnosis of ASD

In strict terms, *screening* tests identify potential ASD, and those who receive positive screening scores go on further for *diagnostic* testing. Some of the literature however use both terms interchangeably. ASD screening and diagnosis in 2022 are broadly two-fold and have barely changed since their inception in the early 1970s; evaluation of early developmental behaviour collected via interview of parents or carers, and direct observation of subject plus questionnaire completion by a skilled professional usually a psychologist, a specially trained PDD assessor, or a psychiatrist. The only change is the occasional but rare updating of the tools or instruments, i.e. questionnaires and methods. Although screening and diagnosis instruments are country-dependent and age-range specific, there are large regional disparities within countries with regard to access, thresholds, and condition management resources. An example of one such diagnostic tool (ADI-R) is presented as Appendix A.

Currently in the UK, guidance on identification and recommendations for carrying out comprehensive assessments are provided by the National Institute for Health and Clinical Excellence (NICE) for children and adolescents up to age 19 (NICE, 2011), and for adults (Wilson, et al., 2014). Recommended diagnostic tools include

- Autism Diagnostic Interview–Revised, or **ADI-R** (Lord, C., et al., 1994).
- Autism Diagnostic Observation Schedule, or **ADOS** (Lord, et al., 2000). Revised version **ADOS-R** or **ADOS-2** was published in 2012 (Lord, et al., 2012).
- Diagnostic Interview for Social and Communication Disorders, or **DISCO** (Wing, et al., 2002).
- Developmental, Dimensional and Diagnostic Interview, or **3Di** (Skuse, et al., 2004).

In their review of clinical practice guidelines for diagnosis of ASD in the UK, Hayes et al. (2018) analysed twenty-one documents on guidelines and recommendations and found that "… *although individual guidelines appeared to present a coherent and systematic assessment process, they varied enough in their recommendations to make the choices available to healthcare professionals particularly complex and confusing* …", and that "… *social factors in operational, interactional and contextual areas added complexity to guidelines but there were few concrete recommendations as to how these factors should be operationalized for best diagnostic outcomes* …".

In the USA, in addition to ADI-R, ADOS, and 3Di, recommended diagnostic tools include

- Childhood Autism Rating Scale, or **CARS** (Van Bourgondien, et al., 1992).
- Diagnostic and Statistical Manual Fifth Edition, or **DSM-5** (Volkmar & Reichow, 2013).

Screening tools used in both UK and USA include

- Gilliam Autism Rating Scale – Second Edition, or **GARS-2** (Gilliam, 1995).
- Modified Checklist for Autism in Toddlers or **MCHAT** (Robins, 2008).
- Ages and Stages Questionnaires, or **ASQ** (Squires & Twombly, 2009).
- Screening Tool for Autism in Toddlers and Young Children, or **STAT** (Stone, et al., 2008).
- Parents' Evaluation of Developmental Status, or **PEDS** (Theeranate & Chuengchitraks, 2005).
- Communication and Symbolic Behaviour Scales, or **CSBS** (Wetherby & Prizant, 2002).

Harris et al. (2014) contend that evaluation tools exhibit inherent biases culturally and linguistically. As example, they refer to Zhang et al.'s publication (2006) that noted that within some Chinese culture pointing with the index finger and eye contact with adults are frowned upon as inappropriate behaviors. However the absence of these two actions are important diagnostic observation components in ADOS tests indicating ASD. Harris et al. (2014) also reference Norbury & Sparks (2013) in the latter's observation that "… *potential cultural differences surrounding pretend play, public displays of emotion, and the extent to which children (especially boys) play with toy dolls* …", and state therefore that "… *these culturally imbedded behaviors and experiences will significantly impact the results of ASD assessments* …". After evaluating six screening and four diagnostic tools, Harris et al. (2014) concluded that screening and diagnosis tests lack the context of family cultural expectations, hence significant numbers of children are potentially being misidentified or not identified at all, and thus unable to access support, interventions and treatment.

Prominent in the literature a few decades ago was the Baron-Cohen et al. (1985) claim that autistic children did not posses a *theory of mind*, i.e. the ability to ascribe mental states to other people and thereby surmise other people's point of view. Their model of metarepresentational development was claimed to measure and predict this cognitive deficit leading to social impairment. Their conclusion that this was specific to autism is now demonstrably inaccurate in the light of new knowledge showing this deficit to be present not only in a wide range of PDDs but also in transient psychological setbacks like anorexia nervosa (Bora & Kose, 2016), alcoholic toxicity (Uekermann & Daum, 2008), and cocaine addiction (Sanvicente-Vieira, et al., 2017). Moreover, this impairment is exhibited in only a small subtype of ASD (Craig, et al., 2021). This example is cited here to further demonstrate the often inaccurate beliefs about ASD not only in the general populace, but also the sometimes erroneous and subjective nature of accepted "facts" even in peer-reviewed literature. With ASD, as with much else in this world, what is considered *bona fide* fact today quickly becomes patently flawed as more knowledge is acquired.

C. Machine and Deep Learning Methods in Autism Research

Machine learning (ML) methods applied to research in autism can be seen in the literature from the early 2000s, initially predominantly supervised learning models, not only for diagnosis but also for other aspects as well. Serious deep learning (DL) approaches in autism research are observed in the literature from the early 2010s. Over the years, publications of unsupervised learning methods in ASD research have increased to be on a par with supervised ML.

In supervised ML, one logistic regression study investigating month of conception and risk of ASD found the months of December, January, and February showed a 6% increase in risk, implicating environmental factors (Zerbo, et al., 2011). Decision tree algorithms have been used, where one study claims to have obtained 92.11% accuracy in diagnosis by computing and then using as features the rotation range and rotation per minute of a subject's head in its pitch (head nodding direction), yaw (head shaking direction) and roll (lateral head inclination) directions in answer to ten yes/no questions (Zhao, et al, 2021). In 2016 Beggiato et al. used discriminant analysis to investigate which screening score items in one particular screening test resulted in the disparity in reported ASD prevalence in males and females (Beggiato et al., 2017). They concluded that potential gender bias in interpretation of answers to questionnaire, for example the range of facial expressions used to communicate, imaginative play, circumscribed interests, and unusual pre-occupations all have different ranges and thresholds in females, and that the lack of correction factors depending on the sex of the subject constituted gender bias that resulted in the underestimation of the prevalence of ASD in females.

Discernible from the literature is a trajectory of purist ML increasingly incorporating Bayesian methods into their models. This is seen in many deep learning artificial neural networks, mostly with computer vision techniques to extract and train on neuroimage features, which are then used to predict and therefore diagnose, as well as contribute to answering questions of neurobiology and aetiology. In an attempt to derive the benefits of larger sample sizes from multiple sites whilst overcoming the disadvantage of legitimate inter-group neural differences being masked by non-neural inter-site variability arising out of different scanners with different acquisition parameters, Ingalhalikar et al. (2021) harmonised multi-site neuroimaging data by using an empirical Bayes approach known as the ComBat technique. They used multi-site Autism Brain Imaging Data Exchange (ABIDE) data to successfully classify ASD individuals from typically developing (TD) control individuals, utilising connectivity data from resting state functional magnetic resonance imaging (rs-fMRI). They used network ablation analysis to augment further insights into ASD brain networks connectivity that correlated with important verbal communication impairments in autism. They state in their conclusion that "*ComBat has the potential to make AI-based clinical decision-support systems more feasible …*".

Tetsuya Iidaka's publication in 2015 indicates further potential for probabilistic AI utility in both aetiology and diagnosis. He used a probabilistic neural network to successfully distinguish ASD individuals from control subjects with 90% accuracy, 92% sensitivity, and 87% specificity (Iidaka, 2015). Correlation matrices were computed from rs-fMRI images of 312 ASD patients and 328 TD controls, all under 20 years of age. The publication author declared that his study provided a possible biomarker of ASD produced from the intrinsic connectivity matrix of rs-fMRI data, and gives further credence to the hypothesis of altered brain network connectivity contributing to the neurobiology of ASD.

Unsupervised learning approaches have also been used in attempts to distinguish ASD from other developmental and social deficits, and to identify subtypes of ASD presentation and pathophysiology. Using *k*-means and multiple linear regression with retrospective data on challenging behaviors and treatment progress for 854 children with ASD, Gardner-Hoag et al. (2021) identified seven clusters with significant differences in treatment outcomes. Their conclusions include prioritising those with the worst challenging behaviors and treatment response with targeted interventions instead of standard treatment. Deng et al. (July 2017) were the first to deploy deep Generative Adversarial Network (GAN) to classify children's speech affected by developmental disorders. Their dataset (alarmingly small at first sight but justified in experimental design) was derived from primary school children and consisted of 11 ASD, 10 PDD-NOS, 13 speech/specific language impairment (SLI), and 68 TD control group, partitioned 60:20:20 for training, validation, and testing respectively. Their twelve hours of audio recordings from this dataset was evaluated against the *Child Pathological & Emotional Speech Database* (CPESD, the standard French speech deficit screening system of acoustic feature spectral analysis) (Ringeval, et al, 2011) (Ringeval, et al, 2016). Their results and conclusion showed that the hitherto small data size limitation of speech-aided ASD diagnosis could *in principle* be overcome by utilising a deep GAN in generating additional data representations that enable classification accuracies comparable to state-of-the-art non-GAN non-speech-aided ASD AI diagnostic tools.

It is noteworthy that all such state-of-the-art ML and DL diagnosing tools are currently at best prototypes.

D: Bayesian Networks as diagnostic tool

A Bayesian network (BN) is a probabilistic graphical model built as a Directed Acyclic Graph that combines conditional probabilities of sets of variables to predict outcomes. BNs are superior to ML models due to their ability to combine data with expert knowledge and capture complex interdependencies of variables to yield more accurate answers (Fenton & Neil, 2019). While ML models often work better with dimensionality reduction, BN models have no such limitation.

Causal BNs, where edge-to-node indicates causality and imposes directional probability density functions, are of great potential utility to medical and healthcare diagnosis, prescribing, and prognosis, stemming from the fact that it is now routine, at least in the literature, for computer systems to outperform physicians and other medical professionals in practically all tasks. Additionally, normal medical deductions and clinical assessments are inherently and naturally Bayesian in approach, i.e. *priors* are updated given new evidence and information to obtain better *posteriors*.

Rooted in Sewall Wright's work on directed acyclic graphs (Wright, 1921), many publications of applied BN studies have exhibited statistically significant correlations and good ROC-AUC curves (receiver operating characteristic-area under curve) when used as tools for diagnosing disease or condition. In 2001 Kahn et al. (2001) used a BN model to differentiate among 5 benign and 5

malignant primary bone tumours using the patient's sex, age and 17 radiographic features. The dataset comprised 28 patients. Their model was evaluated with trainee physicians and found to correctly diagnosis 68% of tumours, with 89% correct of the two most probable tumours.

Seixas et al. (2014) proposed using a BN model to support diagnosis of dementia, Alzheimer's disease, and mild cognitive impairment. They combined data and expert knowledge and built their network structure from a supervised learning algorithm from a dataset of real clinical cases, with learned features being predisposal factors, neuropsychological test results, patient demographic data, symptoms and signs. Model evaluation was performed using sensitivity analysis and quantitative methods. Their model yielded better diagnosis results for each of the diseases than most other well-known ML classifiers (Seixas, et al., 2014).

A 2014 BN model named AutismNET was quantified entirely by probability distributions elicited from medical literature, domain expert knowledge and no data. (Szczygieł, et al., 2014). It was developed as a web-based interface to enable parents enter observations and determine the likelihood of their child being autistic. Although their model is simplistic – the first version consisted of 3 nodes, the second 10 nodes, and the third 17 nodes – it demonstrated proof of concept. The authors admitted several shortcomings they plan to address in future versions, among them a revision of numerical parameters to address high sensitivity to observed symptoms. They also planned a mobile device user interface.

Despite several publications since the early 2000s with a near explosion of published models since 2015, all endeavoring to contribute to elucidating ASD neurobiology and thereby augment its diagnosis and symptoms management, ML models are not widely utilised in clinical settings. Cavus et al. (2021) in their review of available models claim "*The gap in the existing literature is the absence of a definitive explanation on the sufficiency and readiness of the ML models toward real-life implementation."*.

A definitive explanation of precisely this in BN models but applicable to ML approaches too in this context is provided by Mclachlan et al. (2020) when they state "*… We believe that to be effective, any approach to real-time online Bayesian computation should seek to be computationally lightweight, capable of on-the-fly prediction, and accessible to patient and clinician alike using existing common consumer technology …*". Kyrimi et al. identified the *ad hoc* nature of most published medical BNs as offering little opportunity for methodological improvement (Kyrimi, et al., 2020), stating "*Most published BNs are presented as faits accomplis with little explanation of how the network structure was developed and without justifying whether the structure is correct for a given scientific application ...*" and "*… a clear description of the modelling approach is necessary if clinical and patient communities are to adopt the methodology or resulting BN into healthcare practice …*". They suggested an extension of the idiom-based approach introduced by Neil, Fenton, and Lagnado (Lagnado, et al., 2013) to medical BNs (Kyrimi, et al., 2020).

III. METHODOLOGY

A. BN Architecture

The model built and used in this research report was constructed using AgenaRisk software (Fenton & Neil, 2019). Model variables are represented as nodes, with influencing and causal relationships represented as directional edges in a *parent-to-child* graph. The initial task was the building of the BN *architecture*, the second task being model *parameterisation.* A model thus built learns computationally from data, or from a combination of data and computational extraction of expert knowledge skilfully represented to the node probability tables (NPTs). AgenaRisk's notable utility is in combining data, expert knowledge, and information deduced from the literature. Also notable is its ability to enable capture and encapsulation of *fuzzy* concepts and knowledge in reproducible mathematical formalism. It is head and shoulders above current standard BNs in enabling model builder to incorporate far greater numbers - and also greater complexity - of mathematical and programming expressions. Furthermore, it enables finer modelling of variables with desirable individual prior weighting. Most of all, in addition to categorical and discrete numeric variables, it enables continuous numeric variable modelling with high accuracy through dynamic discretisation (Gama, et al., October 1998).

a) Network Variables (Nodes)

The variables to include in this network were chosen by adhering to the reasoning behind medical idioms (Kyrimi, et al., 2020). From medical literature, a deduction and elicitation was made of all the regressors intrinsic to ASD diagnosis, and represented as nodes. Naming protocol was as would be used in a clinical setting. All clinical setting idioms were considered and included, not only in diagnosis but in treatment as well (please see Appendix B Figure 2 and Appendix C Figure 5).

b) Node Types

Discrete node types were determined by reason of variable properties, and also in anticipation of the probability distribution that best describes that variable in the NPT. Examples of node types are 'Boolean', 'Ranked', 'Labelled', 'Integer interval', 'Continuous interval', and 'Discrete real'.

c) Node States

Depending on the node type, a number of applicable node states are considered and the most appropriate is selected, or manually created if 'Labelled', or both. Appendix B Figures 3 and 4 show the states for the nodes 'Reliability of reported phobias' and 'MRI Scan Type' respectively.

d) Idioms

The idiom-based approach to BN creation introduced by Lagnado et al. (2013) and extended to medical BNs by Neil et al. (Kyrimi, et al., 2020) comprises assembling *modules* of small networks built according to knowledge of a particular domain and linking these modules according to the serial, parallel, logical, or other procedural convention commensurate to the causal flow of the phenomena being modelled. For medical problems and applications, idioms are implemented using medical classification systems, procedures, guidelines, terminology, as well as the order of reasoning and decision-making processes employed by experts of that domain (Neil, et al., 2000) (Fenton & Neil, 2019) (Kyrimi, et al., 2020). Such an approach may also facilitate real-world professional adoption of these AI models (Mclachlan, et al., 2020) (Kyrimi et al., 2020). Consequently this network was built by creating and assembling modules of nodes based on ASD 'risk factors', 'signs and symptoms',

'medical tests', 'comorbidities', 'treatments', and other such considerations as displayed in Appendix C Figure 5.

e) Causal Directions/Influences (Edges)

AgenaRisk software enables straightforward linking of nodes with directional arrows as edges once the causal or influential flow direction has been predetermined by knowledge. This step was undertaken as the final step in building the network structure, paving the way then for subsequent network parameterisation.

f) Node Probability Table (NPT)

In analogy to the biological Class: *Cephalopoda*; Genus: *Octopus*, the NPTs can be considered as the peripheral "mini brains" of the network that work in synchronicity with the central "brain". The complexity of an NPT is dependent on the number as well as the types and states of parent nodes ("a" to "e" above). Using a combination of manual input, formulating expressions, and then designating partitioned expressions, modelling was performed in conformity to the most likely statistical mass or density distribution of each variable. The functions defined therein enabled the model as a whole to learn algorithmically (i.e. central brain) from data and/or elicited expert knowledge input to each specific node. The data, expert knowledge, and information from literature used to inform the NPTs are summarised in Appendix (*tbc*).

g) Forward and Backward Reasoning

When a BN's structure reflects or models actual causal relationships between regressors, then input of evidence in any node results in an automatic update of probabilities for other nodes connected to it when the model is run. This is due to the computational capacity of the network for *forward* as well as *backward reasoning*. While forward reasoning follows the direction of the edges and replicates causality, backward reasoning runs counter to the direction of the edges and replicates diagnosis.

B. BN Parameters

Subsequent to building the network structure was the modelling of ASD diagnosis by constructing node parameters that reflect current knowledge and interplay requisite for diagnosis. The following section describes the rationale behind how NPTs were created in this project:

Ten broad risk factors were identified (Appendix C Figure 6). Despite an ASD 4:1 male:female ratio cited in most publications, a 3:1 ratio was instead implemented in this network, and explained under section V "Discussion". Although 'Genomic Susceptibility' and 'Family Medical History' first appear to be modelling the same thing, the former comprises ailments that are implicated to a greater extent, and can thus be weighted extra in the overall disease model.

Similarly, the two manifestation idioms of 'signs and symptoms' and 'diagnostic tests' could, at first sight, be seen as a duplication of information. The justification for including both in this model is two-fold: firstly, the purpose of this model is to assist professional medical diagnosis as well as aid non-professional but informed lay users to accurately analyse risk and make sound decisions regarding whether to seek official diagnosis, and/or avail themselves to treatments likely to be beneficial, such as modified/adapted ketogenic diet and microbiome therapy. In view of the well-known difficulty and long waiting times traditionally experienced in obtaining diagnosis, this model is therefore designed to provide as reliable a diagnosis as possible without using current official tools - in such instances observations into the 'diagnostic tool' nodes can be omitted, and as much information as possible entered for other nodes. Where diagnostic tool information is available and entered into this model, corresponding signs and symptoms observations can be omitted to prevent duplication. With further development this model could ultimately be adopted as a more accurate and reliable diagnostic tool in its own right. Secondly, as previously mentioned, current diagnostic tools are not tampered or dampened by ingrained cultural and religious behaviours, important traits modelled by this AI tool. It was decided not to model the specificity and sensitivity of the official diagnostic instruments, as various systematic reviews present widely different and inconsistent values for these tools, with some exception for ADOS-2 and ADI-R (Falkmer, et al., 2013) (Wigham, et al., 2019) (Lebersfeld, et al., 2021).

Bayesian networks and inference utilise Bayes theorem:

$$P(H \mid E) = \frac{P(E \mid H) \times P(H)}{P(E)}$$

where

P(H|E) = posterior (i.e. revised) probability of hypothesis *H* given evidence *E*; in this instance the probability of being autistic given observed specific risk factors, comorbidities, and symptoms.

P(E|H) = probability of evidence *E* given hypothesis *H*; in this instance the probability of observing specific risk factors, comorbidities, and symptoms given being autistic.

P(H) = prior probability of hypothesis *H*; in this instance the probability of being autistic.

P(E) = prior probability of evidence *E*; in this instance the probability of observing specific risk factors, comorbidities, and symptoms.

Each incorporation of new evidence results in update of posterior conditional probability.

The disease condition 'Autistic?' was created as a Boolean node to return 'Yes' or 'No' in relative percentage terms based on the comparative expression defined in its NPT. As the pivot of the entire network, it models the uncertain relationships between observable risk factors and the disease condition with forward reasoning, and the uncertain relationships between disease condition and the remaining idioms and variables with backward reasoning. Both forward and backward reasoning combine overall to universally update the probability of each node in the network. The following examples of this model demonstrate the use of familiar mathematical and programming language syntax to construct balanced expressions that return calibrated 'Yes' or 'No' to disease condition according to the following logic:

a) "and" (&&) implies all stated conditions are true, and "or" (||) implies any one of stated conditions is true.

b)

if(genomic_susceptibility>=0.6&&vaccination_history>=0.5&&environmental_factors>=0.5&&pregnancy_factors>=0.5&&sex>=0.5&&family_medical_history>=0.5&&brain

_morphology>=0.25&&individual_genome>=0.25&&mitochondrial_dysfunction>=0.25&&brain_physiology>=0.25, "Yes","No")
Here each risk factor node would have to return a probability of at least its assigned value, taking back-propagation into account, for the diagnosis to be positive.

c)
wmean(1,genomic_susceptibility,1,vaccination_history,1,environmental_factors,1,pregnancy_factors,1,family_medical_history,1,sex,2,individual_genome,2,mitochondrial_dysfunction,2,brain_morphology,2,brain_physiology)
Here a weighted mean of risk factor variables is used to return a positive diagnosis, where each of the four direct empirical medical laboratory testable attributes counts twice as much as each of the other six risk factor attributes.

d)
mfromn(4,10,genomic_susceptibility>=0.8,vaccination_history>=0.7,environmental_factors>=0.8,pregnancy_factors>=0.7,family_medical_history>=0.8,sex>=0.75,individual_genome>=0.25,mitochondrial_dysfunction>=0.25,brain_morphology>=0.25,brain_physiology>=0.25)
Here if any four conditions out of the ten specified evaluate to true, the whole expression evaluates as true and returns a positive diagnosis.

The values in all the expressions are carefully calibrated, and it is possible to appropriately nest expressions where the NPT suitably demands it. For brevity only the few above are described, further options can be utilised including "noisy OR" and "noisy AND".

In an ideal situation, nodes such as 'ADI-R score', 'ADOS-2 score' (i.e. clinical psychology diagnosis idiom nodes) would be modelled as "integer interval" or "discrete real" nodes, and the various "measure" and "outcome" factors as "continuous interval" nodes. Doing so activates the choice of more advanced functionalities in their NPTs. However, given time constraints and in the interest of simplicity in this version 1.0, these nodes were implemented as either "ranked", "Boolean", or "labelled" nodes. This does not necessarily reduce the quality of the model, and the advanced functionalities will be implemented in future development of the model.

In BNs that model personalised risk for diseases like Covid-19 or pre-diabetes and their interrelated factors like disease severity, deaths, treatment effects, etc., the cumulative probability of the disease state or node can be influenced by linked "treatment" nodes. The BN in this project has been constructed in a manner such that linked "treatments" have no effect on the disease state or node, in replication of the real world where ASD treatment may assuage comorbidities but has no bearing on whether one is autistic or not.

IV. RESULTS

When the model is ran without any prior observation, it returns a probability of being autistic as 1%, the implication being that a person chosen at random without any further information, has a 1% probability of being autistic. This BN therefore accurately models the worldwide population prevalence rate (Zeidan, et al., 2022) (WPR, 2022) at baseline level when no observation is input. It successfully re-calculates this probability when any single or multiple observations are input to the model.

Scenarios

Scenarios are specific instances of the network with a particular set of observations. They represent specific diagnosing attempts where observations or known data are input to the model, thereby activating revised prior and conditional probabilities in the node probability tables to yield revised posterior probability of the subject being autistic. Appendix D Figure 7 shows the model displaying all risk graphs when no observations are input, which is the base rate scenario. The following are a few randomly selected scenarios illustrating this causal BN's diagnostic capabilities:

a) Genomic susceptibility/high-risk family medical history:

Sarah is an adolescent worried that she might be autistic. The only information she has is her cousin Luke suffers from Rett's syndrome. Sarah accesses this application online and enters this observation into the model. She obtains the probability of being autistic as 1.75% (Appendix D Figure 8a). Looking over her shoulder is her brother Bob, who has a go and enters the same information but as a male instead of female. He obtains a probability of 2.487% (Appendix D Figure 8b). The same set of results would be obtained for anyone with only the knowledge of any of the following high-risk family history factors: autism, fragile X syndrome, Down's syndrome, tuberous sclerosis complex, mitochondrial dysfunction, phenylketonuria, Cornelia de Lange syndrome, and Angelman syndrome. Hence given the knowledge of this susceptibility being true, the probability of being autistic is observed to double in females and triples in males.

b) Environmental factors exposure with low-risk family medical history:

Amar is a GP who receives a query from the worried parents of an infant regarding the utility of seeking official ASD diagnosis for their male child. The only information they provide is that their major roadside residence and hence high-dose exposure to vehicle exhaust toxicants such as lead and nitrogen dioxide is coupled to a nephew with a diagnosis of neurofibromatosis type I. Amar accesses this BN tool and inputs the information, and obtains an ASD probability of 3.453%. The same results would be obtained for any male with similar environmental exposure and any of the following low-risk family history factors: schizophrenia, Huntington's disease, motor neurone disease, rheumatoid arthritis, multiple sclerosis, lupus MELAS syndrome, and chronic fatigue syndrome. Amar can consequently advise his patients that their infant has an ASD probability nearly quadruple the population baseline.

c) Five risk factors:

Akosua is a Consultant Paediatrician. One of her cases is the Williamson family with 4 children, 2 male and 2 female, all with developmental delay. Akosua's medical notes from observation of and familiarity with the Williamson family show that in addition to high-risk genomic susceptibility and low-risk family history, the following are common to all the children:

1. at least one of the following pregnancy risk factors: advanced parental age, parental metabolic syndrome, maternal obesity or diabetes, maternal viral or bacterial infection during pregnancy, extreme premature birth/low birth weight, prolonged/persistent *in-utero* exposure to substances such as paracetamol (i.e. acetaminophen), and

aniline (from household products, vanishes, cigarette smoke).
2. vaccination history risk factors: each child has received many aluminium adjuvant vaccines requisite for neonates, infants, and toddlers in many developed countries.
3. environment risk factors: exposure to organophosphates from pesticides, insecticides, herbicides, etc.

Inputting this data to the model with 'Sex' unspecified returns a general ASD probability of 6.115% for each of the children.

d) Signs and symptoms with clinical diagnosis:

Jasper is a young adult who has lived with various foster parents and about to begin university education. He has no formal diagnosis but always suspected he might be autistic, and speculates if seeking official diagnosis is worthwhile. He is sensitive to bright lights, extremely fearful of crowded places (agoraphobic), exhibits repetitive and ritualised behaviour, has a narrow range of interests, and struggles to make eye contact. All these are modelled in the "Signs and Symptoms Manifestation Idiom" (Appendix C Figure 5). Jasper goes online, accesses this tool and inputs this data. He runs the model and is not surprised to find out that he has a nearly 8-fold risk increase in ASD (i.e. 7.627%). He seeks official diagnosis. Two years later, having finally obtained a high ADI-R score from his regional health service, he accesses this BN model again and inputs this information, together with now developed anxiety comorbidity. With these information, the model returns an ASD risk probability of 41.976%.

e) Medically testable risk factors:

There are four medically testable risk factors in this model, excluding sex as being obvious (expanded under "Discussion"). These are "Individual Genome", "Mitochondrial Dysfunction", "Brain Morphology", and "Brain Physiology" (Appendix C Figures 5 and 6). Recent literature has highlighted a number of potential diagnostic markers for ASD, from genetics/genomics (Warrier, et al., 2022) to radiomics. There are already medical tests for the presence or absence of specific genetic variants, and of aberrations, for example particular CNVs (Sebat, et al., 2007) that can potentially be re-purposed to detect ASD with high causative correlational likelihood. Similarly a number of medical imaging method, especially MRI methods such as morphometries that are voxel-based, surface-based, and tensor-based can identify brain morphology features that correlate highly with ASD (Chen, et al., 2011) (Iidaka, 2015) (Rochat, et al., 2020). These medically testable risk factors have thus been assessed by this author as providing more objectivity contextually in ASD diagnosis than current methods, and modelled as such.

The scenario: Being highly educated and untrusting of psychiatrists, Kofi and Abena decide to take the medical laboratory route rather than rely on psychiatrists to determine if their two children Ajoa and Kwame are autistic. Having obtained positive results in detection of de novo CNV in some ASD genes, Kofi and Abena input this information into this BN model. The probability of ASD is obtained to be 18.483% for Ajoa (female) and 19.094% for Kwame (male). Kofi and Abena then have their children tested for mitochondrial dysfunction and obtain positive results for both. When this information is added, the model returns 33.035% and 33.538% respectively for Ajoa and Kwame. With brain morphology and brain physiology confirmed and input to the model, these respectively rise to 54.81% and 55.149%. In the eventuality of Ajoa and Kwame presenting with additional comorbidities of depression, anxiety, and insomnia, their ASD risk rises to 99.345% and 99.354% respectively according to this causal BN model (Appendix D Figures 9a and 9b).

f) Eye contact:

Fang and Lixin exhibit severe avoidance of eye contact. As children of Chinese immigrants in UK, they are academically very bright but their London school teachers are concerned about this apparent anti-social trait. The headteacher convinces Fang and Lixin's parents to seek formal ASD diagnosis. They each obtain high scores in 4 well-known official standard diagnostic tests. The parents are however not convinced. They access this BN tool online and input 'lack of eye contact' together with the scores obtained in the 4 diagnostic tests. The model returns an ASD probability of 9.266% for Fang (female) and 16.849% for Lixin (male). Cognisant that their cultural heritage, in which it is disrespectful to stare as well as directly look grown-ups in the eye, could likely engender this misunderstanding, they consider it a Godsend when they realise that finally there is a tool that takes this into consideration. They proceed to input this information into the respective nodes of the "Culture and Religion Idiom: Diagnosis Mitigation". Their relief is palpable when they observe Fang's ASD probability risk fall to 4.317% and Lixin's to 8.216% ; practically halving the ascribed likelihoods from the formal tests (Appendix D Figures 10a and 10b).

V. DISCUSSION

It is almost impossible to objectively discuss autism without a fervent reaction from one or more of the several factions that passionately contest the subject. Gill et al. (2021) state that "... At present, ASD is the most common serious developmental disorder in the USA and the world ...". The impact of ASD in suffering is immense, and although ASD sufferers value their autistic identity and would not have it any other way, most abhor the debilitating and comorbid aspects of the condition, with only a minority claiming to like these. This version 1.0 of the model has been constructed as objectively as humanly possible with the current peer-reviewed evidence and state-of-the-art BN and AI tools.

Most risk factors for autism are not unique to ASD but can be present in other PDDs as well, so an autism diagnosis must be performed cautiously. Of the many proposed AI tools for ASD diagnosis in the literature, one of the novelty features of this particular BN model is that to the best of this author's knowledge, it is the only one that incorporates and corrects for confounding behavioural factors that are learned or acquired but not innate or intrinsic. This is achieved through modelling of a "Culture and Religion Idiom: Diagnosis Mitigation" (Figures 5, 10a, and 10b). It is arguably more desirable to model this mitigation factor directly unto the 'Autistic?' node rather than through the professional diagnostic tools.

Further to the above and introduced earlier under "Methodology" section, a different confounder inherent in the current psychiatric diagnostic tools probably leads to over-estimation of the average ratio of male:female prevalence in ASD. In most publications and on the websites of most autism support organisations the prevalence ratio for the sexes is stated as 4:1 male:female, sometimes higher. It is

now recognised, at least in the literature, that the sections of diagnostic instruments in current use that utilise role play with dolls could potentially be introducing a bias. An "awkwardness" observation and score in some males may not be symptomatic of ASD at all, but due to either intrinsic or learned attitude to playing with dolls. Moreover, it is widely recognised that females may be better at "behavioural masking", i.e. deploying coping mechanisms that hide signs and symptoms, and thus evade diagnostic instruments. The BN built in this project therefore conservatively models the ratio as 3:1 male:female in anticipation of future more reliable statistics that would correct current bias. A truer explanation for the pathophysiology of the observed sex inequality is that a minority of ASD genes may be located on the X chromosome and recessive, thus expression of these genes are physiologically masked in females, as a female must be homozygous to exhibit phenotypic expression. Males on the other hand express these genes unmasked - they do not possess an extra X chromosome to mask.

This model currently incorporates what may be classified as objective testables, i.e. endophenotypes. Later versions would include more of them. Endophenotypes are quantitative medical laboratory determinable biomarkers that correlate with illnesses traditionally determined and diagnosed by psychiatric non-objectivity and verbosity (e.g. Appendix A). Current knowledge in endophenotypes rarely identifies single diseases, but rather narrows down to spectrum disorders stemming from common aetiopathogenesis (Gottesman & Gould, 2003) (Manji, et al., 2003) (Glahn et al., 2014). Many proven genomic and radiomic methods continue to be used in ASD elucidation, endophenotypic refinement, and nosology. In June 2022 ground-breaking research that accurately distinguished autism from attention deficit hyperactivity disorder (ADHD), and both autism and ADHD from controls, with potential to diagnose either condition using biomarkers from a simple eye test, was published (Constable, et al., 2022). They used an electroretinogram (ERG), a standard test used by opticians to identify retinal disorders, to record electrical activity in the retina by showing the subject patterned flashes of light while an electrode, in the form of a contact lens or thin fibre, is in contact with the cornea.

All these developments justify another characteristic of this model in emphasising the role of the medically testable risk factors, reckoning them as more objective, and thus weighting them proportionally higher than the myriad of largely subjective signs and symptoms currently relied upon heavily by other diagnostic approaches. It is a source of amazement and wonder why the stupendously subjective nature of ASD screening and diagnosis, totally dependent on where one lives and the health services in that administrative catchment area, continues to be adhered to in modern times. It has been expressed in some quarters that it may be time to challenge the predominance of the current system of quaint, laborious, sclerotic, extremely subjective, and some might say self-serving ASD diagnosing regimes, bodies, and authorities, and gradually replace them with demonstrably accurate, objective, relatively quick (but not shoddy), cost-effective screening and diagnostic tools that actually serve autistics, their families, and their carers. BN and AI tools are poised to play substantial roles in this anticipated future of ASD diagnosis. In defence of ASD diagnosing bodies and authorities, most of the advances in ASD research are relatively recent, and although published in peer-reviewed journals, require time to be established beyond doubt through experimental replication (i.e. reproducibility) and systematic reviews. Also, it is not easy attempting to identify and categorise what are essentially heterogeneous fine gradual continua of phenotypic expressions (i.e. penetrance). The notion that all the diverse behavioural and personality traits examined on a typical diagnostic questionnaire (Appendix A) can be adequately observed or not observed in a typical standard 45-minute to 2-hour observation assessment has been branded as not only fanciful but also ludicrous. Again, diagnosing bodies and authorities compensate by consistently recommending that multiple instruments/tools are used rather than any single diagnostic test.

This model incorporates environmental factors including childhood vaccines as risk factors. Although fiercely contested, this is supported by many peer-reviewed publications (Palmer, et al., 2009) (Jager, 2013) (Dorea, 2015) (Schofield, 2017) (Watad, et al., 2017) (Plotkin, et al., 2020), (Angrand, et al., 2022) to mention a few. Pesticide and herbicide organophosphate load can also accumulate to toxic levels from concentration up the food chain.

This author is by no means anti-vaccine, as scientific evidence is overwhelming and conclusive that the principle of inoculation and therefore the practice of vaccination constitutes an effective and indispensable part of any modern health system and service. It is however known that although very rare and negligible in percentage terms but significant in terms of sheer numbers (a minuscule percentage of a very large number is still large), a range of complications, not all of which are adequately studied, may or may not arise *if at the time of vaccination* a person is already immunocompromised, or is physiologically maladjusted in other ways. This is especially the case with attenuated live vaccines. Despite claims to the contrary, the extent to which certain metal-based adjuvants and excipients further complicate this remains unresolved to fair-minded observers.

It is the certainty with which the WHO, some medical professionals, and a number of autism support organisations summarily dismiss some environmental factors as if settled beyond doubt, that is puzzling. Statements like "*... there is also no evidence to suggest that any other childhood vaccine may increase the risk of autism. Evidence reviews of the potential association between the preservative thiomersal and aluminium adjuvants contained in inactivated vaccines and the risk of autism strongly concluded that vaccines do not increase the risk of autism ...*" from the WHO website (WHO, March 2022) are commonly found across all literature, with a list of common frequently cited publications in support. In view of the fact that none of the supporting research publications employed the scientific standard of double-blind placebo-controlled clinical trials, would it not be scientifically prudent if such statements were *qualified* rather than *emphatic*? Similar *fait* statements about ethylmercury in thiomersal-preservative vaccines were common throughout the medical literature and community until eventually the science caught up, to the effect that the UK, USA, European Union, and a few other advanced countries found it necessary, or at least precautionary, to remove thiomersal from childhood vaccines. Developing countries are still lumbered with this ethylmercury-based vaccine excipient on the basis of costs – it appears if you do not reside in a wealthy country, then it's OK to have your children poisoned in acts of charity.

This author concedes that it would be unethical to withhold crucial vaccines from subsets of children for the purpose of using them as experimental controls. There are

however geographical regions of the world where people actively choose, legally and of their own volition, to have their children not vaccinated to the hilt, i.e. they choose to receive a few important vaccines rather than the large number required in some developed countries, for instance UK (14 *different* vaccines by the age of 4 years), and USA (15 *different* vaccines by the age of 6 years) - a fair number of these different vaccines administered in *multiple* doses. It is feasible to truly investigate the effects of aluminium adjuvants and other vaccine products, admittedly without randomisation, but with high quality blinded research employing controls, corrected for geographical factors like diet, sunshine (vitamin D3), hygienic environment, and other confounding factors.

Memorable physical chemistry (thermodynamics and electrochemistry) enables appreciation of the following theoretical but very plausible logical scenario :
Vaccine dilution and administration invariably results in changes in activity α and chemical potential μ (i.e. *effective* concentration; $\alpha_i = \gamma_i m_i$ where γ is activity coefficient, m is molality, and $\mu_i = \mu_i^{\ominus} + RT \ln \alpha_i$ where $\ominus$ = standard/single component, R = gas constant, T = temperature, ln = natural logarithm, and i = aluminium adjuvant particle). Vaccine dilution and administration also results in changes in zeta potential ζ (i.e. solvated particle slipping plane electric potential; $\zeta_i \propto -\log\alpha_{H+} \,/\, I$, where $-\log\alpha_{H+}$ is pH of medium and I is ionic strength of medium). The resultant reverse-aggregates of aluminium adjuvant particles would likely not always be monomers but rather irreproducible combinations of dimers, trimers, tetramers etc with different particle sizes, shapes, charge densities, solvation power, and hence zeta potentials. Thus distribution effects of unknown nature may likely arise. Particle adsorption of serum peptides etc may in turn profoundly influence cellular mechanisms that impact their diffusion (passive and active) into all cells, phagocytotic uptake into immune cells, and therefore the immunogenicity and *induction of pro-inflammatory cytokines that borderline or exceed desired control*. Contrary to expectation, the literature shows scant characterisation and minimal data on aluminium adjuvant physico-chemical properties. Helpfully, interleukin 6 (IL-6) measurement is modelled in this BN as one of the node states in the "Brain Physiology" endophenotype risk factor node (Wei, et al., 2012).

It may well be that physico-chemical characterisation studies have been performed in detail, but proprietary and intellectual property concerns of the various competing pharmaceutical corporations result in such data being guarded assiduously. Incidentally, Badran et al. (2022) have observed and documented some aggregation characteristics of aluminium oxyhydroxide and aluminium hydroxyphosphate in vaccine solutions using scanning as well as transmission electron microscopy and other methods.

ASD risk by ethnicity and race is not modelled in this network because, in addition to the absence of universal data, the literature is fragmented with contradictory findings across regions and time. As example, a 2017 publication of ASD prevalence among US children using data from 2002 to 2010 found higher prevalence in ethnic whites than blacks and that the disparities were not all explained by socio-economic status (Durkin, et al., 2017), while a 2021 publication of data from 2017 of over 7 million pupils in England found higher prevalence in blacks than whites (Roman-Urrestarazu, et al., 2021). Roman-Urrestarazu et al. report "…important variability across geographic areas …". Ethnicity/race nodes would be included in this BN when the picture becomes clearer.

VI. CONCLUSION

From the results obtained, this causal BN has been shown to model real world scenarios with excellent diagnostic performance. It makes an important contribution to the field, which is the modelling of acquired cultural behavioural mitigation during diagnosis.

VII. FUTURE WORK

Further development of this model to make it ideal for the purpose which it is built would comprise:

1. Some factors that are currently modelled as node states, such as MRI scan types, can be built as full nodes in their own right.
2. NPTs in all nodes can be tweaked further, using further information from expert knowledge, to make the overall diagnosis more accurate and reliable.
3. The eventual BN may likely expand and necessitate decomposition into a Multiobject Bayesian Network Model (MBNM), i.e. an object-oriented BN (OOBN).
4. A comprehensive investigation of the model's accuracy measures of specificity and sensitivity for publication in a peer-reviewed journal.
5. Compatibility programming and API development of the eventual model to port unto PamBayesian CardiPro, an online medical diagnosing application developed by the Neil-Fenton Group for easy general adoption.

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APPENDICES

A. Appendix A

Figure 1: Sample ADI-R diagnostic tool.

Autism Diagnostic Interview-Revised (ADI-R)

A WPS TEST REPORT by Ann Le Couteur, M.B.B.S., Catherine Lord, Ph.D., Michael Rutter, M.D., F.R.S.

12031 Wilshire Blvd., Los Angeles, California 90025-1251

Version 1.210

Diagnostic Algorithm

Subjects Aged 4 Years, 0 months or more

Name of Subject: Donal
Date of Birth: Not Entered
Chronological Age: 12 year(s) 0 month(s)
Name of Respondent: Not Entered
Clinician Name: Not Entered
School/Clinic: Not Entered

Subject ID: Sample
Date of Interview: 05/10/06
Gender: Male
Relation to Subject: Not Entered
Date Processed: 05/10/06

Subject is Verbal (Item 30 = 0)

A: Qualitative Abnormalities in Reciprocal Social Interaction

Codes are "Most Abnormal 4.05.0" for all items in A1 to A4 (except 31, 58, and 65).

		Code	Score
A1: Failure to use nonverbal behaviors to regulate social interaction			
Direct Gaze	(50)	2	2
Social Smiling	(51)	3	2
Range of Facial Expressions Used to Communicate	(57)	2	2
		Total A1	6
A2: Failure to develop peer relationships			
Imaginative Play With Peers	(49)	2	2
Interest in Children	(62)	2	2
Response to Approaches of Other Children	(63)	2	2
Group Play with Peers (score if 4.0 to 9.11 years)	(64)	2	
OR (score either 64 or 65, depending on age of subject)			2
Friendships (score if 10.0 years or older)			
"Most Abnormal 10.0 - 15.0"	(65)	2	
		Total A2	8
A3: Lack of shared enjoyment			
Showing and Directing Attention	(52)	3	2
Offering to Share	(53)	2	2
Seeking to Share Enjoyment With Others	(54)	2	2
		Total A3	6
A4: Lack of socioemotional reciprocity			
Use of Other's Body to Communicate (Score "Ever")	(31)	0	0
Offering Comfort	(55)	2	2
Quality of Social Overtures	(56)	2	2
Inappropriate Facial Expressions (Score "Ever")	(58)	2	2
Appropriateness of Social Responses	(59)	2	2
		Total A4	8
A Total = A1 + A2 + A3 + A4		**A Total (cutoff = 10)**	28

B: Qualitative Abnormalities in Communication

Codes are "Most Abnormal 4.05.0" for all items in B1 and B4.
B2(V) and B3(V) codes apply only for verbal subjects (Item 30 = 0), using "Ever" codes.
Only B1 and B4 codes apply for nonverbal subjects (Item 30 = 1 or 2).

		Code	Score
B1: Lack of, or delay in, spoken language and failure to compensate through gesture			
Pointing to Express Interest	(42)	2	2
Nodding	(43)	2	2
Head Shaking	(44)	2	2
Conventional/Instrumental Gestures	(45)	3	2
		Total B1	8
B4: Lack of varied spontaneous make-believe or social imitative play			
Spontaneous Imitation of Actions	(47)	3	2
Imaginative Play	(48)	2	2
Imitative Social Play	(61)	1	1
		Total B4	5

Verbal Subjects Only:

B2(V): Relative failure to initiate or sustain conversational interchange			
Social Verbalization/Chat	(34)	2	2
Reciprocal Conversation	(35)	2	2
		Total B2(V)	4
B3(V): Stereotyped, repetitive or idiosyncratic speech			
Stereotyped Utterances and Delayed Echolalia (Score "Ever")	(33)	1	1
Inappropriate Questions or Statements (Score "Ever")	(36)	1	1
Pronominal Reversal (Score "Ever")	(37)	0	0
Neologisms/Idiosyncratic Language (Score "Ever")	(38)	2	2
		Total B3(V)	4

Verbal Total = B1 + B2(V) + B3(V) + B4	**B(V) Total (cutoff = 8)**	21
Nonverbal Total = B1 + B4	**B(NV) Total (cutoff = 7)**	.

C: Restricted, Repetitive, and Stereotyped Patterns of Behavior

Codes are "Ever" for all items in C1 to C4.

		Code	Score
C1: Encompassing preoccupation or circumscribed pattern of interest			
Unusual Preoccupations	(67)	0	0
Circumscribed Interests	(68)	2	2
		Total C1	2
C2: Apparently compulsive adherence to nonfunctional routines or rituals			
Verbal Rituals	(39)	0	0
Compulsions/Rituals	(70)	1	1
		Total C2	1
C3: Stereotyped and repetitive motor mannerisms			
Hand and Finger Mannerisms	(77)	1	
OR (Score the higher of the two)			1
Other Complex Mannerisms or Stereotyped Body Movements	(78)	1	
		Total C3	1
C4: Preoccupations with part of objects or non-functional elements of material			
Repetitive Use of Objects or Interest in Parts of Objects	(69)	1	
OR (Score the higher of the two)			1
Unusual Sensory Interests	(71)	0	
		Total C4	1
C Total = C1 + C2 + C3 + C4		**C Total (cutoff = 3)**	5

D: Abnormality of Development Evident at or Before 36 Months

Age Parents First Noticed	(2)	36	0
Age of First Single Words	(9)	19	0
Age of First Phrases	(10)	24	0
Age When Abnormality First Evident	(86)	2	0
Interviewer's Judgment on Age When Abnormalities First Manifest	(87)	24	1
		D Total (cutoff = 1)	1

Note:

- = Missing (not answered)
. = Score not calculated.

Summary of Codes

1.	N/A	21.	-		41.	-	-	61.	-	1	81.	-	-
2.	36	22.	-		42.	-	2	62.	-	2	82.	-	-
3.	N/A	23.	-		43.	-	2	63.	-	2	83.	-	-
4.	-	24.	-		44.	-	2	64.	-	2	84.	-	-
5.	-	25.	-		45.	-	3	65.	-	2	85.	-	-
6.	-	26.	-		46.	-	-	66.	-	-	86.	2	
7.	-	27.	-		47.	-	3	67.	-	0	87.	24	
8.	-	28.	-		48.	-	2	68.	-	2	88.	-	-
9.	19	29.	-	-	49.	-	2	69.	-	1	89.	-	-
10.	24	30.	0		50.	-	2	70.	-	1	90.	-	-
11.	-	31.	-	0	51.	-	3	71.	-	0	91.	-	-
12.	-	32.	-	-	52.	-	3	72.	-	-	92.	-	-
13.	-	33.	-	1	53.	-	2	73.	-	-	93.	-	-
14.	-	34.	-	2	54.	-	2	74.	-	-			
15.	-	35.	-	2	55.	-	2	75.	-	-			
16.	-	36.	-	1	56.	-	2	76.	-	-			
17.	-	37.	-	0	57.	-	2	77.	-	1			
18.	-	38.	-	2	58.	-	2	78.	-	1			
19.	-	39.	-	0	59.	-	2	79.	-	-			
20.	-	40.	-	-	60.	-	-	80.	-	-			

Missing codes: 110
Missing required codes: 0

Code Key:

Item 2, 5 - 10, 17, 19, 26, 28, and 87:
age in month OR
code 991 to 999
- = Missing (not answered)

Other Items:
Code 0 to 9
First column: may be "current" or "ever".
Second column (if presented):
may be "most abnormal", "ever" OR "at 5.0 years".
N/A = Not Applicable (no code needed)
- = Missing (not answered)

This report was generated based on WPS TEST REPORT Microcomputer Data Entry.

END OF REPORT

B. Appendix B

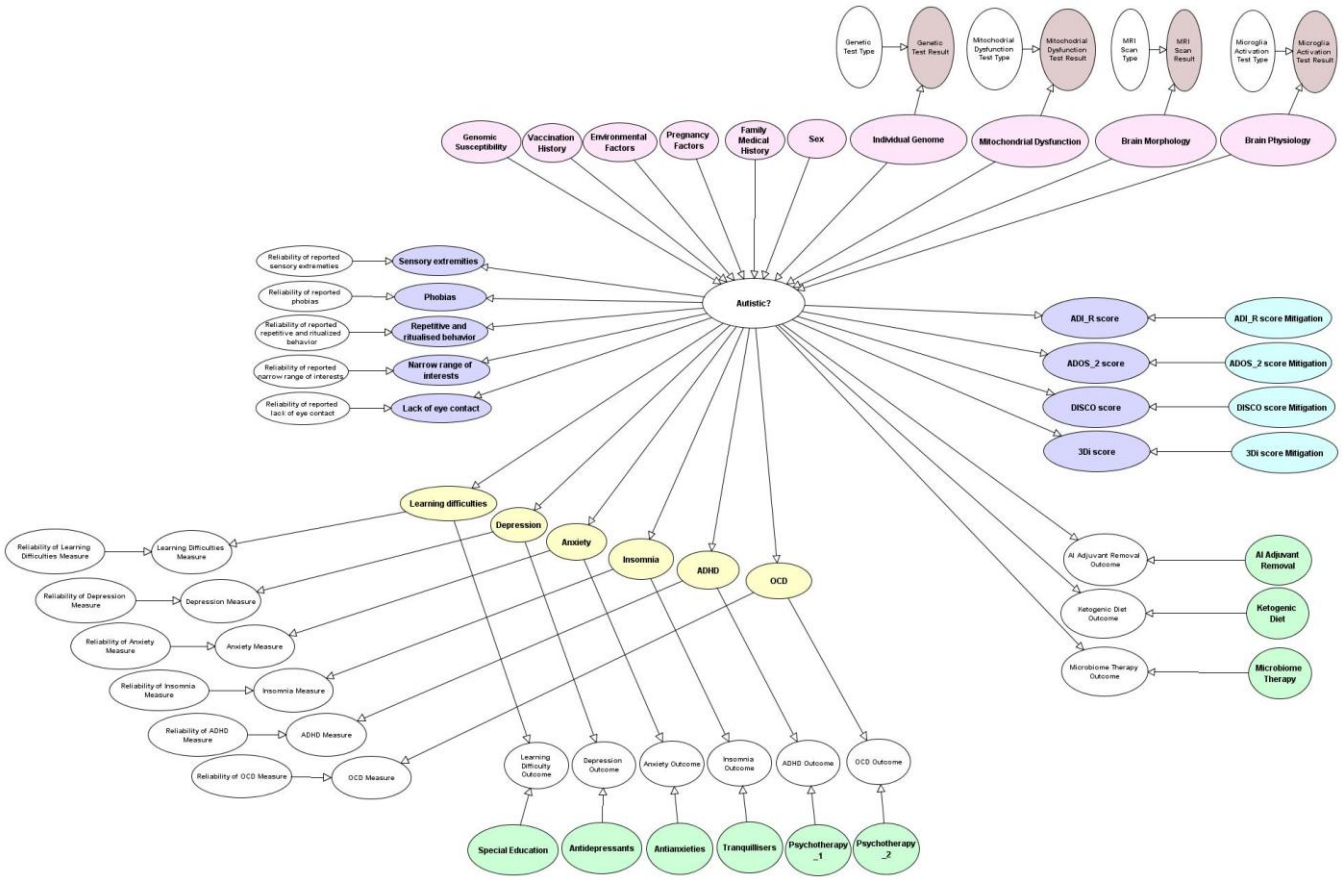


Figure 2: Full ASD diagnostic model showing variables and their causal inter-relationships.

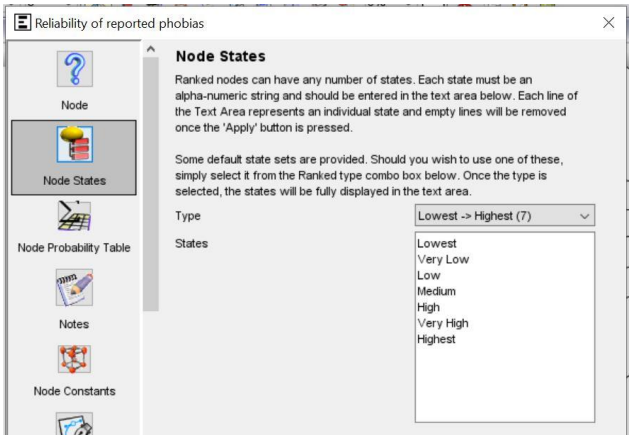


Figure 3: 'Reliability of reported phobias' node states.

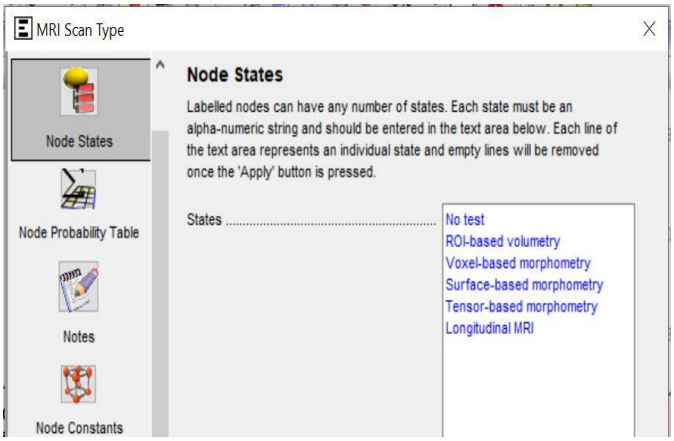


Figure 4: 'MRI Scan Type' node states.

C. Appendix C

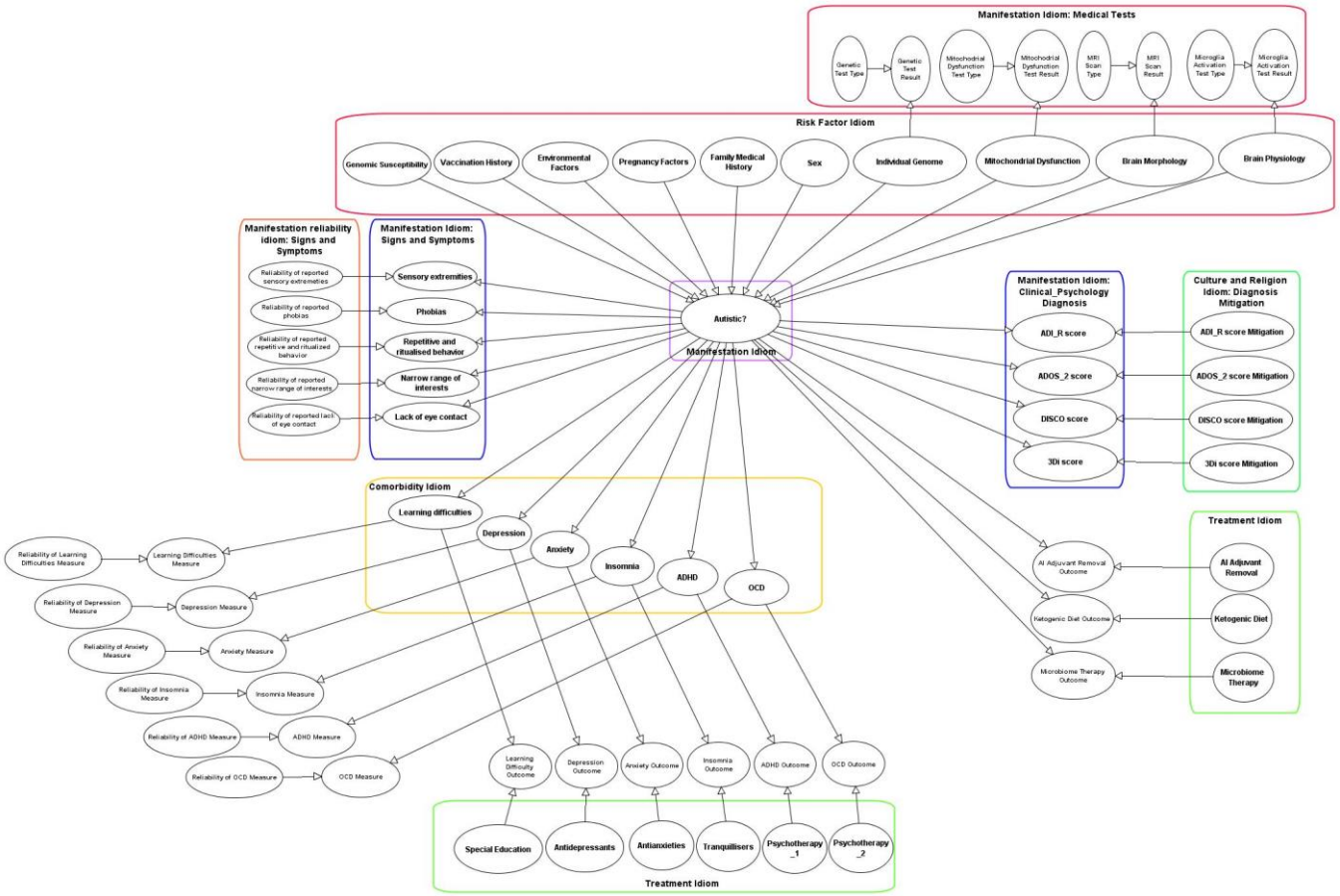


Figure 5: Full ASD diagnostic model displaying idiom map.

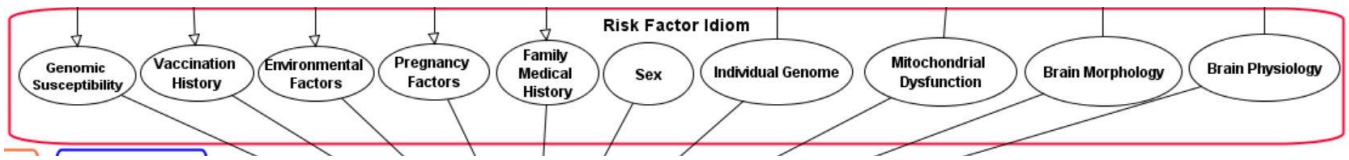


Figure 6: Model section showing risk factors.

D. Appendix D

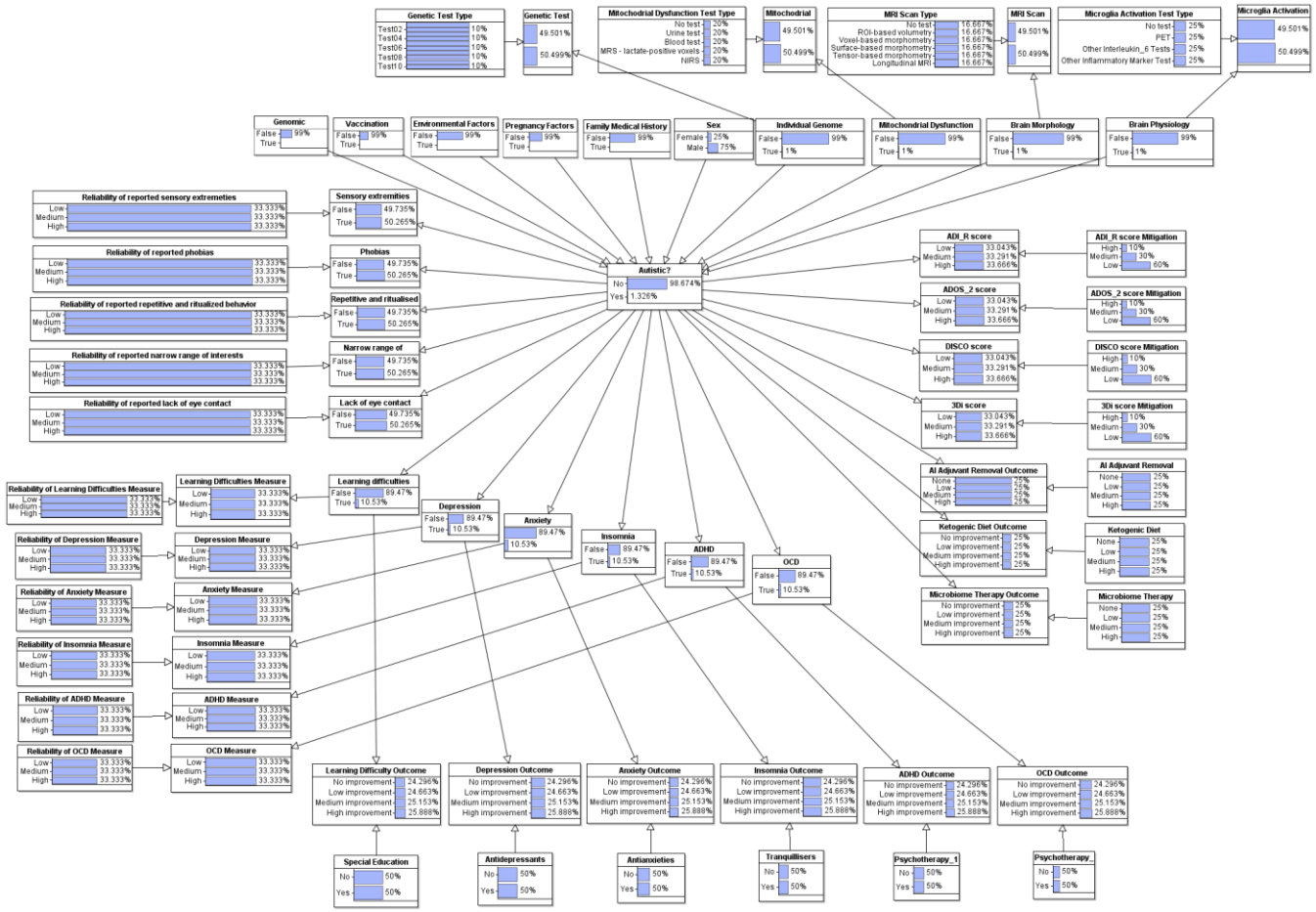
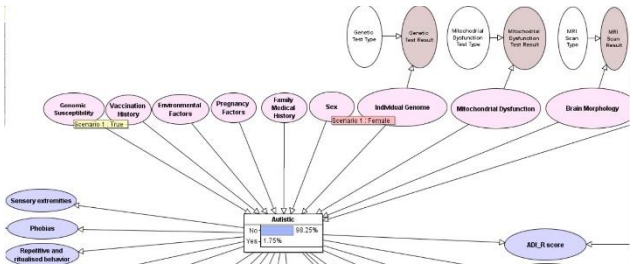
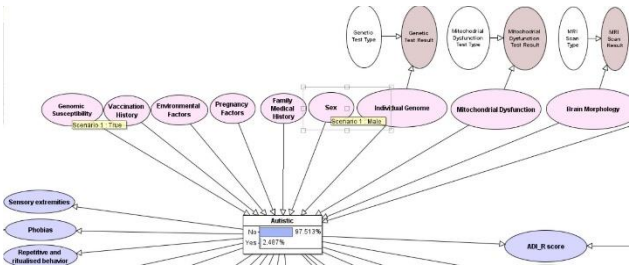


Figure 7: Full ASD model displaying all risk graphs at baseline (before any observation(s)).



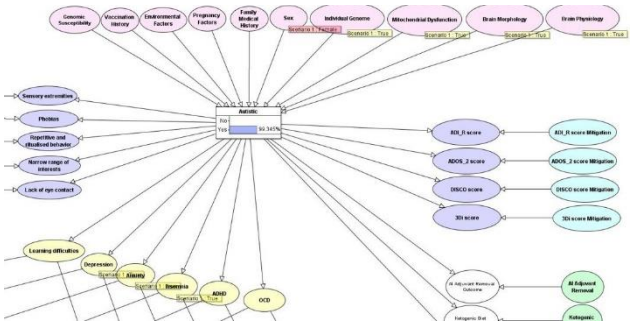
a.

Figure 8a: Model section showing Sarah's diagnosis.



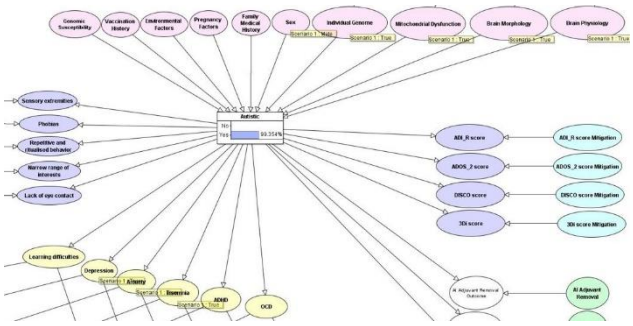
b.

Figure 8b.: Model section showing Bob's diagnosis.



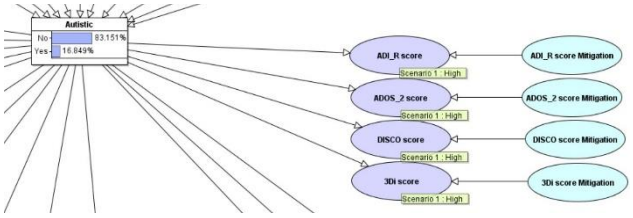
a.

Figure 9a: Model section showing Abena's diagnosis.



b.

Figure 9b: Model section showing Kofi's diagnosis.



a.

Figure 10a: Model section showing Lixin's diagnosis.