Approach and Method for Bayesian Network Modelling: The Case for Pregnancy Outcomes in England and Wales

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Abstract: For predicting and reasoning about outcomes of specific medical condition Bayesian Networks (BNs) can provide significant benefits over traditional statistical prediction models. However, developing appropriate and accurate BNs that incorporate key causal aspects of the condition is challenging and time-consuming. This work introduces a novel development approach, merging expert elicitation, literature knowledge, and national health statistics that enables such BNs to be developed efficiently. The approach is applied to build a BN for pregnancy complications and outcomes in England and Wales using 2021 data. The BN showed comparable predictive performance against logistic regression and nomograms, but additionally provides powerful support for decision-making and risk assessment across diverse pregnancy-related conditions and outcomes.

1 INTRODUCTION

Traditional pregnancy prediction models focus on singular health issues such as gestational diabetes mellitus (GDM) or preeclampsia (PE) without considering the broader context of the pregnancy. Typically, these models are statistical, relying on a limited set of risk factors which leads to several limitations (a full set of references for this and other imputations in this paper can be found in the expanded preprint version: McLachlan et al, 2024). These limitations include: (i) a focus on predicting the presence of a condition without considering the absence of that condition; (ii) overfitting to available data, leading to poor performance in the presence of uncertain or missing data; (iii) lack of transparency and interpretability, making it difficult to understand how the model makes its predictions; and (iv) limited ability to generalize to new populations or settings. To address these limitations we propose a new approach to pregnancy prediction based on Bayesian networks (BNs). BNs are a type of probabilistic model that can represent complex relationships between variables and have been shown effective in a wide range of medical applications.

Our proposed approach involves using BNs to model the entire pregnancy rather than focusing on singular health issues. This allows us to draw on a wider range of information including symptoms, risk factors, and medical history and to simultaneously make predictions about multiple health issues.

We have evaluated our proposed approach using the domain of pregnancy outcomes and found that it can outperform traditional methods in terms of accuracy, generalisability, and interpretability. We believe our approach has potential to transform how prediction models, and particularly pregnancy outcome prediction models, are developed and used. The resulting model is extensively validated using vignettes and concurrency analysis.

The rest of the paper is structured as follows: Section 2 covers theoretical and application domain backgrounds and reviews literature related to the research problem. Section 3 outlines approach and method for knowledge, data, and expert-driven

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modelling using causal BNs. Section 4 presents the results of applying this approach to develop a BN for pregnancy complications and outcomes. Section 5 discusses the experience of utilizing the approach and method, highlighting potential limitations in application to other problem domain spaces.

2 BACKGROUND AND RELATED WORKS

In our contemporaneous work, we screened a collection of 100 works published between 2000 and 2023 that proposed predictive risk screening models for pregnancy complications (Dube, Kyrimi & McLachlan, 2023).

2.1 Risk Factors and Symptoms

Risk screening typically occurs during the initial maternal clinic visit known as the *booking visit* (Tandu-Umba et al, 2014). While risk screening scores may be updated throughout antenatal care as new clinical and non-clinical information emerges, the specific signs, symptoms or clinical tests used vary depending on the adopted guideline or scoring model (Tandu-Umba et al, 2014; Stott et al, 2016). Some models rely on common factors like maternal age, BMI, and pregnancy history collected during the booking visit (Tandu-Umba et al, 2014), while others incorporate antenatal care records, pregnancy outcomes, or even novel variables like paternal DNA or vaginal swab results (Stott et al, 2016).

2.2 Common Issues

Developing healthcare risk, probability and decision support models can be challenging because: (i) obtaining a sufficiently large and high-quality dataset remains a hurdle and data may only be available for small patient groups, with demographic or clinical risk factors significantly reducing subgroup sample sizes (North et al, 2011; Pitchforth & Mengersen, 2013); (ii) traditional model evaluation relies on internal statistical methods (Dube et al, 2023) such as ROC curves and CIs that have limitations in assessing BNs (Pitchforth & Mengersen, 2013); (iii) prediction accuracy varies when some observations are missing or the patient lacks the predicted health condition, often due to overfitting that occurs when models are trained solely on data identifying the medical condition of interest, excluding information about what isn't that condition (Kumar et al, 2022); and (iv)

most are not presented with clear examples like risk-scored vignettes, hindering clinical comprehension and adoption (North et al, 2011; Mehta-Lee et al, 2017).

3 METHOD

Our research initially focused on constructing causal models for singular health issues affecting patients with rheumatoid arthritis, angina, acute traumatic coagulopathy, and GDM (McLachlan et al, 2020). However, we too overlooked the broader perspectives of general health, the accumulated effect of comorbidity, and healthcare access and experience within an entire population. We now stress the importance of adopting a holistic approach to model not only the patient, but also the community and disease; in essence, a complete *digital twin* that can be used to establish the credibility of our models in: (a) identifying or explaining risk; and (b) providing computer-based clinical decision support using machine learning (ML) or artificial intelligence (AI). Creating a community-wide baseline is crucial to fully evaluate causal relationships among known and novel symptoms, and modelling treatment and prognostic counterfactuals.

3.1 Hypothesis

This work proposes a broadly accurate BN model for diagnosis and treatment outcomes can be constructed using expert clinical knowledge, privacy-preserving datasets and population-wide statistics. By analysing commonly recorded medical observations, the model can predict health outcomes, incorporating causal interactions among clinical data, patient information and publicly available clinical data. *Notably, this approach is unprecedented in using large-scale health and outcome statistics.*

3.2 Bayesian Networks

BNs, also termed probabilistic graphical models, offer a graphical framework for probabilistic reasoning under uncertainty through a directed acyclic graph (DAG) consisting of structure and parameters. The structure includes nodes representing variables and edges indicating causal relationships. Parameters consist of conditional probability functions for each node, representing its strength given its parents. Bayesian probabilistic reasoning involves updating prior beliefs (prior probability) based on new evidence, resulting in posterior
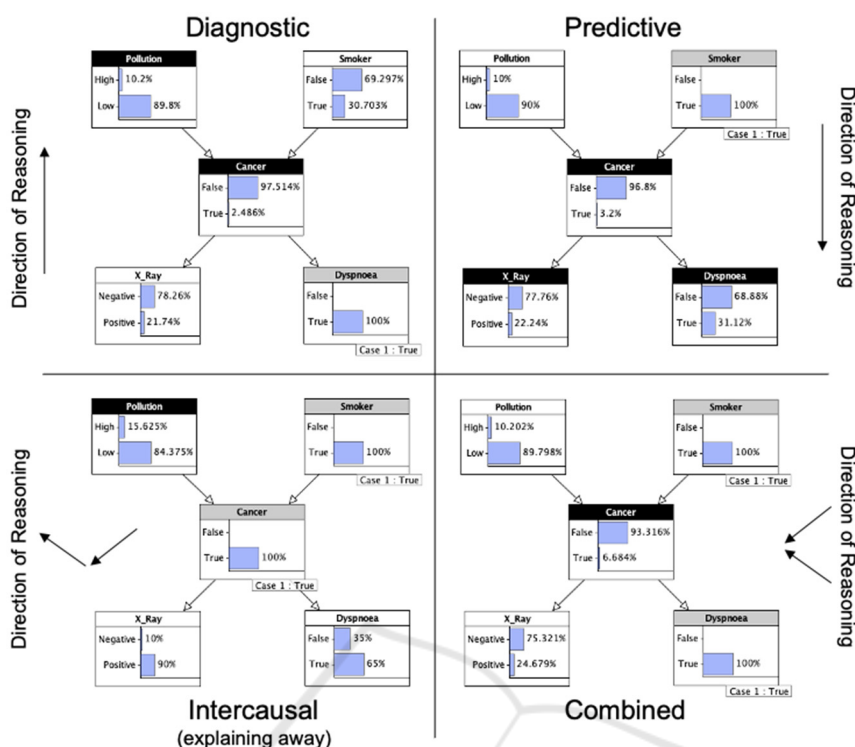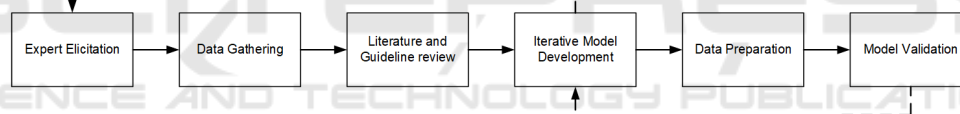
Figure 1: Types of reasoning.

Figure 2: BN Development Process Flow Diagram.

probability. In Figure 1, various scenarios illustrate reasoning from evidence using a lung cancer model. A node head in grey indicates observed evidence, while black determines the question being reasoned about. Forward reasoning - following the arc direction, and backward reasoning - counter to the arc, represent causal or predictive and diagnostic reasoning, respectively. Combining forward, intercausal and backward reasoning produces intercausal and combined reasoning. The approach used in this work ensures the model's capacity for all four modes of reasoning.

3.3 Study Population

The model in this study used publicly available privacy-preserving aggregate statistics from various sources. The data covered 624,828 pregnancies in England and Wales during 2021 encompassing live births, stillbirths, and neonatal deaths. Additionally, evidence for risk factors and causal relationships was

drawn from guidelines and academic studies published between 2019 and 2022, focusing on UK populations in 2021.

3.4 BN Development

Our main design objective was to create a model that credibly encapsulates current clinical knowledge on pivotal risk factors and interacting signs and symptoms affecting pregnancy outcomes. This objective is pursued through a six-phase development process outlined in Figure 2 and detailed in the subsequent section.

3.4.1 Expert Elicitation

The BN's structure and parameters can be derived entirely from data with an extensive dataset. However, BNs exhibit flexibility, capable of seamlessly integrating less comprehensive datasets, multiple expert's knowledge, and diverse information sources

	%
Asian	12.58
Black	4.95
Mixed	7.12
Other	2.35
White	73.0

One Dimensional NPT
Ethnicity

	Asian	Black	Mixed	Other	White
NO	0.967	0.932	0.966	0.966	0.966
YES	0.033	0.068	0.034	0.034	0.034

Two Dimensional NPT
Incidence of hypertension (HTN) in pregnancy by ethnicity

	Asian		Black		Mixed		Other		White	
AGE	<40	40>	<40	40>	<40	40>	<40	40>	<40	40>
NO	0.943	0.94	0.914	0.906	0.944	0.941	0.944	0.941	0.944	0.941
YES	0.057	0.06	0.086	0.094	0.056	0.059	0.056	0.059	0.056	0.059

Three Dimensional NPT
Incidence of hypertension (HTN) in pregnancy by ethnicity and age

	Asian						Black					
AGE	<40			40>			<40			40>		
BMI	Low	Med	High	Low	Med	High	Low	Med	High	Low	Med	High
NO	0.94	0.89	0.79	0.943	0.90	0.80	0.906	0.83	0.67	0.914	0.85	0.70
YES	0.06	0.11	0.21	0.057	0.10	0.20	0.094	0.17	0.33	0.086	0.15	0.30

Four Dimensional NPT
Incidence of hypertension (HTN) in pregnancy by ethnicity, age and BMI
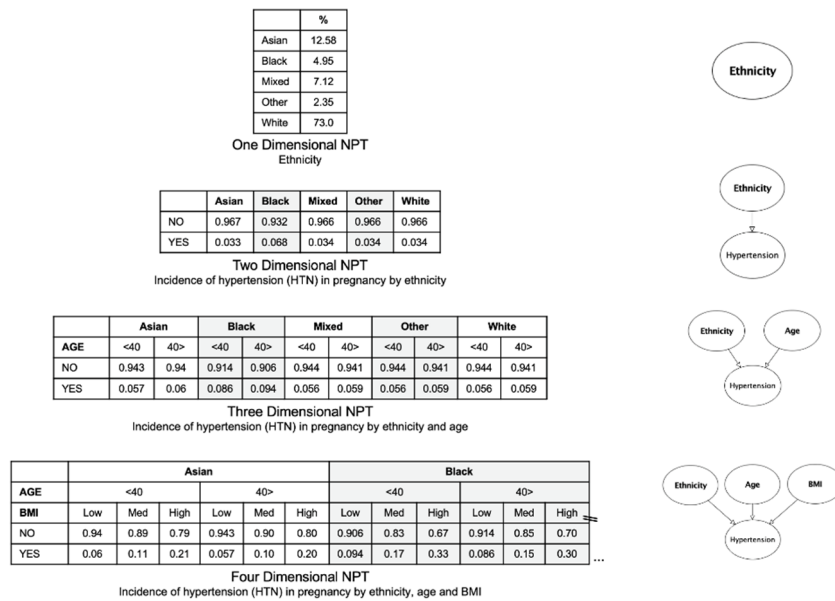
Figure 3: Examples of dimensionality in NPTs.

(Christophersen et al, 2018). Expert input enriches BN's design, ensuring up-to-date domain knowledge (Sanford & Moosa, 2015) Expert elicitation yielded caremaps; visualisations of disease progression, diagnosis, treatment processes and potential patient outcomes through flow diagrams or process maps. The caremap development process, has been detailed previously (McLachlan et al; 2020a).

3.4.2 Data Gathering

We sought national datasets that described the incidence of pregnancy complications and outcomes for an entire population. A key focus was publicly available privacy-preserving datasets whose use would not require, or violate, institutional ethics policies. This limited us to secondary or aggregate statistical sources such as those of national health services, health departments or statistics agencies. We collected datasets for the year 2021 as these were the most recent complete and published statistical datasets available for the UK.

3.4.3 Literature and Clinical Guideline Review

We performed a search to locate literature, clinical practice guidelines and protocols relevant to the medical condition(s) being modelled. The literature included was aligned to the data gathered in Phase 3.4.2. Priority was given to articles published during the same time period that described incidence of the medical condition(s) in like populations.

3.4.4 Model Development

The iterative model development process was: (1) medical idioms identifying key structural fragments were identified from the combination of caremap and knowledge derived from the clinical experts; (2) data was identified from statistical and literary sources to populate node probability tables (NPTs), describing incidence of the variable described by the node and incidence of interaction across arcs between that node and parent or child nodes; (3) structural fragments were brought together to form a single contiguous BN; and (4) the resulting model structure was reviewed with clinical experts and where changes were identified, the process returned to the first step. The process for identifying medical idioms and using these to support expert elicitation was previously described in (Kyrimi et al, 2020).

3.4.5 Data Preparation

Each node within a BN has a NPT. Absolute parent nodes (such as the pollution node in the example in Figure 1) have a single dimensional NPT. Where a node has a single parent (such as the dyspnoea node in the example in Figure 1) it will have a two-dimensional NPT. Where a node has two parents (such as the cancer node in the example in Figure 1) it will have a three-dimensional NPT etc. Nodes with six parents or greater are generally avoided due to complexity of elicitation and computation. Examples of data dimensionality in NPT are provided in Figure 3.
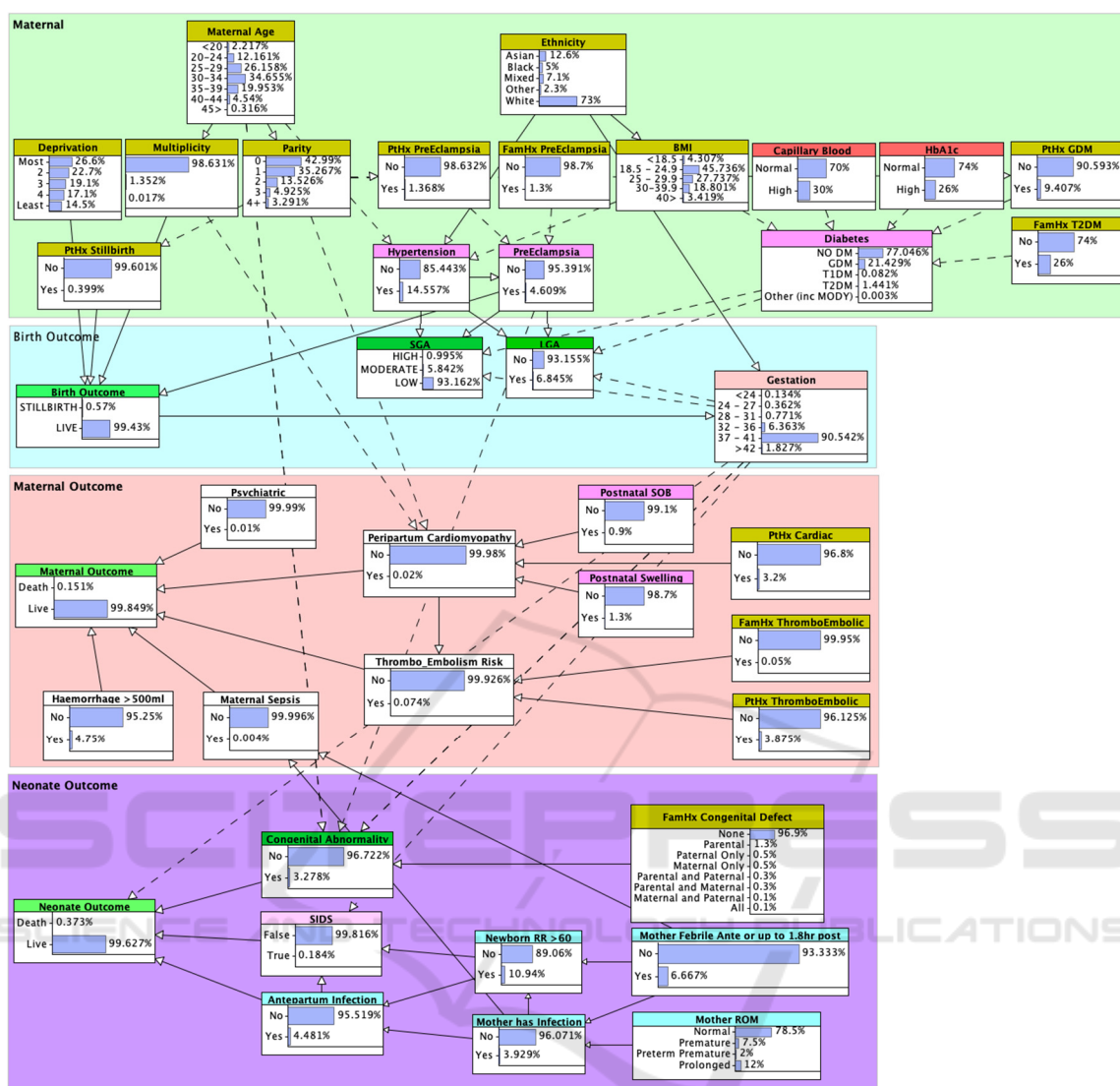
Figure 4: BN model showing background priors.

The content of each column in an NPT should sum to 1.0 (100%). Discretisation allows the modeller to convert continuous variable factors like BMI and capillary blood glucose (CBG) by assigning them clinically relevant intervals, ordinal states or categories (for example: low, medium, high). Some variables such as BMI in the example shown in Figure 3 were discretised in this way. Tables using population-level continuous variable data were prepared in Microsoft Excel and converted on ingestion by the Agenarisk BN modelling tool.

3.4.6 Model Validation

The validation process for our BN models followed a multi-step methodology recommended by various authors (Pitchforth & Mengersen, 2013). We initially undertook face validity with clinical experts (Pitchforth & Mengersen, 2013). However, we recognised the potential weakness in situations wherein experts involved in design are unlikely to disagree with their own judgment as reflected in the resulting model. To mitigate this we also used: (i) content validity to assess the BN structure against identified literature and clinical practice guidelines, evaluating the relationships between crucial risk factors and symptoms (Pitchforth & Mengersen, 2013); and (ii) concurrent validity to compare BN predictions against published models using clinical vignettes (Pitchforth & Mengersen, 2013). Due to the extreme rarity of the primary model outcomes;

"Stillbirth" as Birth Outcome and "Death" as Maternal Outcome, classical validation tests for model's accuracy, discrimination and calibration were not performed.

4 RESULTS

Figure 4 presents the Maternal Outcomes BN model, comprising four fragments that are used to group nodes relevant to: (1) maternal risk factors and common health conditions that may affect the pregnancy; (2) the immediate pregnancy outcome for the neonate and (3) mother; and (4) survival of the neonate.

The model structure allows the relevant impact of observations on factors in the primary maternal zone to carry over onto maternal and neonate outcomes. Solid lines indicate direct relationships, while dashed lines indicate the presence of hidden nodes used for alternate discretisation of variables. Model priors are also shown in Figure 4.

4.1 BN Validation

This section provides an overview of the processes used to validate the maternal outcomes model.

4.1.1 Face Validity

Throughout development of our BN, a collaborative effort with a small group of clinical experts ensured validation through comparisons with literature and clinical guidelines. Face validity ensures the model's visual representation aligns with expectations. The iterative development process incorporated clinical insights and weighed variables and causal pathways against evidence from clinical texts, medical journals, and available data. For parameterisation, clinicians played a crucial role in providing initial estimates for BN parameters. We updated these in the final model using national statistics for the entire England & Wales population.

The model holistically addresses primary pregnancy outcomes: *(1) Birth Outcome:* This fragment encompasses live birth or stillbirth, including considerations for late-term miscarriage based on nuanced definitions (NHSInform, 2022); *(2) Maternal Outcome:* Predicting maternal death aligned to 2021 mortality statistics (ONS, 2023)*; (3) Neonate Outcome:* Predicting death in live-born babies aligned to 2021 ONS and MBRRACE-UK birth outcome statistics.
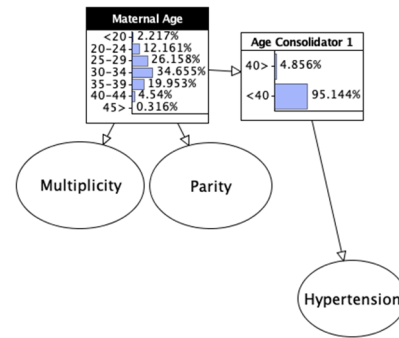

Figure 5: Maternal Age substructure showing hidden Age Consolidator node.

Secondary outcomes linked to the baby are also identified, including: *(1) Small for Gestational Age (SGA):* Stratifying risk into three categories, the model offers a nuanced perspective on this outcome, grounded in a total incidence for 2021 derived from substantial data (NMPA Project Team, 2021)*; (2) Large for Gestational Age (LGA):* Incorporating the impact of gestational diabetes mellitus (GDM), the model aligns with 2021 datasets, capturing the nuanced nature of this outcome*; (3) Congenital Abnormality:* Grounded in probability and informed by UK national statistical data and research on increasing prevalence rates due to inheritance, the model projects a prior probability of 3.278% for this outcomes.

The collaborative and iterative approach, coupled with reliance on expert input and robust statistical grounding, ensures a model's robustness and relevance in reasoning complex outcomes.

4.1.2 Content Validity

The key demographic risk factors identified in predictive models included: *(1) Maternal Age (74%):* Models varied in representing maternal age, reflecting it either as a continuous variable or discretizing it into intervals. Our model employs five-year increments that align with national maternity statistics (ONS, 2023). To simplify situations where a binary identifying advanced maternal age was required, a hidden boundary age node was included as shown in Figure 5; *(2) BMI (59%):* BMI statistics, categorized into five groups, were derived from Public Health England's report (PHE, 2019). BMI is strategically placed between ethnicity and child nodes representing diabetes, hypertension, and pregnancy outcomes; *(3) Parity (42%):* Nulliparity and grand parity were categorized into five groups to aid consideration of their impact on conditions and outcomes. Maternal age is linked, especially in

extreme cases, updating probabilities for nodes like diabetes, hypertension, and birth outcomes (Ananth et al, 1996); *(4) Ethnicity (36%):* Ethnicity's influence is integrated across the model, impacting hypertension, gestation and BMI, with connections to various pregnancy outcomes; *(5) Gestation (32%):* Gestation can be both an outcome and a risk factor, and affects various pregnancy outcomes including prematurity and post-term deliveries. The gestation node is informed by the 2021 dataset (ONS, 2023) to ensure accuracy in predicting maternal and neonate risks and outcomes.

4.1.3 Concurrent Validity

We re-examined papers included in our screening review (Dube et al, 2023) to locate any works that included a vignette with prediction suitable for use in concurrent validity testing, identifying only two.

North et al (2011) propose a model using statistical methods to predict incidence of pre-eclampsia. Their model is based on demographic and risk factors of the first-time mother along with observable signs and symptoms routinely collected by the midwife during the initial (booking) patient appointment. They used their model to compute the following vignette:

> *A 28 year old nulliparous woman whose birth weight was 2400 g, with a mean arterial pressure of 96 mmHg, BMI 30, a family history of pre-eclampsia, and no protective factors, her probability of pre-eclampsia is 39%.*

Making the same observations (maternal age, BMI, parity, family history of pre-eclampsia, and maternal hypertension) our model indicates a 43% probability for pre-eclampsia. The 4% difference can be attributed to: (i) diverse country origins in their dataset (England, Wales, Ireland, New Zealand, and Australia) versus our England and Wales focus; (ii) their 2004-2008 data versus our 2021 dataset; (iii) their 4961 pregnancies versus our larger 624,828; and (iv) reported increasing incidence of pregnancy-related conditions globally between 2010-2020 (Cameron et al, 2022).

Mehta-Lee et al (2017) used statistical methods on pregnancy data collected between 2004-2009 to develop a nomogram for predicting preterm delivery. They began with a larger number of potential factors, but the resulting nomogram includes only the nine factors they identified as most predictive from a cohort of 192,208 pregnancies. Their vignette describes:

> *A 35 year old (13 points) African American (41 points) woman planning to get pregnant for the first time (46 points) who has no history of diabetes (0 points) but who smokes (12 points) would have a total of 112 points. This approximates to a baseline probability of preterm birth of 12-13% prior to conception.*

Using the same observations, our model predicted an 8.7% preterm birth rate - which is the sum of predictions for all gestations prior to 37 weeks with the exclusion of smoking as a factor (Smith et al, 2023). Discrepancies observed with how other models incorporated smoking may have arisen due to underreported smoking rates influenced by social stigma (Smith et al, 2023). Global variations in reporting, and confounded outcomes in UK studies, only contribute to the confusion (Smith et al, 2023). UK studies generally report lower smoking rates compared to the USA, with some incredibly reporting no smoking at all (Stott et al, 2016). Vaping, a smoking alternative, poses uncertainties in long-term pregnancy outcomes. Omitting smoking from our model considers these issues and ensures robust predictions unaffected by potential smoking-related biases (Smith et al, 2023).

Finally, Du & Li (2021) developed a nomogram for prediction of the baby's survivability in pregnancies complicated by GDM using data collected from 626 Chinese mothers receiving outpatient antenatal care between 2016 and 2019. We used their nomogram to evaluate the following scenario:

> *A 35 year old (22 points) Asian woman at 31 weeks or 217 days gestation (10 points) with a BMI of 35 (25 points), first degree family history of T2DM (10 points), history of GDM in a previous pregnancy (4 points) and a mildly high fasting plasma glucose (FPG) of 6.0 mmol (47.5 points). This gave a total of 118.5 points which their nomogram approximated to 82-83% survivability for the baby.*

Our BN model with these observations predicted a live birth, birth outcome of 84.7%. The dataset of pregnancies used in Du & Li (2021) were temporally the closest to those used to develop our model, and the resulting predictions are not significantly different.

5 DISCUSSION

During our model validation, two unaddressed issues in reviewed models emerged. First, some works included potentially unquantifiable elements: self-assessed, unmeasurable, or flexible factors (Mehta-Lee et al, 2017). Second, some models included potentially unknowable elements: data challenging to reliably procure (North et al, 2011).

While resource-intensive, our model's design proves efficient. It eliminates redundant data entry across different predictive models, streamlining the process for clinicians. Rather than inputting the same variables multiple times for various conditions, our model allows one-time entry, computing probabilities for both primary and subsequent conditions along the disease pathway (Angeli et al, 2011). Traditional models often focus on prediction of a singular health condition, neglecting a holistic view of health. Our model considers the patient comprehensively, capturing interactions between risk factors, symptoms, and various health issues. Unlike condition-limited models, our approach models the patient as an entire organism, preserving information about the overall impact of common symptoms or concomitant diseases on health outcomes.

While adapting the model for New Zealand, future work includes exploring treatment selection and outcome counterfactuals. This involves testing alternate hypotheses, such as the potential outcomes with or without specific interventions. Limitations include the need for granular national health statistics and access to expert support for model development and face validity assessment. Resources and time are substantial in constructing complex models like ours, contrasting with the preference for simpler, single-condition statistical models.

6 CONCLUSIONS

This work has introduced a novel pregnancy risk prediction model addressing limitations in existing approaches. Our holistic model considers not only the condition of interest but also related conditions and outcomes. Unlike models relying on limited local data, we utilise publicly available national health statistics, allowing versatile model development. Employing a causal Bayesian probabilistic approach, we navigate uncertain or missing data. Validation involves ongoing face, content, and concurrent methods, revealing an accurate description of pregnancies nationally and individually. Three case vignettes provide exemplar predictions for future model comparisons. The model's reliability and clinical holism, achieved at low cost, can instil confidence in both clinicians and patients.

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