



# Approaches for drawing causal inferences from epidemiological birth cohorts: A review



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## ABSTRACT

Large-scale population-based birth cohorts, which recruit women during pregnancy or at birth and follow up their offspring through infancy and into childhood and adolescence, provide the opportunity to monitor and model early life exposures in relation to developmental characteristics and later life outcomes. However, due to confounding and other limitations, identification of causal risk factors has proved challenging and published findings are often not reproducible. A suite of methods has been developed in recent years to minimise problems afflicting observational epidemiology, to strengthen causal inference and to provide greater insights into modifiable intra-uterine and early life risk factors. The aim of this review is to describe these causal inference methods and to suggest how they may be applied in the context of birth cohorts and extended along with the development of birth cohort consortia and expansion of “omic” technologies.

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## 1. Introduction

Large-scale population-based birth cohorts recruit women during pregnancy or at birth over a defined time period and follow up their offspring through infancy and into childhood and adolescence. The longitudinal design of these cohorts is a key feature, providing the opportunity to monitor and model early life exposures in relation to developmental characteristics and later life outcomes, with prospective data collected at repeat follow-ups. Data are often collected on both parents and offspring and include information on demographic, socio-economic and lifestyle characteristics and environmental exposures obtained from questionnaires, clinic data for assessing health and development, and data from biological samples. Some cohorts have been designed as multipurpose resources, whilst others focus on specific health or exposure-related research questions. The size of birth cohorts varies considerably, from a few hundred individuals to over 100,000 in countries where population-based record linkage is possible.

A major focus of such studies is exposure to risk factors during early life developmental periods which can have important consequences for health and disease. The “Developmental Origins of Health and Disease” (DOHaD) hypothesis outlines how the risk of chronic disease in adult life is initially induced through biological programming of the foetus or infant in response to early environmental signals [1,2]. These responses include molecular, hormonal, metabolic or physiological changes which may have negative impacts on later health. Of particular interest is the data captured on maternal exposures acting during pregnancy, driven by the notion that the intra-uterine environment is a critical period for influencing offspring development and programming events [3,4].

Studies have reported associations between foetal growth, maternal nutrition, exposure to drugs, pollutants and hormones in-utero and a whole host of perinatal and later life offspring traits. The influence of postnatal factors has also been explored, including early life growth [5] and breastfeeding [6]. Of particular value are historical birth cohorts which can be used to study the influence of early life exposures on later disease [7]. As well as DOHaD, other aspects of research within lifecourse epidemiology may be investigated within the context of a birth cohort [8,9] and details of these can be found elsewhere [10].

An attractive feature of birth cohorts is the ability to obtain information on other family members, not only the mothers of the offspring, but sometimes fathers, siblings and grandparents. Family-based sampling can facilitate inter-generational studies of the influence of parental characteristics on a range of offspring outcomes and may aid in disentangling the genetic determinants of disease from environmental risk factors [11].

Increasingly, birth cohorts collect and store biosamples from their participants, which can be used to obtain genetic, epigenetic and metabolic profiles, and to measure biomarkers of environmental exposures such as smoking and pollutants. Biosampling allows the exploration of how social and environmental factors leave biological imprints, independent of or in combination with genetic background. The ‘omics’ revolution [12] offers the potential to explore putative mechanisms by which specific exposures convey disease risk, whereby identified molecules provide robust biomarkers of early life exposure or may act as intermediates in pathways between exposure and risk of later outcomes.

In addition to the wealth of data collected, longitudinal birth cohorts can offer more to observational epidemiology than other study designs because they allow for prospective time-ordering of the associations of interest i.e. with exposures preceding outcomes, which is useful for establishing causality. However, a key limitation to causal inference in epidemiological birth cohorts is potential confounding, leading to spurious observational associations [13,14]. Distinguishing causality from correlation is essential to identify key early life modifiable causes of ill health and disease and to uncover new mechanistic pathways for therapeutic intervention. A suite of methods has been developed in the last decade to minimise problems afflicting observational epidemiology and to strengthen causal inference. The aim of this review is to describe the causal inference methods that have been used to provide greater

insights into modifiable intra-uterine and early life risk factors in the context of large epidemiological birth cohorts and to suggest how we may improve methodological approaches, especially in relation to the expansion of “omics” technologies.

## 2. Challenges of establishing causality in birth cohorts

Key problems of observational epidemiology which limit its ability to establish causal effects include: 1) reverse causation—where the outcome of interest affects the exposure; 2) confounding—the presence of common causes of the risk factor of interest and the outcome; 3) selection bias—when the study participants are selected in a manner that biases the effect estimate in an association; and 4) measurement error in the exposure, confounding factors or outcome. The characteristics of birth cohorts are such that some of these problems can be minimised. For example, their prospective study design means that there is no biased retrospective assessment and the likelihood of reverse causation is reduced due to the time-ordering of the exposure-outcome associations. These studies also allow for repeated measures to be taken at different time points and appropriate analytical techniques may be used to account for missing data, reducing the role of measurement error and selection bias [15,16].

Observational epidemiology undertaken in the context of a birth cohort generally relies on the assumption that confounding characteristics have been identified and measured with little or no error. However, confounders may be inadequately measured (residual confounding) or there may be unobserved factors (unmeasured confounding) [17] which can lead to spurious associations and conclusions about intra-uterine and early life risk factors [18,19]. Inconsistent findings between cohorts and randomised controlled trials (RCTs) highlight the methodological challenges in establishing robust causal links [13,20]. For example, in observational studies maternal vitamin C intake has been found to be associated with higher birth weight in the offspring [21]. However, large RCTs where pregnant women have been randomised to vitamin C supplements [22–24] have found no benefit of supplementation on birth weight. These conflicting findings are likely due to confounding in the observational association, as mothers with higher vitamin C intake tend to have lower rates of smoking and are from a higher socioeconomic background, which influence birth weight [25].

Other limitations introduced by the very nature of birth cohorts include the long time gap between outcomes and exposures, increasing the likelihood of confounding. Another implication of this time gap is the relevance of early life exposures experienced when the birth cohorts were established to contemporary cohorts. Finally, given the high correlation between maternal exposures and behaviours in pregnancy with those postnatally it is often difficult to tease apart intra-uterine from postnatal effects [26].

## 3. Classic epidemiological approaches for drawing causal inferences

Data collected on parents, offspring and other family members in epidemiological birth cohorts may be integrated in a suite of methods which minimise problems of confounding, strengthen causal inference and provide greater insights into modifiable early life risk factors. The strength of evidence obtained from these methods can be placed between observational associations and RCTs in the hierarchy of evidence for clinical guideline production. Table 1 includes a selection of large, well-established cohorts and the data available in these cohorts which may permit the application of the causal inference methods described in this review. Table 2 outlines each of the main causal inference methods, with examples and linked schematic diagrams in Fig. 1.

## 4. Randomised controlled trials

Well-conducted, large RCTs, where study participants are randomly allocated to a treatment to avoid potential confounding between

treatment and outcome, are the gold standard for estimating causal effects in population health. This is also the case in the setting of early life influences, for example with the randomization of women to different interventions in pregnancy. A number of RCTs of pregnancy and early life interventions originally set up to investigate short-term outcomes have been extended to follow up offspring at multiple ages. One example of a birth cohort nested within an RCT is the PROBIT trial [27,28]. This cluster-randomised controlled trial involved randomization to a breastfeeding promotion intervention which resulted in longer duration of any and exclusive breastfeeding and has been used to investigate the causal effect of breastfeeding on later health outcomes, including obesity, blood pressure, cognitive function and eating attitudes [29–33]. RCTs require large investment and their experimental nature means that they should be reserved for interventions that have strong support from observational epidemiology. In addition, for some exposures it is not possible or would be unethical to randomise participants and where RCTs are conducted, they are often done so in selected populations and so findings may not be generalizable.

## 5. Cross-cohort comparisons

Support for the initiation of the PROBIT trial came from observational studies which have shown breastfeeding to be protective against a wide range of later outcomes. However, not all of these associations persist in a randomised trial setting [29–31]. This discordance can be explained by the fact that the majority of observational studies have been conducted in higher-income countries where breastfeeding is strongly related to higher socio-economic circumstances, maternal non-smoking and healthy diet. The links between breastfeeding and these factors would generate non-causal observational associations between breastfeeding and health outcomes, and the ability to fully evaluate and statistically adjust for such confounding is limited. One way to circumvent this problem, without initiating an RCT, would be to compare associations between two or more populations in which the underlying confounding structures are markedly different. For example, if the associations found in higher-income countries are causal then one would expect them to be found in low- and -middle- income countries where breastfeeding is often not associated with socio-economic position [34]. An analysis of a UK-based cohort study, ALSPAC, and a Brazilian-based cohort study, the Pelotas 1993 Cohort, showed that the inverse association of breastfeeding with later offspring body mass index (BMI) and blood pressure found in higher income countries is not present in low- and middle- income countries. By contrast, a positive association with intelligence quotient (IQ) was found in both settings [34]. These findings have been validated by results of the PROBIT study, based in the middle-income country of Belarus [27,28]. The assumption about different confounding structures in different cohorts may not be correct and has to be thoroughly investigated. In addition, harmonisation of variables between cohorts is required in order to minimise the influence of statistical heterogeneity.

## 6. Negative controls

It is also possible to infer a causal effect by comparing an observed association between a particular exposure and an outcome with a negative control. A negative control situation is one that cannot involve the hypothesised causal mechanism, but which is likely to involve the same sources of bias or confounding as in the original association [18,35,36]. Any evidence of association over and above that observed in the negative control is indicative of a causal effect. For example, the association of an exposure and outcome may be compared with that of another exposure, which is equally socially patterned, and the same outcome. A study conducted in the Norwegian Mother and Child cohort (MoBa) compared the magnitude of association between maternal folic acid supplementation in pregnancy and children's risk of autistic disorders with the association between maternal fish oil supplementation and

autistic disorders. A reduced risk of autistic disorder in children of folic acid users was evident but no such association was found with prenatal fish oil use, even though fish oil use was associated with similar socio-economic characteristics as folic acid use [37].

Negative controls can also be used if one wishes to investigate whether an association between a particular exposure and outcome arises in a proposed critical period, such as in-utero. For example, maternal smoking after pregnancy would not be expected to have the same influence on offspring outcomes as smoking during pregnancy if the mechanism of influence is through the intra-uterine environment [38]. However, the high correlation of pre- and postnatal smoking makes it difficult to disentangle causal effects [26] and women who do not smoke in pregnancy but do postnatally may be characteristically different from women who continue to smoke, which may re-introduce confounding. This can be avoided through the use of within-individual comparisons or when the influence on exposure patterns is externally generated [18,19]. For example, the Dutch Hunger Winter study demonstrates the specific effect of imposed nutritional deprivation during early pregnancy on a number of health outcomes, compared with women who experienced famine at other stages in pregnancy [39].

## 7. Parental comparisons

A negative control design that is primarily used for exploring the extent to which associations of intra-uterine exposure might be causally related to offspring outcomes in later life is the parental comparisons approach. If there is a causal intra-uterine effect, one would expect a stronger maternal-offspring association than paternal-offspring association for the same exposure assessed at the time of pregnancy. Where associations are similar for both parents it is likely that there is confounding by genetic or shared environmental characteristics [11,18,36]. Proof of concept has been illustrated with maternal smoking in pregnancy which is strongly associated with lower offspring birth weight, whereas paternal smoking is only weakly associated. When both maternal and paternal smoking during pregnancy are taken into account, the former association is little attenuated whereas the latter association is essentially abolished, arguing for a biological effect of maternal smoking in pregnancy on offspring birth weight [18].

It has been hypothesised that maternal obesity and metabolic profiles related to this may, during pregnancy, programme the offspring for greater risk of obesity in later life [40,41]. This could result in inter-generational acceleration, with ever-increasing levels of obesity in the population [42]. Some parental comparison studies find stronger associations of maternal BMI than paternal BMI with offspring BMI [43–45], although these have often been of small sample size, with different sources and degrees of validity for BMI measures, and non-paternity for biological measures has generally not been taken into account [46]. Subsequent studies addressing these issues have found that maternal and paternal BMI relate very similarly to offspring adiposity [46–50], arguing against a major specific effect of the intra-uterine environment and suggesting that the associations are driven by shared familial genetic or lifestyle characteristics.

Some evidence has been found which supports potential male-line transgenerational responses, invoking parent of origin, imprinting and epigenetic phenomena [51,52]. Maternal and paternal associations of similar magnitude may therefore be interpreted as showing intra-uterine maternal influences which are offset by these paternal pathways. However, it has been posited that the likelihood of such perfectly matched effects being produced by mechanistically distinct processes is low [18,53].

## 8. Sibling comparisons

It may be possible to compare outcomes within siblings who are concordant or discordant for early life exposures. Since familial

**Table 1**

Characteristics of a selection of birth cohorts described in this review and the data currently available which may permit causal inference.

Birth cohort	Study description	Initial sample size	Data collection during pregnancy	Data on both parents	Prospective/retrospective	Follow-up	Frequency of follow-up	Methods of data collection	Biological samples	Dna extracted	Gwas data	Epigenetic data	Metabolomic data	Sibling data
Avon Longitudinal Study of Parents and Children (ALSPAC) (UK)	Prospective pregnancy cohort study set up from 1991 to 1992 in the south west of England and the surrounding areas	15,247 pregnancies (14,541 in initial recruitment, 706 added a later time)	Yes	Yes	Prospective	From around 8th gestational week to 21+ years postnatal for parents and between birth and 21+ years of age for child.	68 data collection time points for child. 19 data collection time points for mother	Questionnaires, clinical assessments, medical and educational records	In offspring (at birth and later ages), mothers (during pregnancy and postnatally) and fathers	~10,000 mothers and offspring; ~2000 fathers	8365 children, 8340 mothers, fathers in process	450 K DNA methylation available in ~1000 mother-child pairs at multiple time points	NMR metabolomic profiling in ~5000 children, ~4000 mothers and 2000 fathers planned, at multiple time points	Only if born during recruitment period.
1958 British birth cohort (National Child Development Study) (UK)	Longitudinal study of all children born in England, Scotland and Wales in one week in March 1958. Initially a study on perinatal mortality, but later extended to lifelong tracing of participants.	17,416 births	No, some retrospective data from medical records and perinatal survey.	Yes	Prospective though some retrospective data about pregnancy.	Between birth and 55 years of age	Since 1958, 9 further 'sweeps' of all cohort members	Maternal interview at birth; obstetric data from medical records; parental interviews, medical examinations, school attainment and questionnaires in childhood; interviews and questionnaires for offspring (and parents) in adulthood. Biomedical assessment and blood collection at age 44-45. Data from medical records.	In offspring	~7500 offspring	~3000 offspring (~7000 metabochip and immunochip)	MeDIP in subsample	No	No
Pelotas Birth Cohort Studies (1982) (Brazil)	One of three parallel longitudinal studies of all infants being born to mothers living in Pelotas in 1982, 1993 and 2004.	5914 births	No, though some retrospective data from perinatal survey	Yes, though limited for partners	Mostly prospective data collection. Retrospective data about pregnancy.	Between birth and 30 years	On entire cohort at age 2, 4, 22 and 30 years but more frequent follow-up of subsamples	Maternal questionnaire and offspring anthropometric assessment at birth; follow-up interviews, anthropometric assessments and questionnaires; some national record linkage.	In offspring	~4000 offspring	~3500 offspring	No	No	Only if born during recruitment period.
The Norwegian Mother and Child Cohort Study (MoBa) (Norway)	Prospective pregnancy cohort which enrolled women at week 17-18 in pregnancy from all over Norway between 1999 and 2008, with record linkage.	>114,500 children born to >95,000 mothers	Yes	Yes	Prospective	From pregnancy week 17-18 to date. 7 year and further follow-ups are being processed.	3 questionnaires during pregnancy, further questionnaires at 6 months, 18 months and 3 years.	Questionnaires and record linkage with Norwegian Patient Registry	In offspring (at birth), mothers (during pregnancy and at birth) and fathers	~70,000-95,000 offspring, mothers and fathers	~3000 mothers and children. 14,000 mothers and children and 11,000 fathers available in 2015	450 K DNA methylation data available in 1,000 mother-child pairs	No	Includes almost 18,000 pairs of siblings

Generation R (The Netherlands)	Population-based multi-ethnic birth cohort study which enrolled mothers living in a defined area of Rotterdam, Netherlands with a delivery date between April 2002 and January 2006.	9778 mothers and children	Yes	Yes	Prospective	From early pregnancy to date. Data collection at age 10 years will be completed in 2015	3 assessments in the prenatal phase, frequent follow-ups from birth to 48 months and data collection at focus visit at age 5-6 years	Observational assessments, parental and child interview and questionnaires, records of child health care centres, obstetric records	In mothers (during pregnancy), children (at birth and age 6) and fathers	~6500 offspring, 8,000 mothers and 5,000 fathers	Available on ~6000 children. Not yet scheduled for parents.	450 K DNA methylation data available in 1,000 cord blood samples	No	Only if born during recruitment period.
The Danish National Birth Cohort (DNBC) (Denmark)	Prospective cohort study which enrolled pregnant women from all over Denmark between 1996 and 2003, with record linkage.	92,274 mothers with a total of 100,418 pregnancies	Yes	Yes	Largely prospective with some retrospective data collection about medical history.	From early pregnancy to date	2 telephone interviews and 1 food questionnaire in pregnancy, further follow-ups at 6 months, 18 months, 7 years and 11 years. The plan is for the study to be lifelong.	Computer-assisted telephone interviews; questionnaires; data from Routine Health Registers and National Hospital Discharge Registry.	In offspring (at birth) and mothers (during pregnancy)	~91,000 samples on mothers	GWAS data available on ~8000 mothers	450 K DNA methylation in ~1300 offspring of GOYA study on available soon	No	Only if born during recruitment period.
The Dutch Hunger Winter Families Study (The Netherlands)	Longitudinal cohort study of part of the population that was in the fetal stage at the time of the 'Hunger Winter' of 1944-45. Aimed to examine how maternal under-nutrition during specific gestational time windows may affect the subsequent life course.	3307 live birth singletons at 3 institutions in famine-exposed cities in Western Netherlands were identified. 1075 (751 cases and 324 sibling controls) not lost to follow-up.	No, apart from information on stage of pregnancy when famine may have been experience	Yes	Largely retrospective	One follow up in adulthood	Follow-up took place once between 2003-2005 at around age 59 years.	Telephone interview, questionnaires and clinical assessment	In offspring	~1000 offspring	No	450 K DNA methylation available on ~600 offspring	No	324 siblings of cases formed the control group for the study
Promotion of Breastfeeding Intervention Trial (PROBIT) (Belarus)	Cluster-randomised control trial initiated in Belarus to investigate the influence of a breastfeeding promotion intervention. Recruitment from 1996-1997 and mothers eligible if they intended to breastfeed and had given birth to a healthy singleton infant.	17,046 mother-infant pairs	No	Yes	Prospective though sometimes retrospective if participant missed one or more follow-up study visit.	From early post-partum to date. Data from age 16 years is currently being processed.	After post-partum survey, 6 further follow-ups took place before 12 months, one at 6.5 years and one at 11.5 years.	Polyclinic and home visits for observational assessment, interviews, parent and child-reported questionnaires and administered tests; data from routine check-ups abstracted from medical records, teacher-reported questionnaires	In offspring at age 11.5	No	No	No	No	No



background will generally be similar for siblings, comparing outcome differences in relation to discordant exposures within sibships effectively “matches” on family characteristics, providing a stronger means of controlling for certain confounding factors [11]. Such study designs have been used to show that gestational diabetes [54,55], gestational weight gain [56] and extreme BMI [57,58] are likely to be causally related to later offspring obesity and other metabolic outcomes [41], with findings being translated into long-term follow-up of participants in randomised controlled trials [59,60].

Again there are instances where this causal analysis method has provided contrasting results in different studies. For example, sibling studies have been used to explore whether the positive association between birth weight and later IQ [61] is causal. Whilst some studies suggest that birth weight differences within sibships are related to differences in intelligence, implying an intra-uterine effect [62,63], others show no evidence of association [64,65], arguing that the association observed in the population may be explained by factors such as family socioeconomic background.

It is important to bear in mind that, although sibling comparison estimates will not be influenced by unmeasured familial confounders, there are notable limitations to this study design which may explain the discrepancy in findings [66]. Such estimates are more severely biased by non-shared confounders than population-level comparisons [67] and are more sensitive to misclassification of the exposure and measurement error [66,68]. Use of a sibling comparison design also limits the population included, affecting power and demonstrating the need for large sample sizes to obtain robust causal evidence.

## 9. Mendelian randomization

Mendelian randomization (MR) is a method that utilises genetic variants robustly associated with modifiable exposures to infer causality [69]. The MR design is analogous to an RCT [70] and creates a similar scenario by exploiting Mendel's laws (segregation and independent assortment). Given these laws, at a population level genetic variants should not be associated with genetic or environmental confounding factors that can distort conventional observational studies. Analysing data according to genotype will therefore compare groups that differ by an on-average level of a modifiable exposure, but not by a myriad of behavioural, social and physiological variables that may confound observational associations [71,72]. In addition, in a genetic association the direction of causation is from genetic variation to the outcome, and not vice versa as disease processes do not alter germline genotype. Genetic variants are also subject to relatively little measurement error or bias and variants will generally be related to a modifiable exposure throughout life, avoiding attenuation by errors [73].

Where maternal genotype is taken to be a proxy for environmentally-modifiable exposures in pregnancy, this may provide unique insights into the causal nature of intra-uterine environment influences on later offspring outcomes [18]. For example, variation in *MTHFR* is associated with methylenetetrahydrofolate reductase activity and hence with circulating folate and homocysteine levels. Maternal *MTHFR* variants have been found to influence risk of neural tube defects (NTD) in offspring [74], implying a causal effect of low maternal folate. These findings are consistent with the results of RCTs of maternal folate supplementation which is associated with reduced risk of offspring congenital abnormalities [75,76]. In this example, the effect of maternal genotype on risk of NTD was greater than paternal or offspring genetic estimates, implying an independent maternal effect [74] which is consistent with the hypothesis that maternal folate intake is the exposure of importance.

Limitations of the Mendelian randomization approach have been outlined in detail elsewhere [77,78], and include low statistical power due to the small amount of variance in a trait explained by the genetic variant; population stratification, which may induce confounding when allele frequencies and disease risk differ according

to the genetic ancestry of populations within the study; and pleiotropy, where the genetic variant influences more than one post-transcriptional process and may affect the outcome via a pathway that is independent of the exposure. Methods may be implemented to address these limitations and extensions of the MR approach applied to avoid them [77,78].

## 10. Non-genetic instrumental variable analysis

The use of genotype in MR studies is an application of instrumental variable (IV) analysis [79,80], which may be used to obtain an estimate for the magnitude of a causal effect. An IV is a variable that is associated with the outcome only through its robust association with the exposure, and therefore an IV will typically not be associated with factors that confound the association of exposure and outcome. Examples of non-genetic instrumental variables include external factors which influence a population largely at random, such as the famine experienced in the Dutch Hunger Winter [39], climate conditions [81], or cigarette taxation [82]. However, in these cases the external or “exogenous” factor is generally rare or of small effect. Another non-genetic IV which is more commonplace is the phenotype of a family member in family-based studies, which may be used to proxy for own phenotype. For example, offspring anthropometry has been used as an IV for examining the causal effect of own anthropometry on mortality [83,84]. As offspring anthropometry is likely influenced by the same socio-economic, lifestyle and genetic confounders as parental anthropometry, this method is used primarily to deal with reverse causation, under the assumption that offspring's anthropometry will not be influenced by parent's illness.

## 11. Triangulation of causal inference methods

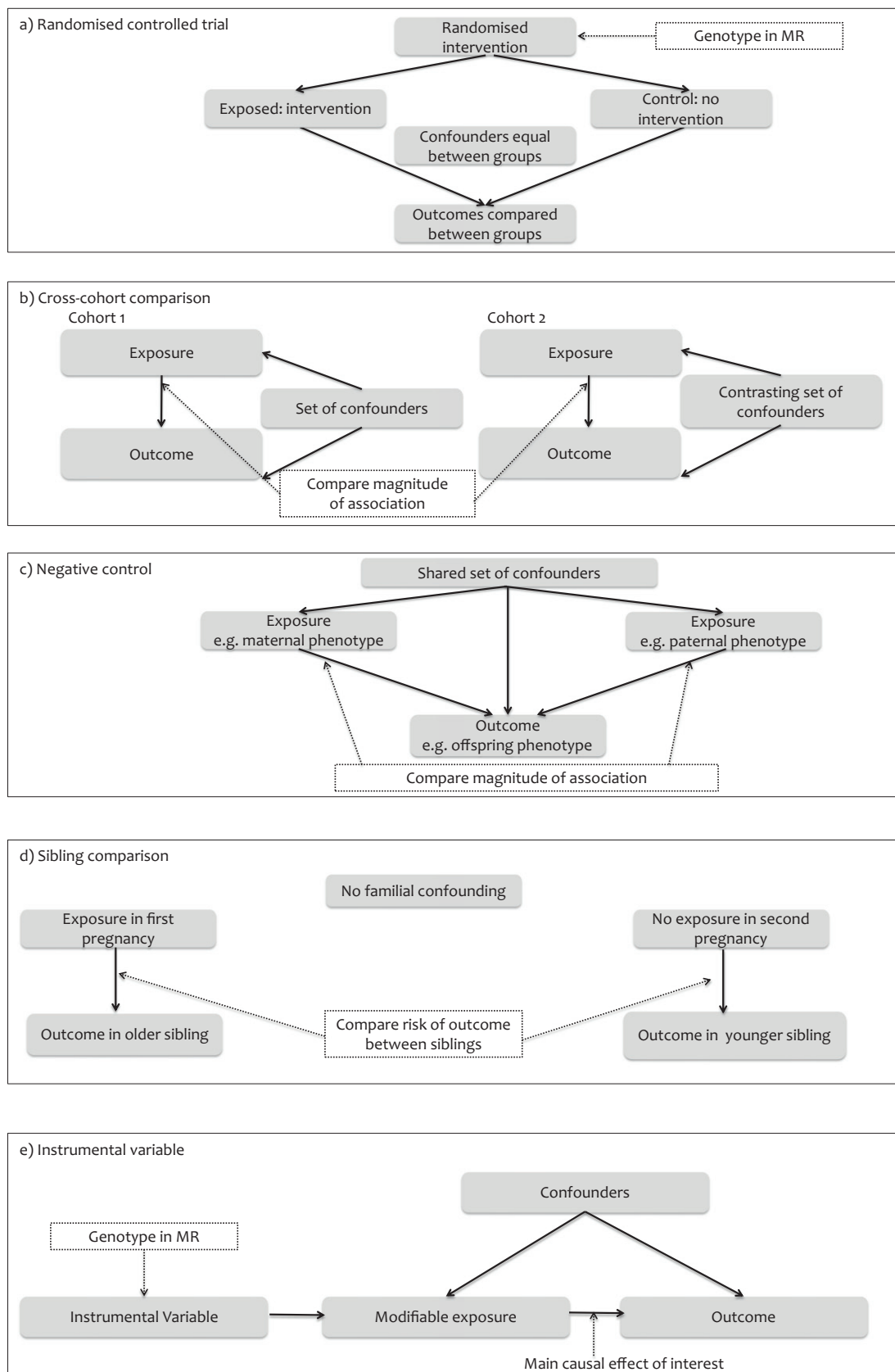
The above causal inference methods have different underlying assumptions, strengths and limitations and an integration of different approaches to the same research question may be used to improve the identification and estimation of causal effects through the “triangulation” of findings. This may be done under the supposition that independent biases are unlikely to lead to the same result across a range of methodological approaches. If causal effects are consistently estimated, the likelihood that they are unbiased is high. If they differ between the approaches, there is a further need to investigate whether the underlying assumptions for each approach have been violated. One example of triangulation has already been alluded to, which is the similarity in findings between a cross-cohort comparison study [34] and a randomised controlled trial investigating the effect of breastfeeding on offspring BMI, blood pressure and IQ [29–32]. Conventional multiple regression, parental comparison, between-sibling analyses, Mendelian randomization, non-genetic instrumental variable and RCT studies have all been consistent in their findings of a causal effect of maternal smoking in pregnancy on offspring birth weight [85]. “Triangulation” methods have also been exemplified within single studies where two complementary approaches have shown consensus on early life causal effects [45,54]. The approach of privileging a hypothesis which fits with the overall pattern of findings and knowledge across all informative sources is within the tradition of “inference to the best explanation” approaches to causal reasoning [86].

## 12. Consortia

One characteristic which all of the described causal inference methods have in common is that they are often underpowered and generally require large sample sizes. Therefore, as well as using triangulation, there is a need for independent replication of findings in order to avoid spurious conclusions in causal inference analysis. Cross-cohort analysis can improve power and statistical precision, and can provide high quality evidence on the causal effects of early life exposures on later health and disease. Collaboration is already evident in some instances, with the pooling and harmonising of data to

**Table 2**  
An outline of the causal inference approaches described in this review.

Causal inference approach	Approach summary	Biases addressed	Strengths	Potential limitations	Example	Schematic
Randomized control trial (RCT)	Subjects are randomly allocated to either exposure or control groups with assumption that there is no difference between the two groups except for the intervention they are receiving	Confounding, reverse causality, selection bias, loss-to-follow up bias (using intention-to-treat analysis), measurement error	Gold standard for estimating causal effects. Any effect is very likely to be causal if study has large number and trial is reliably performed	Generalizability may be questionable; impossible or unethical to randomize to certain exposures; can be expensive	Association between maternal breastfeeding behaviour and childhood outcomes. <a href="#">27–33</a>	a
Cross-cohort comparison	Associations are compared between two or more populations with markedly different confounding structures. If the observed association is causal, it should be present in both cohorts	Confounding, Selection bias	Exploring residual confounding. Reliable findings if cohorts are markedly different and have large sample size	Assumptions about different confounding structures may not be correct; need for variable harmonisation between cohorts	Association between breastfeeding and IQ, obesity and blood pressure in two cohorts. <a href="#">34</a>	b
Negative control approaches (approach used to rule out possible non-causal interpretation of results by performing study where hypothesised causal mechanism is removed; expected to produce null result)	Control exposure	Confounding	Provides information on the specificity of the exposure being tested, and whether the observed association is simply due to confounding by other associated factors and study biases	Assumption about the structure of confounding for negative control, some uncontrolled confounders	Association between maternal use of folic acid supplements (and comparison with fish oil) and risk of autism in children. <a href="#">37</a>	c
	Control outcome	Confounding	Provides information on the specificity of the outcome being tested, and whether the observed association is simply due to confounding by other associated factors and study biases	Assumption about the structure of confounding for negative control, some uncontrolled confounders	Association between use of folic acid supplements in pregnancy and severe language delay in children (and comparison with motor skills). <a href="#">126</a>	
	Natural experiment	Confounding, reverse causality	Can study settings which would be impractical or unethical to produce by researchers	Selection bias as exposure cannot be manipulated by researcher, some unobserved confounding may remain	Association between imposed nutritional deprivation during early pregnancy on a number of health outcomes, compared with those who experienced famine at other stages in pregnancy <a href="#">39</a>	
	Parental comparison	Confounding	Improves causal inference of intrauterine effect if exposures are measured in both parents at same time in pregnancy, and non-paternity is taken into account for phenotypic traits.	Assumption that paternal exposures share same confounding structure as maternal exposure may not be correct; where parental associations are similar magnitude this may be due to offsetting paternal pathways rather than shared confounding	Association between parental smoking and birth weight. <a href="#">18</a>	
Sibling comparison	Compares outcomes when siblings are discordant for an exposure. If causal then there will evidence of a difference in outcome in relation to discordant exposure levels within sibships	Confounding	Improves causal inference of intrauterine exposures. Controls for familial background and related confounding factors	Assumes a stable family environment; confounding by factors not perfectly shared by siblings; potential for measurement error of exposure; limited power	Effect of maternal gestational diabetes on height, weight and BMI of offspring and their siblings. <a href="#">55</a>	d
Mendelian randomization (MR)	MR is the use of a genetic variant robustly associated with an exposure/risk factor of interest as an instrumental variables to test and estimate the causal effect of that exposure/risk factor with a disease or health related outcome.	Confounding, reverse causality, selection bias, measurement errors, generalizability	Genetic instruments are not subject to confounding from environmental or lifestyle factor, are not influenced by the outcome, do not change over time and are measured with high accuracy	Low power, lack of instrumentation, pleiotropy and linkage disequilibrium, population stratification, non-linear associations, developmental canalisation	Association between maternal <i>MTHFR</i> variants and risk of neural tube defects (NTD) in offspring. <a href="#">74</a>	a, e
Non-genetic instrumental variable (IV)	Similar to MR except that it uses a phenotype rather than a genetic variable as an IV for obtaining and estimating causal effects.	Sometimes confounding, reverse causality	IV is associated with the outcome only through association with exposure and will typically not be associated with confounding factors.	True exogenous factors are generally rare or of small effect. When exposure in one family member is used as IV for exposure in another family member, residual confounding is likely.	Association between own BMI and mortality using son's BMI as an IV. <a href="#">83</a>	e



**Fig. 1.** Schematic diagrams outlining the main causal inference methods. MR = Mendelian randomization.

address research questions on environmental exposures [87,88] and genetic associations [89–91]. There are several examples of birth cohort collaborations, including CHICOS (<http://www.chicosproject.eu/the->

[project/management/](http://www.chicosproject.eu/the-project/management/)), EAGLE (<http://www.copsac.com/content/eagle-consortium/>), EGG (<http://egg-consortium.org/>) and ENRIECO (<http://www.enrieco.org/>) [92] and a tool for accessing information



on each birth cohort has been made available at <http://www.birthcohorts.net/> [93]. Also of importance in this field is the inclusion of birth cohort studies from low- and middle-income countries [94, 95], where variation in environmental exposures, health outcomes and confounding structures may be used to improve causal inference [34]. To date, collaborations have been used to replicate findings from causal inference analysis in multiple cohorts, including parental comparisons [96] and Mendelian randomization [97].

### 13. New data

As has already been mentioned, an attribute of many birth cohorts is their biological sampling which includes the collection of blood, urine and hair samples. New technologies permit genotyping and profiling of methylation, metabolites and biomarkers of environmental exposures, and open up new avenues for exploring underlying causal pathways. Of particular value is the collection of serial samples from the same individuals in some birth cohorts, which allows assessment of change in molecular measures over time.

#### 13.1. Genetics

As shown in Table 1, many birth cohorts now have genome-wide data available on a large number of individuals, including both offspring and parents. These may be used in Genome Wide Association Studies (GWAS), where associations between a wide range of phenotypes and genetic variants across the genome are determined in a hypothesis-free approach. More recently, an innovative method utilising genome-wide data in mothers and offspring has been developed which allows the delineation of maternal-specific influences on offspring outcomes [98]. The ability to identify many robust genotype–phenotype associations is of merit for Mendelian randomization analysis which has classically involved the use of a single variant to proxy for a particular modifiable exposure. GWAS has uncovered a host of genetic variants which explain an increasing proportion of the variance in a trait and may act as a stronger instrument for improving the precision of causal estimates [99]. The use of genetic scores, created by adding up the total number of risk alleles a person has, offers particular promise in this regard [100,101]. However, as the function of a variant identified

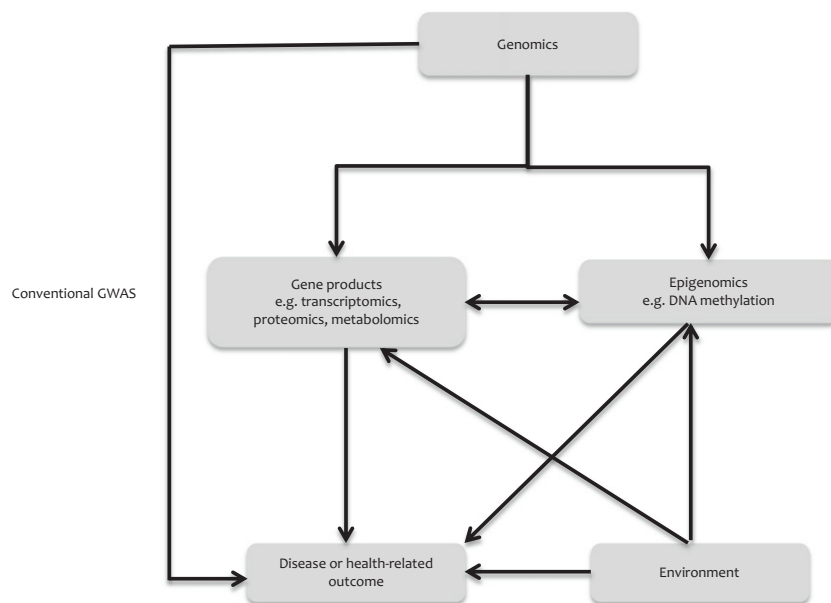
in GWAS is often unknown, the assumption that it will only influence the outcome through its direct effect on the exposure is difficult to assert. Nonetheless strategies exist for assessing potential pleiotropy [72,99].

Building on the success of GWAS and the availability of cost effective and robust technologies is the use of “omics” within population health science. This is largely concerned with understanding how gene regulatory mechanisms or gene products interact with the environment to influence health-related outcomes and is useful for investigating the molecular pathways that may underpin causal effects. Of particular utility are large-scale epigenetic and metabolomic scans for formulating novel hypotheses on biological processes. However, in contrast to germ-line genetic variation, epigenetic and metabolomic signatures are largely phenotypic, and are subject to the same problems of confounding and reverse causation which afflict conventional epidemiology [53,102,103] (Fig. 2). The extension of causal inference approaches is therefore of particular relevance in determining causal associations between “omic” markers and a range of exposures and outcomes [77].

### 14. Epigenetics

Epigenetic mechanisms are involved in regulating gene activity which creates phenotypic variation without altering the underlying DNA code. Epigenetics is a potentially major mechanism by which environmental factors can affect physiological function and disease risk. In particular, DNA methylation has become increasingly integrated into population-based studies as a potential modifiable indicator of the underlying biological changes.

Epidemiological approaches can be used to identify whether epigenetic processes are involved in mediating the association between various risk factors and common complex disease [104,105]. Longitudinal cohort studies that make use of multiple time points are useful for investigating how the epigenome changes over time, as a result of varying exposures, and how this contributes to disease development [106]. In particular, there is considerable interest in the role of epigenetic mechanisms in DOHaD as epigenetic states are often established in early development [107–109]. This makes birth cohorts with sample collection from pregnant women and offspring at birth of particular value for providing insights into the temporal relationship between early life



**Fig. 2.** Diagram outlining the interplay between genomics, other “omics” and environmental factors in relation to disease or health-related outcomes. GWAS = Genome-wide association study.

exposures and epigenetic changes [110–112], which may then predict later health-related outcomes [113–115].

It is important to bear in mind that epigenetic profiles can be influenced by technical or genetic factors, cellular and tissue heterogeneity, time-varying artefacts and stochastic changes. These sources of noise threaten the detection of biological signals and the ability to infer causality from associations [53,103]. Careful study design, data collection and control of sources of variability are therefore required, as are methods which will contribute to the identification of predictive epigenetic biomarkers and modifiable targets for intervention [102,116,117].

Many of the approaches already listed to address causality in conventional epidemiological settings can also be used to interrogate causality in associations involving epigenetic changes. For example, maternal smoking in pregnancy has been shown to be associated with DNA methylation in newborns and the finding of no paternal associations highlights the prominent intra-uterine influence of maternal smoking on offspring DNA methylation at birth [118] and at later ages in the offspring [119]. Mendelian randomization analysis has also been used in the context of epigenetic epidemiology to investigate the causal effect of maternal red blood cell folate on genome-wide methylation in infant cord blood [120], using the previously described *MTHFR* genotype as an instrument. However, further work is needed to investigate whether the identified methylation changes mediate the influence of intra-uterine exposures on developmental outcomes, for example in a “two-step Mendelian randomization” framework [77,102,116,117].

## 15. Metabolomics

Metabolomics is a technology involving the measurement of metabolites which likely act as intermediates in biological pathways. An advantage of using metabolites as intermediate phenotypes is that they are more proximal to biological pathways than downstream phenotypes or clinical endpoints [121], boosting the statistical power to detect associations [122,123]. Metabolites are also useful in birth cohorts when disease endpoints have not yet been reached.

However, as metabolites are influenced by both genetic and environmental factors and by disease processes, they too are prone to the limitations of observational study. Once an association between a metabolite and a trait has been observed, the next challenge is to distinguish causal effects, with potential implications for clinical outcomes and disease pathogenesis, from non-causal associations, which may have potential implications for biomarker discovery [12,124]. Different statistical methodologies may be used to construct a causal framework involving metabolites, and to dissect causal relationships [125]. This framework also suggests the usefulness of “triangulating” causal inference methods in the domain of high-dimensional molecular data as an exploratory tool to infer causal relationships.

## 16. Summary

This review has outlined a suite of causal inference methods including cross-cohort comparisons, negative control studies, sibling studies, Mendelian randomization analysis and instrumental variable techniques. These methods make use of the wide range of data available in epidemiological birth cohorts in order to establish causal links between early life influences and a range of developmental and health outcomes. Such methods have often been shown to produce the same conclusions regarding causal effects as randomised controlled trials, which are not always feasible or ethical, and may be used to inform on interventions. Strengthening causal inference is also an important step in “omics” research for distinguishing causal molecular pathways that may underpin causal effects of early life exposures on complex traits and diseases.

The methods for causal inference described enhance capability to interpret conventional observational associations, though some discrepancies in findings between studies highlight their limitations, in particular their lack of power in small samples. An integration or

“triangulation” of different approaches to the same research question may be used to improve the identification and estimation of causal effects in observational data. In addition, cross-cohort analysis and the independent replication of findings can improve power and statistical precision and provide more high-quality evidence for causality. This may be enabled with collaboration amongst different birth cohorts and the dissemination and harmonisation of techniques through the established consortia.

## Conflicts of interest statement

None declared.

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