Born in Bradford Data Dictionary

Subcohort indicators: who has what data

Contents

Background

This document is a data dictionary for Subcohort indicators: who has what data. It describes 76 variables from 3 sources. This document was built from Born in Bradford database version BUILD-JAN2018.

Born in Bradford

Born in Bradford is a longitudinal multi-ethnic birth cohort study aiming to examine the impact of environmental, psychological and genetic factors on maternal and child health and wellbeing. Bradford is a city in the North of England with high levels of socio-economic deprivation and ethnic diversity. Women were recruited at the Bradford Royal Infirmary at 26-28 weeks gestation. For those consenting, a baseline questionnaire was completed. The full BiB cohort recruited 12,453 women and 3353 of their partners across 13,776 pregnancies and 13,858 children between 2007 and 2010. The cohort is broadly characteristic of the city's maternal population. Mean age of the mothers at study recruitment was 27 years old. Researchers are looking at the links between the circumstances of a child's birth, the context in which they grow up, their health and well-being and their educational progress. Ethical approval for the data collection was granted by Bradford Research Ethics Committee (Ref 07/H1302/112).

Study identifiers

Study identifiers are standardised across Born in Bradford data sources to enable linking of data from different sources.

Variable	Variable Label	Details
ChildID	BiB Child ID	Unique ID assigned to each child at birth. Where birth outcome is unknown for a given pregnancy, ChlidID will be blank and there is no child recruited to the study from that pregnancy. Use MotherID with ChildID to link siblings together. Note that twins have separate ChildIDs but the same PregnancyID.
FatherID	BiB Father ID	Unique ID assigned to partners post-recruitment. Use FatherID with PregnancyID to link fathers across pregnancies. Where FatherID matches across two PregnancyIDs, but those PregnancyIDs are associated with different MotherIDs, this is a father with two separate pregnancies in the cohort with different mothers. Likewise, where MotherID matches across two PregnancyIDs, but those PregnancyIDs are associated with different FatherIDs, this is a mother with two separate pregnancies in the cohort with different fathers.
MotherID	BiB Mother ID	Unique ID assigned to each mother post-recruitment. MotherID should be used when looking for pregnancies or children associated with the same mother. Data collected at pregnancy level will duplicate for MotherIDs that are in the study for more than one pregnancy.
PregnancyID	BiB Pregnancy ID	Unique ID assigned to each mother at recruitment. It is named PregnancyID because a mother can enrol for more than one pregnancy. If a mother returns to enrol for a second or third pregnancy, she is assigned a new PregnancyID. Children and partners from that pregnancy can be linked to the mother by the PregnancyID

Subcohort: Child

Database ID for source: `subcch`

This source is measured at the **child** level. It contains data from 13858 children with one observation per child. There are 49 variables with a total of 13858 observations.

Description

Pre-defined subcohorts at Child level.

Variable	Variable Label	Details
has_all1qs	Has ALL IN 12m questionnaire	Derived: Categorical value
		────────────
		Subcohort indicator: has ALL IN 12 month questionnaire
		────────────
		2553 non-missing values
		────────────
		Coding [`has`]: 1 = has
has_all2qs	Has ALL IN 24m questionnaire	Derived: Categorical value
		────────────
		Subcohort indicator: has ALL IN 24 month questionnaire
		────────────
		2067 non-missing values
		────────────
		Coding [`has`]: 1 = has
has_allinc	Child is in ALL IN study	Derived: Categorical value
		────────────
		Subcohort indicator: child is in ALL IN study
		────────────
		2562 non-missing values
		────────────
		Coding [`has`]: 1 = has
has_b12tab	Has BiB1000 12m questionnaire	Derived: Categorical value
		────────────
		Subcohort indicator: has BiB1000 12 month questionnaire
		────────────
		1313 non-missing values
		────────────
		Coding [`has`]: 1 = has

Variable	Variable Label	Details
has_b18tab	Has: BiB 1000 Questionnaire: bib18_maintable	Derived: Categorical value —————— Has data from source: BiB 1000 Questionnaire: bib18_maintable —————— 1293 non-missing values —————— Coding [has]: 1 = has
has_b24tab	Has: BiB 1000 Questionnaire: bib24_maintable	Derived: Categorical value —————— Has data from source: BiB 1000 Questionnaire: bib24_maintable —————— 1228 non-missing values —————— Coding [has]: 1 = has
has_b36tab	Has: BiB 1000 Questionnaire: bib36_maintable	Derived: Categorical value —————— Has data from source: BiB 1000 Questionnaire: bib36_maintable —————— 1232 non-missing values —————— Coding [has]: 1 = has
has_b6mtab	Has BiB1000 6m questionnaire	Derived: Categorical value —————— Subcohort indicator: has BiB1000 6 month questionnaire —————— 1336 non-missing values —————— Coding [has]: 1 = has
has_bib12n	Has: BiB1000 12 month child nutrients intake	Derived: Categorical value —————— Has data from source: BiB1000 12 month child nutrients intake —————— 1262 non-missing values —————— Coding [has]: 1 = has

Variable	Variable Label	Details
has_bib18n	Has: BiB1000 18 month child nutrients intake	Derived: Categorical value
		——————
		Has data from source: BiB1000 18 month child nutrients intake
		——————
		1257 non-missing values
		——————
		Coding [has]: 1 = has
has_bib1kc	Child was recruited to BiB 1000	Derived: Categorical value
		——————
		Subcohort indicator: Child was recruited to BiB 1000
		——————
		1763 non-missing values
		——————
		Coding [has]: 1 = has
has_cgrchs	Has routine child growth data	Derived: Categorical value
		——————
		Subcohort indicator: has routine child growth data
		——————
		12515 non-missing values
		——————
		Coding [has]: 1 = has
has_chab12	Has: BiB 1000 12m anthropometry	Derived: Categorical value
		——————
		Has data from source: BiB 1000 12m anthropometry
		——————
		1233 non-missing values
		——————
		Coding [has]: 1 = has
has_chab18	Has: BiB 1000 18m anthropometry	Derived: Categorical value
		——————
		Has data from source: BiB 1000 18m anthropometry
		——————
		1149 non-missing values
		——————
		Coding [has]: 1 = has

Variable	Variable Label	Details
has_chab1k	Has: BiB 1000 anthropometry	Derived: Categorical value
		Has data from source: BiB 1000 anthropometry
		1275 non-missing values
		Coding [has]: 1 = has
has_chab24	Has: BiB 1000 24m anthropometry	Derived: Categorical value
		Has data from source: BiB 1000 24m anthropometry
		908 non-missing values
		Coding [has]: 1 = has
has_chab36	Has: BiB 1000 36m anthropometry	Derived: Categorical value
		Has data from source: BiB 1000 36m anthropometry
		998 non-missing values
		Coding [has]: 1 = has
has_chab6m	Has: BiB 1000 6m anthropometry	Derived: Categorical value
		Has data from source: BiB 1000 6m anthropometry
		1299 non-missing values
		Coding [has]: 1 = has
has_chachr	Has: Child Health Record Anthropometry	Derived: Categorical value
		Has data from source: Child Health Record Anthropometry
		12042 non-missing values
		Coding [has]: 1 = has

Variable	Variable Label	Details
has_chaecl	Has: eClipse anthropometry	Derived: Categorical value ——————— Has data from source: eClipse anthropometry ——————— 12684 non-missing values ——————— Coding [has]: 1 = has
has_chasch	Has: Child Anthropometry: school measures	Derived: Categorical value ——————— Has data from source: Child Anthropometry: school measures ——————— 6965 non-missing values ——————— Coding [has]: 1 = has
has_chgb12	Has: BiB 1000 12m Growth	Derived: Categorical value ——————— Has data from source: BiB 1000 12m Growth ——————— 1280 non-missing values ——————— Coding [has]: 1 = has
has_chgb18	Has: BiB 1000 18m Growth	Derived: Categorical value ——————— Has data from source: BiB 1000 18m Growth ——————— 1245 non-missing values ——————— Coding [has]: 1 = has
has_chgb1k	Has: BiB 1000 Growth	Derived: Categorical value ——————— Has data from source: BiB 1000 Growth ——————— 1285 non-missing values ——————— Coding [has]: 1 = has

Variable	Variable Label	Details
has_chgb24	Has: BiB 1000 24m Growth	Derived: Categorical value
		————————
		Has data from source: BiB 1000 24m Growth
		————————
		1132 non-missing values
		————————
		Coding [has]: 1 = has
has_chgb36	Has: BiB 1000 36m Growth	Derived: Categorical value
		————————
		Has data from source: BiB 1000 36m Growth
		————————
		1153 non-missing values
		————————
		Coding [has]: 1 = has
has_chgb6m	Has: BiB 1000 6m Growth	Derived: Categorical value
		————————
		Has data from source: BiB 1000 6m Growth
		————————
		1321 non-missing values
		————————
		Coding [has]: 1 = has
has_chgchr	Has: Child Health Record Growth	Derived: Categorical value
		————————
		Has data from source: Child Health Record Growth
		————————
		12026 non-missing values
		————————
		Coding [has]: 1 = has
has_chgcom	Has: Child Growth Combined Sources	Derived: Categorical value
		————————
		Has data from source: Child Growth Combined Sources
		————————
		13805 non-missing values
		————————
		Coding [has]: 1 = has

Variable	Variable Label	Details
has_chgecl	Has: eClipse growth	Derived: Categorical value
		——————
		Has data from source: eClipse growth
		——————
		13478 non-missing values
		——————
		Coding [has]: 1 = has
has_chgncm	Has: NCMP Growth	Derived: Categorical value
		——————
		Has data from source: NCMP Growth
		——————
		8237 non-missing values
		——————
		Coding [has]: 1 = has
has_chgrgp	Has: Child Growth from GP Record	Derived: Categorical value
		——————
		Has data from source: Child Growth from GP Record
		——————
		10623 non-missing values
		——————
		Coding [has]: 1 = has
has_crdbld	Has baby cord bloods data	Derived: Categorical value
		——————
		Subcohort indicator: has baby cord bloods data (e.g. leptins)
		——————
		7910 non-missing values
		——————
		Coding [has]: 1 = has
has_dnamch	Has: DNA methylation: Child linkage	Administrative: Categorical value
		——————
		Has data from source: DNA methylation: Child linkage
		——————
		951 non-missing values
		——————
		Coding [has]: 1 = has

Variable	Variable Label	Details
has_eclbby	Has eClipse baby data	Derived: Categorical value
		————————
		Subcohort indicator: has eClipse baby data
		————————
		13525 non-missing values
		————————
		Coding [has]: 1 = has
has_edcont	Has: Local Authority Education Record Contextual Data	Derived: Categorical value
		————————
		Has data from source: Local Authority Education Record Contextual Data
		————————
		11711 non-missing values
		————————
		Coding [has]: 1 = has
has_edks11	Has: Key Stage 1 Assessment: Pre 2016	Derived: Categorical value
		————————
		Has data from source: Key Stage 1 Assessment: Pre 2016
		————————
		3622 non-missing values
		————————
		Coding [has]: 1 = has
has_edks12	Has: Key Stage 1 Assessment: 2016 Plus	Derived: Categorical value
		————————
		Has data from source: Key Stage 1 Assessment: 2016 Plus
		————————
		7262 non-missing values
		————————
		Coding [has]: 1 = has
has_edphon	Has: Year 1 Phonics Assessment	Derived: Categorical value
		————————
		Has data from source: Year 1 Phonics Assessment
		————————
		11081 non-missing values
		————————
		Coding [has]: 1 = has

Variable	Variable Label	Details
has_eyfsp1	Has: Early Years Foundation Stage Profile: pre 2013	Derived: Categorical value
		Has data from source: Early Years Foundation Stage Profile: pre 2013
		705 non-missing values
		Coding [has]: 1 = has
has_eyfsp2	Has: Early Years Foundation Stage Profile: 2013 Plus	Derived: Categorical value
		Has data from source: Early Years Foundation Stage Profile: 2013 Plus
		10598 non-missing values
		Coding [has]: 1 = has
has_helix	Child is HELIX participant	Derived: Categorical value
		Subcohort indicator: Child is HELIX participant
		233 non-missing values
		Coding [has]: 1 = has
has_medqst	Has MeDALL questionnaire	Derived: Categorical value
		Subcohort indicator: has MeDALL questonnaire
		2594 non-missing values
		Coding [has]: 1 = has
has_medskp	Has MeDALL skin prick test	Derived: Categorical value
		Subcohort indicator: has MeDALL skin prick test
		2269 non-missing values
		Coding [has]: 1 = has

Variable	Variable Label	Details
has_medspc	Has MeDALL skin prick QC	Derived: Categorical value
		————————
		Subcohort indicator: has MeDALL skin prick test QC
		————————
		228 non-missing values
		————————
		Coding [has]: 1 = has
has_prninf	Has: Maternal records abstraction: BiB infant info	Derived: Categorical value
		————————
		Has data from source: Maternal records abstraction: BiB infant info
		————————
		11010 non-missing values
		————————
		Coding [has]: 1 = has
has_res6mc	Has: Six monthly residential information: Child	Derived: Categorical value
		————————
		Has data from source: Six monthly residential information: Child
		————————
		13856 non-missing values
		————————
		Coding [has]: 1 = has
has_schlbp	Has: School Measures: Child Blood Pressure	Derived: Categorical value
		————————
		Has data from source: School Measures: Child Blood Pressure
		————————
		6900 non-missing values
		————————
		Coding [has]: 1 = has
has_yhcarl	Has: Yorkshire and Humber Congenital Anomalies Register	Derived: Categorical value
		————————
		Has data from source: Yorkshire and Humber Congenital Anomalies Register
		————————
		510 non-missing values
		————————
		Coding [has]: 1 = has

Subcohort: Mother

Database ID for source: `subcmo`

This source is measured at the **mother** level. It contains data from 12453 mothers with one observation per mother. There are 3 variables with a total of 12453 observations.

Description

Pre-defined subcohorts at Mother level.

Variable	Variable Label	Details
has_prnmum	Has: Mother data from pregnancy notes extraction	Derived: Categorical value —————— Has data from source: Mother data from pregnancy notes extraction —————— 10142 non-missing values —————— Coding [has]: 1 = has
has_prnpbi	Has: Maternal records abstraction: Pre-BiB infant info	Derived: Categorical value —————— Has data from source: Maternal records abstraction: Pre-BiB infant info —————— 5602 non-missing values —————— Coding [has]: 1 = has
has_prnpbp	Has: Maternal records abstraction: Pre BiB Pregnancy	Derived: Categorical value —————— Has data from source: Maternal records abstraction: Pre BiB Pregnancy —————— 5611 non-missing values —————— Coding [has]: 1 = has

Subcohort: Pregnancy

Database ID for source: `subcpr`

This source is measured at the **pregnancy** level. It contains data from 13776 pregnancies with one observation per pregnancy. There are 24 variables with a total of 13776 observations.

Description

Pre-defined subcohorts at Pregnancy level.

Variable	Variable Label	Details
has_dnammp	Has: Mother pregnancy bloods DNA methylation linkage	Administrative: Categorical value
		⸻
		Has data from source: Mother pregnancy bloods DNA methylation linkage
		⸻
		934 non-missing values
		⸻
		Coding [`has`]: 1 = has
has_eclprg	Has eClipse pregnancy data	Derived: Categorical value
		⸻
		Subcohort indicator: has eClipse pregnancy data
		⸻
		13361 non-missing values
		⸻
		Coding [`has`]: 1 = has
has_fbqall	Has: Father baseline questionnaire	Derived: Categorical value
		⸻
		Has data from source: Father baseline questionnaire
		⸻
		3387 non-missing values
		⸻
		Coding [`has`]: 1 = has
has_matbld	Has maternal bloods data	Derived: Categorical value
		⸻
		Subcohort indicator: has maternal baseline bloods data
		⸻
		11625 non-missing values
		⸻
		Coding [`has`]: 1 = has

Variable	Variable Label	Details
has_matbvd	Has maternal vitamin D	Derived: Categorical value
		Subcohort indicator: has maternal baseline vitamin D
		1498 non-missing values
		Coding [has]: 1 = has
has_matuss	Has: Ultrasound scans	Derived: Categorical value
		Has data from source: Ultrasound scans
		13248 non-missing values
		Coding [has]: 1 = has
has_mbagtt	Has maternal GTT data	Derived: Categorical value
		Subcohort indicator: has maternal baseline glucose tolerance test data
		12331 non-missing values
		Coding [has]: 1 = has
has_mbqall	Has baseline questionnaire	Derived: Categorical value
		Subcohort indicator: has maternal baseline questionnaire
		11395 non-missing values
		Coding [has]: 1 = has
has_mbqp23	Has baseline questionnaire phase 2 or 3	Derived: Categorical value
		Subcohort indicator: has maternal baseline questionnaire from phases 2 or 3
		9619 non-missing values
		Coding [has]: 1 = has

Variable	Variable Label	Details
has_mbqph1	Has: Maternal Baseline Questionnaire (Phase 1)	Administrative: Categorical value —————— Has data from source: Maternal Baseline Questionnaire (Phase 1) —————— 1571 non-missing values —————— Coding [has]: 1 = has
has_mdndvi	Has: MeDALL residential NDVI and green space	Derived: Categorical value —————— Has data from source: MeDALL residential NDVI and green space —————— 2451 non-missing values —————— Coding [has]: 1 = has
has_mdngst	Has: MeDALL Neighbourhood Green Space Tool	Derived: Categorical value —————— Has data from source: MeDALL Neighbourhood Green Space Tool —————— 821 non-missing values —————— Coding [has]: 1 = has
has_metnmr	Has: NMR metabolomics pregnancy samples	Derived: Categorical value —————— Has data from source: NMR metabolomics pregnancy samples —————— 11479 non-missing values —————— Coding [has]: 1 = has
has_mgrnsp	Has: MeDALL Green Space Questionnaire	Derived: Categorical value —————— Has data from source: MeDALL Green Space Questionnaire —————— 821 non-missing values —————— Coding [has]: 1 = has

Variable	Variable Label	Details
has_pregbp	Has: Pregnancy blood pressure	Derived: Categorical value
		Has data from source: Pregnancy blood pressure
		10534 non-missing values
		Coding [has]: 1 = has
has_prnadm	Has: Maternal records abstraction: Admissions info	Derived: Categorical value
		Has data from source: Maternal records abstraction: Admissions info
		855 non-missing values
		Coding [has]: 1 = has
has_prnbpl	Has: Maternal records: Labour blood pressure	Derived: Categorical value
		Has data from source: Maternal records: Labour blood pressure
		8523 non-missing values
		Coding [has]: 1 = has
has_prnbpo	Has: Maternal records: Postpartum blood pressure	Derived: Categorical value
		Has data from source: Maternal records: Postpartum blood pressure
		10024 non-missing values
		Coding [has]: 1 = has
has_prnbpp	Has: Maternal records: Pregnancy blood pressure	Derived: Categorical value
		Has data from source: Maternal records: Pregnancy blood pressure
		10895 non-missing values
		Coding [has]: 1 = has

Variable	Variable Label	Details
has_prnmed	Has: Maternal records: meds during BiB pregnancy	Derived: Categorical value ———————— Has data from source: Maternal records: meds during BiB pregnancy ———————— 3773 non-missing values ———————— Coding [has]: 1 = has
has_prnoed	Has: Maternal records abstraction: Oedema	Derived: Categorical value ———————— Has data from source: Maternal records abstraction: Oedema ———————— 3256 non-missing values ———————— Coding [has]: 1 = has
has_prnprg	Has: Pregnancy third trimester weight	Derived: Categorical value ———————— Has data from source: Pregnancy third trimester weight ———————— 10939 non-missing values ———————— Coding [has]: 1 = has
has_prnprt	Has: Maternal records abstraction: Proteinurea	Administrative: Categorical value ———————— Has data from source: Maternal records abstraction: Proteinurea ———————— 7375 non-missing values ———————— Coding [has]: 1 = has
has_renalu	Has: Fetal renal ultrasound study	Derived: Categorical value ———————— Has data from source: Fetal renal ultrasound study ———————— 1803 non-missing values ———————— Coding [has]: 1 = has