Session 5.2: Missing data inputation

Spatial and Spatio-Temporal Bayesian Models with `R-INLA`, Imperial College

Learning Objectives

After this session you should be able to:

- Appreciate the importance of thinking about why data are missing, and stating your modelling assumptions

- Understand the disadvantages of complete case analysis

- Learn about how Bayesian methods can be used as 'statistically principled' for handling missing data

- Be able to run the above models in R-INLA

The topics treated in this lecture are covered in Chapter 12 of Gómez-Rubio (2020).

Why we care about missing data

- Missing data are common!

- Usually inadequately handled in both observational and experimental research

- For example, Wood, White, and Thompson (2004) reviewed 71 recently published BMJ, JAMA, Lancet and NEJM papers
  - 89% had partly missing outcome data
  - In 37 trials with repeated outcome measures, 46% performed complete case analysis
  - Only 21% reported sensitivity analysis

- Sterne, White, Carlin, Spratt, Royston, Kenward, Wood, and Carpenter (2009) reviewed articles using Multiple Imputation in BMJ, JAMA, Lancet and NEJM from 2002 to 2007
  - 59 articles found, with use doubling over 6 year period
  - However, the reporting was almost always inadequate

Outline

1. How do missing data arise?

2. Example: children height and weight

3. Bayesian imputation

4. Extending the model

How do missing data arise?
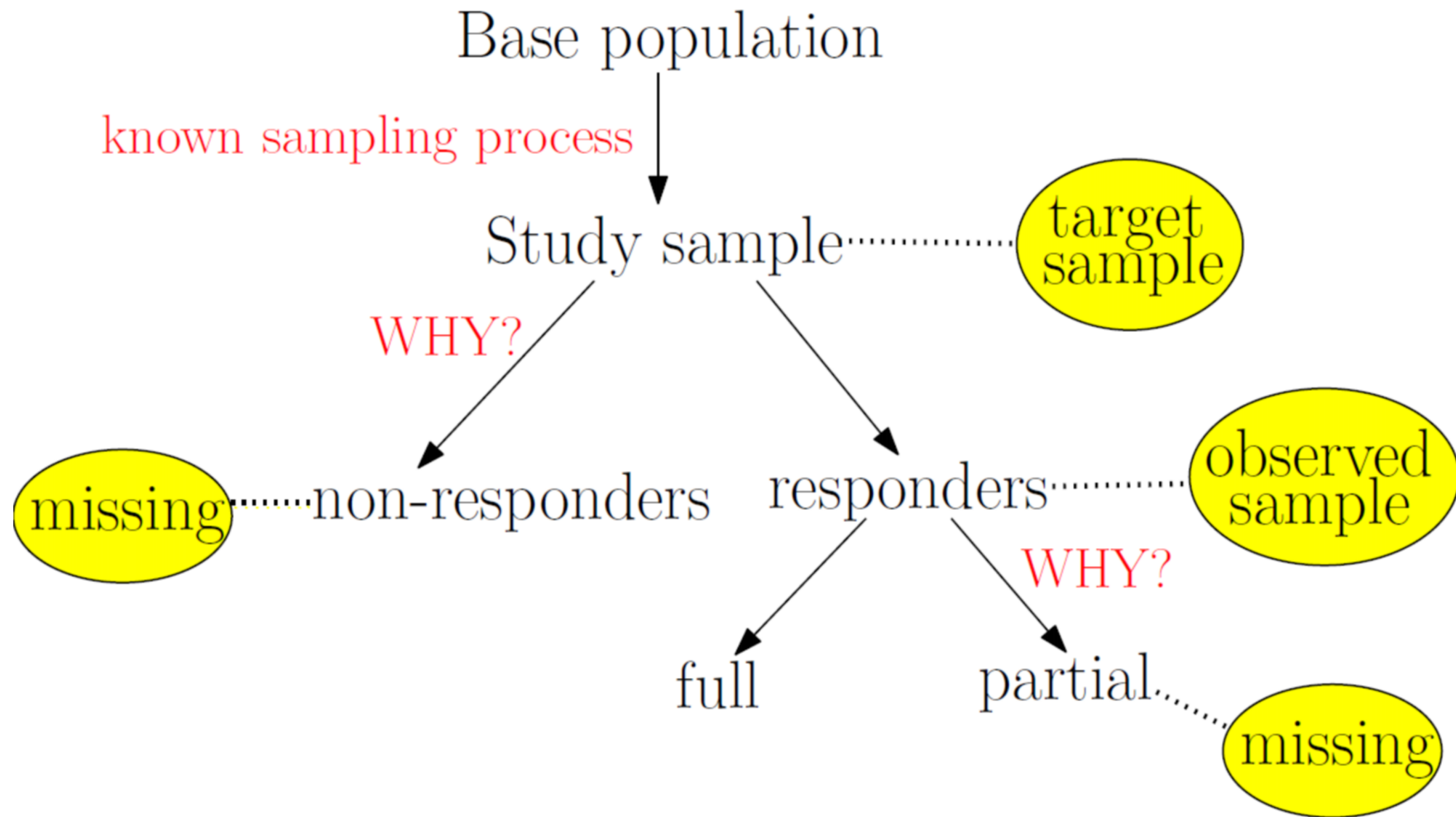
- There are three types of missing data, depending on why the missingness arise. Let's define m_i as the variable indicating if the $i - th$ observation is missing

$$m_i \sim \text{Bernoulli}(p_i)$$

1. Missing completely at random (MCAR) occurs when the missing data are independent from the observed or unobserved data:

$$\text{logit}(p_i) = \theta_0$$

This means that the missing values can be ignored and the analysis can be conducted as usual.

2. Missing at random (MAR) occurs when the missing data depends ONLY on the observed data:

$$\text{logit}(p_i) = \theta_0 + \mathbf{x_i}\theta_1$$

In this case, this can be introduced into the model so that missing observations are imputed as part of the model fitting.

2. Missing at random (MAR) occurs when the missing data depends ONLY on the observed data:

$$\text{logit}(p_i) = \theta_0 + \mathbf{x_i}\theta_1$$

In this case, this can be introduced into the model so that missing observations are imputed as part of the model fitting.

3. Missing non at random (MNAR) occurs when the missing data depends on both the observed and missing data:

$$\text{logit}(p_i) = \theta_0 + \mathbf{x_i}\theta_1 + \lambda\mathbf{y_i}$$

This scenario is difficult to tackle since there is no information about the missingness mechanism and the missing data.

Missing response or missing covariates

- Additionally, it is crucial to distinguish between missing values in the response and in the covariates.

- When the missingness is in the response (and it is MCAR or MAR), these can naturally be predicted as the distribution of the response values is determined by the statistical model to be fit (posterior predictive distribution in the Bayesian approach)

- Missingness in the covariats requires additional steps:

  – a model needs to be specified on the covariate (imputation model) if the missingness mechanism is MCAR or MAR

  – an additional model of missingness needs to be specified if the mechanism is MNAR

  – Here we will consider only missing values in the response

  – `R-INLA` reguires a certain degree of complexity to deal with missing values in covariates, if you are interested in learning more look at Gómez-Rubio, Cameletti, and Blangiardo (2022)

Example: height and weight of children

Example: height and weight of children

- Information of 10,030 children measured within the Fifth Dutch Growth Study 2009 (Schönbeck, Talma, Van Dommelen, Bakker, Buitendijk, HiraSing, and Van Buuren, 2013)

- Data available from the `fdgs` dataset in the `library(mice)` (Van Buuren and Groothuis-Oudshoorn, 2011)

Variable	Description	Missing
id	Child ID	0
reg	Region (5 levels)	0
age	Age (year)	0
sex	Sex	0
hgt	Height (cm)	23
wgt	Weight (kg)	20
hgt.z	Re-scaled height (as a Z-score)	23
wgt.z	Re-scaled weight (as a Z-score)	20

Summarising the data

- The data can be summarised using

```
> summary(fdgs)
```

```
       id                reg              age               sex            hgt              wgt              hgt.z
 Min.   :100001   North: 732   Min.   : 0.008214   boy :4829   Min.   : 46.0   Min.   :  2.585   Min.   :-
 1st Qu.:106352   East :2528   1st Qu.: 1.618754   girl:5201   1st Qu.: 83.8   1st Qu.: 11.600   1st Qu.:-
 Median :203855   South:2931   Median : 8.084873               Median :131.5   Median : 27.500   Median :-
 Mean   :180091   West :2578   Mean   : 8.157936               Mean   :123.9   Mean   : 32.385   Mean   :-
 3rd Qu.:210591   City :1261   3rd Qu.:13.547570               3rd Qu.:162.3   3rd Qu.: 51.100   3rd Qu.:
 Max.   :401955                Max.   :21.993155               Max.   :208.0   Max.   :135.300   Max.   :
                                                               NA's   :23      NA's   :20        NA's   :2
```

- Note that several variables in the dataset have missing observations. In particular, height (`hgt`) and weight (`wgt`), which are common variables used as response or predictors in models

Subsetting the data

- In order to provide a smaller dataset to speed up computations, only the children with missing values (in height and weight) and another 1000 ones taken at random will be used in the analysis

```
> # Subsect 1, observations with NA's
> subset1 <- which(is.na(fdgs$wgt) | is.na(fdgs$hgt))
>
> #Subset 2, random sample of 500 individuals
> set.seed(1)
> subset2 <- sample((1:nrow(fdgs))[-subset1], 1000)
> # Subset 1 + subset 2
> fdgs.sub <- fdgs[c(subset1, subset2), ]
> summary(fdgs.sub)
```

```
       id              reg            age               sex            hgt               wgt               hgt.z
 Min.   :100098   North: 78   Min.   : 0.07118   boy :493   Min.   : 46.00   Min.   :  2.585   Min.    :-4.
 1st Qu.:106293   East :275   1st Qu.: 1.74264   girl:550   1st Qu.: 86.28   1st Qu.: 11.960   1st Qu.:-0.
 Median :204306   South:298   Median : 8.59411              Median :136.05   Median : 29.000   Median :-0.
 Mean   :183214   West :250   Mean   : 8.56536              Mean   :127.04   Mean   : 33.614   Mean    :-0.
 3rd Qu.:211388   City :142   3rd Qu.:14.16427              3rd Qu.:165.10   3rd Qu.: 53.100   3rd Qu.: 0.
 Max.   :401949               Max.   :21.88364              Max.   :199.00   Max.   :117.300   Max.    : 3.
                                                            NA's   :23       NA's   :20        NA's    :23
```

Bayesian imputation

Model specification

- We first predict weight as a function of age and sex. We specify:

$$wgt_i \sim \text{Normal}(\alpha + \beta_1 sex_i + \beta_2 age_i, \sigma^2)$$

- where `wgt` is missing we will have `NA` in the corresponding vector, e.g.

```
> fdgs.sub$wgt[1:10]
```

```
[1] 23.200     NA     NA     NA  8.445     NA  6.960 10.420     NA 14.100
```

- Remember the posterior predictive distribution (presented in lecture 2.2):

$$p(\mathbf{y}^*|\mathbf{y}) = \int p(y^*|\theta)p(\theta|\mathbf{y})d\theta$$

- here $\mathbf{y}^*$ identifies the missing values, while $\mathbf{y}$ is the set of observed values for `wgt`

```
> library("INLA")
> wgt.inla <- inla(wgt ~ age + sex, data = fdgs.sub,
+ control.predictor = list(compute = TRUE), control.compute=list(return.marginals.predictor=TRUE))
> wgt.inla$summary.fixed
```

	mean	sd	0.025quant	0.5quant	0.975quant	mode	kld
(Intercept)	6.259187	0.43627989	5.403400	6.259187	7.114973	6.259188	1.409212e-12
age	3.330942	0.03371347	3.264811	3.330942	3.397073	3.330942	2.344304e-12
sexgirl	-2.378944	0.44640004	-3.254580	-2.378944	-1.503304	-2.378945	1.430725e-12

```
> wgt.inla$summary.hyperpar
```

	mean	sd	0.025quant	0.5quant	0.975quant	mod
Precision for the Gaussian observations	0.01972496	0.0008752915	0.01805436	0.01971032	0.02147894	0.0196809

- Note that we need to include `control.predictor=list(compute = TRUE)` so INLA can estimate the predictive distribution for the missing observations, while `control.compute=list(return.marginals.predictor=TRUE)` tells inla that we want to access the entire posterior distribution of the prediction (rather than only the summary)

Getting the posterior prediction

We now subset the children indexes with missing values so we can report their predictive distributions:

```
> wgt.na <- which(is.na(fdgs.sub$wgt))
> rownames(fdgs.sub)[wgt.na]
```

```
[1] "275"  "1278" "1419" "2135" "2684" "2940" "3069" "3189" "3543" "4262" "5687" "6485" "7101" "7108" "75
```

```
> # Obtain the predictive distribution
> wgt.inla$summary.fitted.values[wgt.na, c("mean", "sd")][1:5,]
```

```
                         mean        sd
fitted.Predictor.0002 23.067927 0.3204041
fitted.Predictor.0003 27.617341 0.3332160
fitted.Predictor.0004 54.019923 0.3769133
fitted.Predictor.0006 13.144501 0.3931169
fitted.Predictor.0009  7.838159 0.3940881
```

Remember that you can also access the marginal posterior distributions (rather than the summary) using
`wgt.inla$marginals.fitted.values`

Imputing hgt using the same approach

- Similarly, a model can be fit to explain height based on age and sex and to compute the predictive distribution of the missing observations:

```
> hgt.inla <- inla(hgt ~ age + sex, data = fdgs.sub,
+ control.predictor = list(compute = TRUE),
+ control.compute = list(return.marginals.predictor=TRUE))
> hgt.inla$summary.fixed
```

	mean	sd	0.025quant	0.5quant	0.975quant	mode	kld
(Intercept)	77.148121	0.71996137	75.735870	77.148122	78.560365	77.148124	1.315960e-12
age	6.022575	0.05540469	5.913895	6.022575	6.131254	6.022575	2.314710e-12
sexgirl	-4.716077	0.73001342	-6.148035	-4.716079	-3.284104	-4.716084	1.218303e-12

```
> hgt.inla$summary.hyperpar
```

	mean	sd	0.025quant	0.5quant	0.975quant	
Precision for the Gaussian observations	0.007400594	0.0003314709	0.00676327	0.007397839	0.008064696	0.007

Imputing hgt using the same approach

- We can obtain the predictions using

```
> hgt.na <- which(is.na(fdgs.sub$hgt))
> hgt.inla$summary.fitted.values[hgt.na, c("mean"
```

```
                           mean        sd
fitted.Predictor.0001 122.24529 0.5354315
fitted.Predictor.0005  83.24902 0.6831827
fitted.Predictor.0007  74.64156 0.6785295
fitted.Predictor.0008  82.80382 0.6857695
fitted.Predictor.0010  88.26140 0.6012610
fitted.Predictor.0012  96.55557 0.6134972
fitted.Predictor.0013  86.31596 0.6657742
fitted.Predictor.0016  81.84746 0.6913755
fitted.Predictor.0017  77.75821 0.7160705
fitted.Predictor.0018  81.59988 0.6371494
```

- We can plot the entire posterior distributions for each child with:

```
> # First child with missing value
> plot(hgt.inla$marginals.fitted.values[[hgt.na[1
```
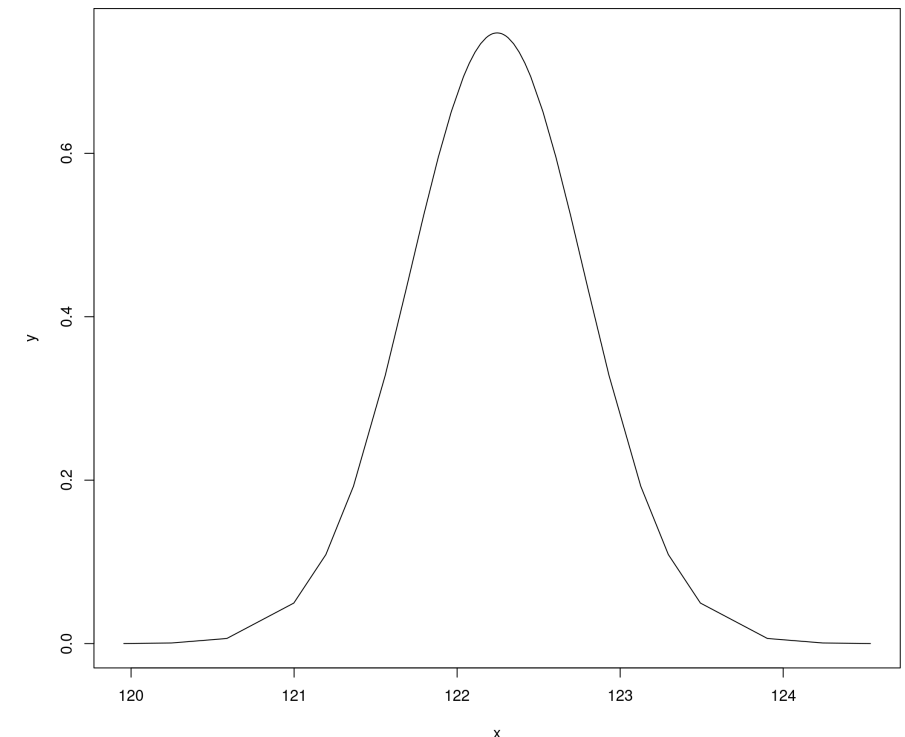
Extending the model

Joint model of height and weight

- The two previous models consider height and weight separately, but it is clear that there is a high correlation between height and weight, which is caused by the age and sex of the child.

```
[1] 0.9999865
```

- We can build a joint model for height and weight to exploit a correlated effect between the coefficients of age in both models.

$$hgt_i = \alpha_h + \beta_{h1}sex_i + \beta_{h2}age_i + \epsilon_{1i}$$
$$wgt_i = \alpha_w + \beta_{w1}sex_i + \beta_{w2}age_i + \epsilon_{2i}$$

with

- α_h, α_w model intercepts
- β_{h1}, β_{w1} the effect of sex
- β_{h2}, β_{w2} the effect of age
- ϵ_1, ϵ_2 the error terms (note that this specification is equivalent to the one above for the separate models)

Joint model of height and weight: prior

- The vectors (β_{1h}, β_{1w}) and (β_{2h}, β_{2w}) are modeled using a multivariate Gaussian distribution with mean 0 and covariance matrix with $1/\tau_{hj}$ and $1/\tau_{wj}$ as variances and $\rho_j / \sqrt{(\tau_{jh}\tau_{jw})}$ as the covariance where ρ_j is the correlation parameter.

- First, the bivariate response variable needs to be put in a two-column matrix given that the model will be made of two data distributions

```
> n <- nrow(fdgs.sub)
> y <- matrix(NA, nrow = 2 * n, ncol = 2)
> y[1:n, 1] <- fdgs.sub$hgt
> y[n + 1:n, 2] <- fdgs.sub$wgt
```

- Similarly, as we have two intercepts, we need to define these explicitly as covariates with all values equal to one:

```
> I <- matrix(NA, nrow = 2 * n, ncol = 2)
> I[1:n, 1] <- 1
> I[n + 1:n, 2] <- 1
```

Correlated effects

- Now we need to define the correlated effects. We will use the random effect specification similar to what we saw with the hierarchical models (`iid`), but modified to have the two coefficients as correlated `f(...,model=iid2d)`.

- In order to do so we need to modify the variables `age` and `sex` as they will be passed to the model as weights of the latent random effects `iid2d` specification. We need them to be twice as long to match the dimension of the response:

```
> age.joint <- rep(fdgs.sub$age, 2)
> sex.joint <- rep(fdgs.sub$sex, 2)
```

- Finally we need two index vectors to indicate which coefficient to use from the `iid2d` model is required. These indexes will be 1 for the first half of observations (to indicate that the coefficient is β_h and 2 for the second half (to indicate that the coefficient is β_w).

```
> idx.age = rep(1:2, each = n)
> idx.sex = rep(1:2, each = n)
```

The model is fit and summarized as seen below

```
> # Model formula
> joint.f <- y ~ -1 + I + f(idx.sex, sex, model="iid2d", n=2) + f(idx.age, age, model = "iid2d", n = 2)
> # Model fit
> fdgs.joint <- inla(joint.f,
+   data = list(y = y, I = I, sex = sex.joint, age = age.joint, idx.age = idx.age, idx.sex= idx.sex),
+   family = rep("gaussian", 2),
+   control.predictor = list(compute = TRUE))
> # Summary fixed (intercept)
> fdgs.joint$summary.fixed
```

```
        mean        sd 0.025quant   0.5quant 0.975quant       mode          kld
I1 81.016834 1.1187456  78.824974 81.015596  83.216242 81.014056 5.459222e-10
I2  8.391859 0.6534032   7.094048  8.396656   9.660892  8.404877 6.700648e-09
```

Hyperparameters and variable effects

- The hyperparameters can be obtained through

```
> fdgs.joint$summary.hyperpar
```

	mean	sd	0.025quant	0.5quant	0.975quant	
Precision for the Gaussian observations	0.007337564	0.0004351792	0.006731568	0.00731645	0.008057808	0.(
Precision for the Gaussian observations[2]	0.019735832	0.0011908765	0.018050540	0.01962622	0.022008854	0.(
Precision for idx.sex (component 1)	0.479444359	0.2656799385	0.110371521	0.43197154	1.116284475	0.3
Precision for idx.sex (component 2)	1.510806333	0.7345656354	0.466994457	1.38398023	3.289255210	1.1
Rho1:2 for idx.sex	0.850682971	0.0750803297	0.663412322	0.86527502	0.953101619	0.8
Precision for idx.age (component 1)	0.224562551	0.0969687283	0.080319436	0.20975570	0.454733424	0.1
Precision for idx.age (component 2)	0.608992589	0.4076230902	0.153968261	0.50568852	1.683601440	0.3
Rho1:2 for idx.age	0.782644550	0.1210974817	0.487197186	0.80549517	0.950876221	0.8

- While the coefficients for `age` and `sex` are part of the random effects of the model:

```
> #Sex
> fdgs.joint$summary.random$idx.sex
```

```
> #Age
> fdgs.joint$summary.random$idx.age
```

ID	mean	sd	0.025quant	0.5quant	0.
1 1	-4.194114	0.6133787	-5.399120	-4.193921	-
2 2	-2.202628	0.3518744	-2.882278	-2.206638	-

| ID	mean	sd	0.025quant	0.5quant	0.975
1 1	6.027020	0.05568376	5.917811	6.027021	6.1
2 2	3.328184	0.03383798	3.261822	3.328183	3.3

Estimates of missing values

- Finally to access the predicted values for the children with missing data we need to remember that we now have the response `y` stacked (first height, then weight)

- As height is the first variable we can use `hgt.na` to get to the indexes of the children with missing data

- For weight we need to use `wgt.na` and add `n` to each index, as this is the total number of observations, so the data for weight will start on the index 1044

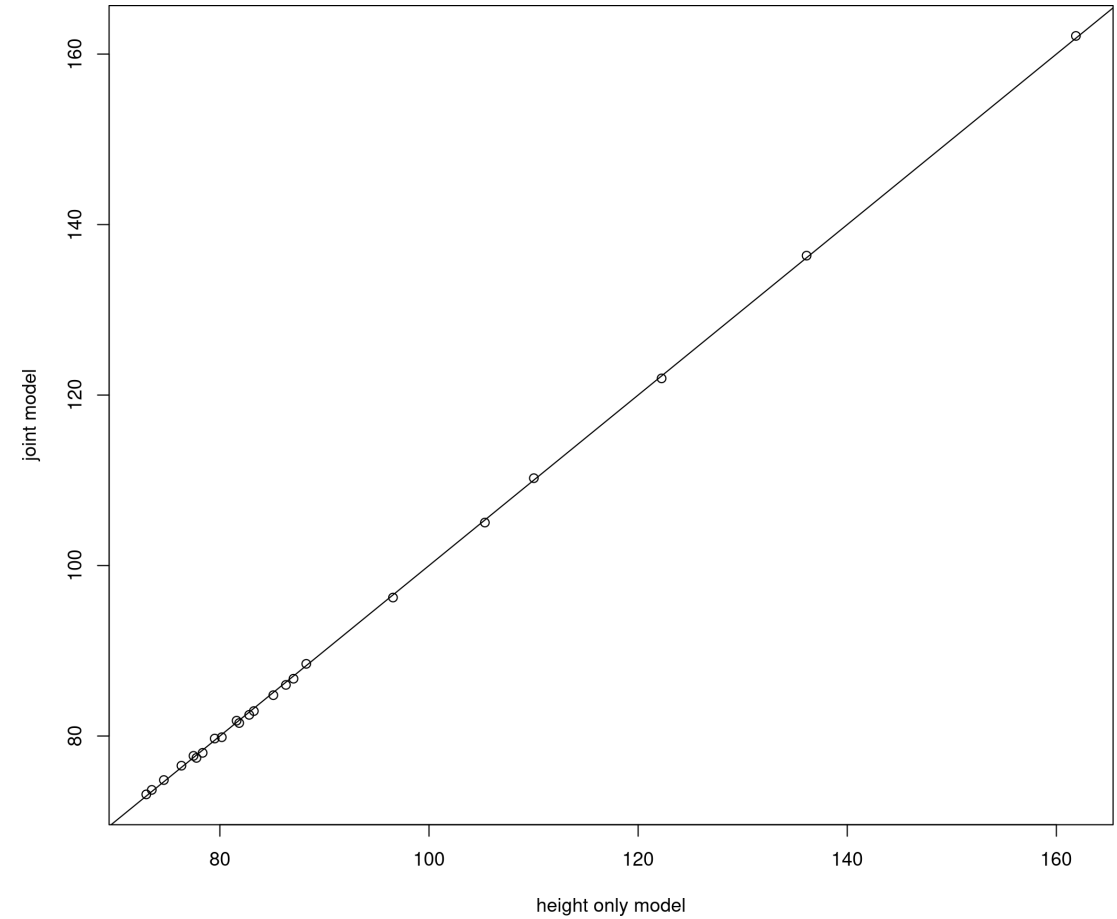```
> joint.wgt.na = wgt.na+n
```

```
> #Height
> fdgs.joint$summary.fitted.values[hgt.na, c("mean", "sd")][1:10,]
> #Weight
> fdgs.joint$summary.fitted.values[joint.wgt.na, c("mean", "sd")][1:10,]
```

Comparing the results of the joint and separate models

Weight
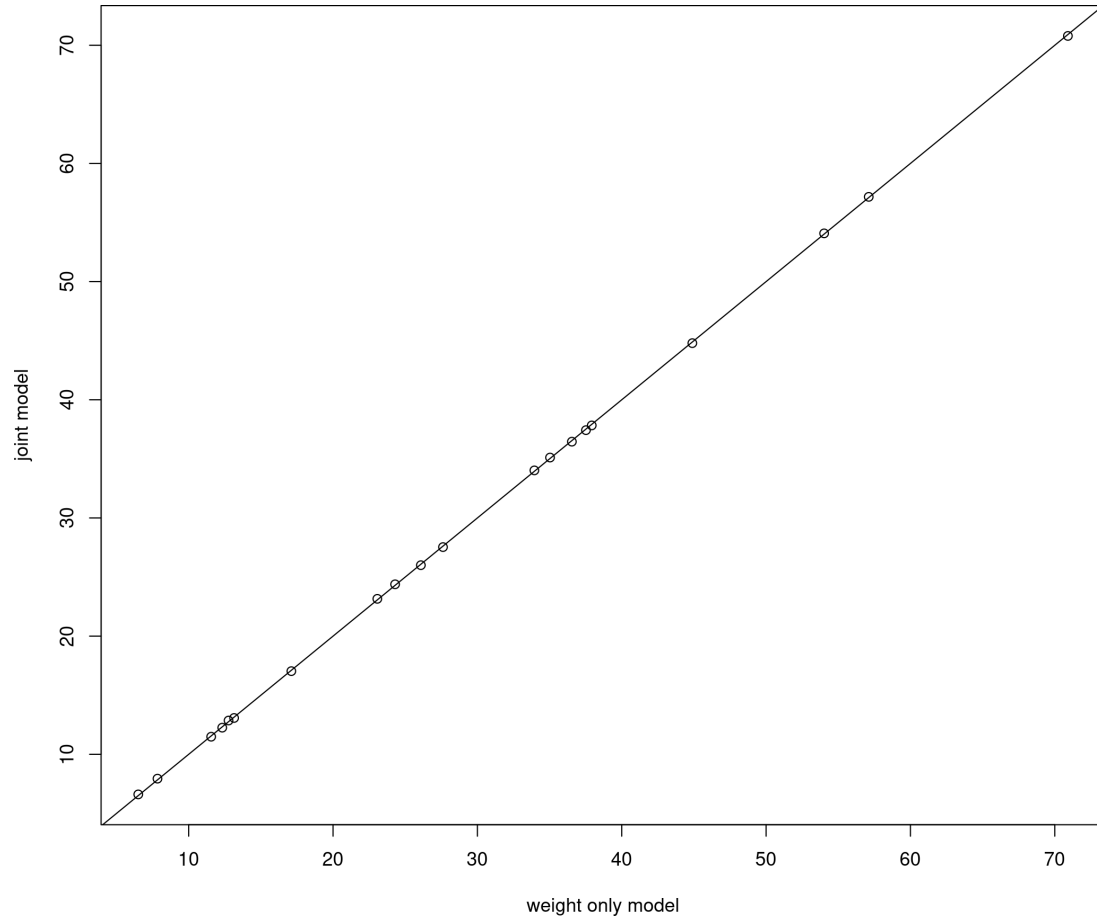
Height

References

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Schönbeck, Y., H. Talma, P. Van Dommelen, et al. (2013). "The world's tallest nation has stopped growing taller: the height of Dutch children from 1955 to 2009". In: *Pediatric research* 73.3, pp. 371-377.

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