

Statistics with SpaRRows II

Many models, matrices, and magic

Julia Schroeder

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Bivariate models, and what they have to do
with variance/covariance

Bivariate models, and what they have to do with variance/covariance

Bivariate analysis

From Wikipedia, the free encyclopedia

Bivariate analysis is one of the simplest forms of quantitative (statistical) analysis.^[1] It involves the analysis of two variables (often denoted as X , Y), for the purpose of determining the empirical relationship between them.^[1]

Bivariate models, and what they have to do with variance/covariance

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Bivariate models

- Are an extension from linear models

Bivariate models

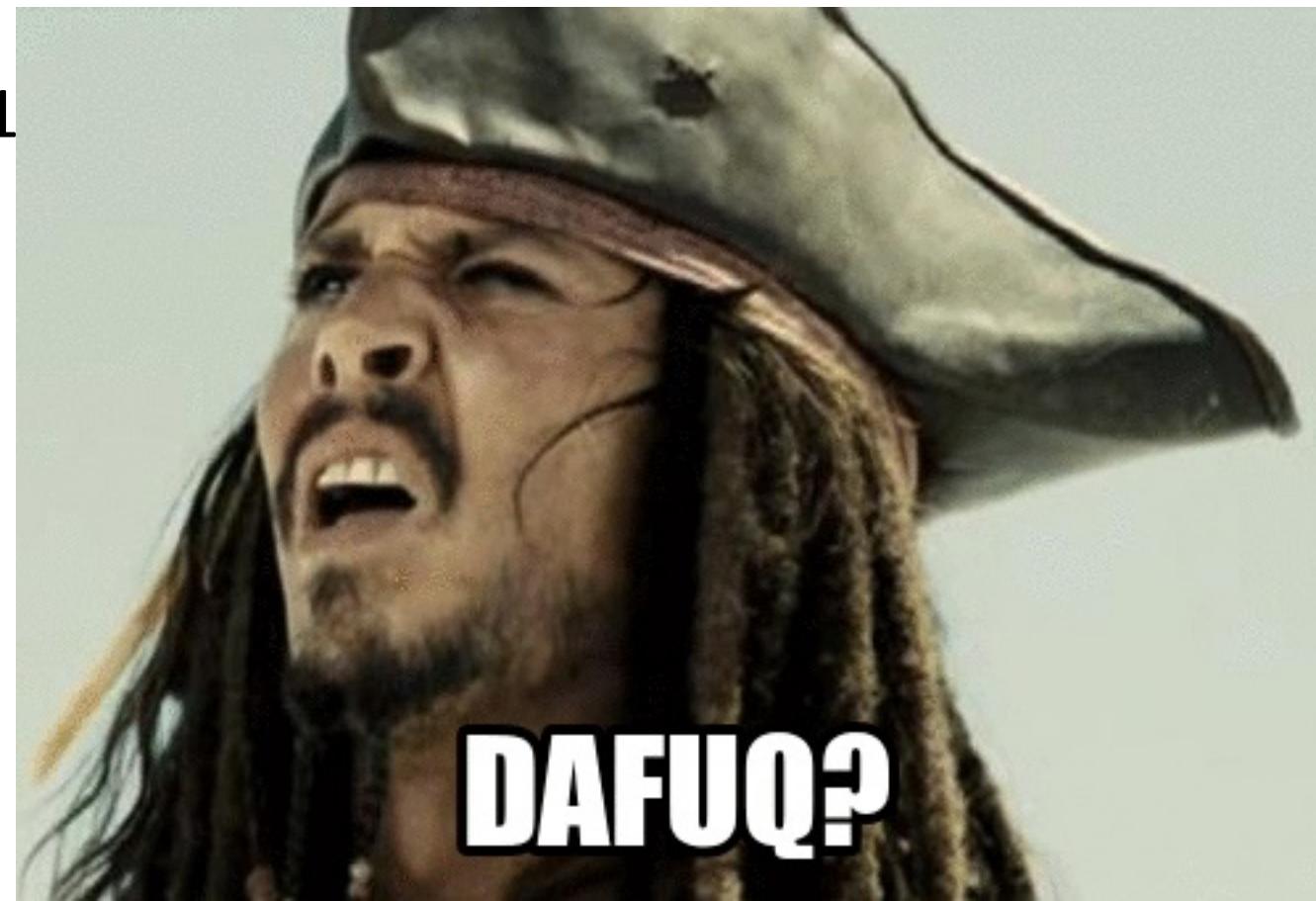
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Bivariate models

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Let me break it down

- Terminology:
- Bivariate analysis: 1 response – 1 explanatory variable

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Model

$$(y_i, z_i) = b_0 + \varepsilon_i$$

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$$\begin{pmatrix} y_1 & z_1 \\ y_2 & z_2 \\ \dots & \dots \\ y_i & z_i \end{pmatrix}$$

Model

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Model

$$(y_i, z_i) = b_0 + \varepsilon_i$$

The diagram illustrates the components of the model equation. At the top, the equation $(y_i, z_i) = b_0 + \varepsilon_i$ is shown. Below it, a black arrow points from the matrix of observations $\begin{pmatrix} y_1 & z_1 \\ y_2 & z_2 \\ \dots & \dots \\ y_i & z_i \end{pmatrix}$ to the intercept term b_0 . A red arrow points from the matrix of error terms $\begin{pmatrix} \varepsilon_{1,y} & \varepsilon_{1,z} \\ \varepsilon_{2,y} & \varepsilon_{2,z} \\ \dots & \dots \\ \varepsilon_{i,y} & \varepsilon_{i,z} \end{pmatrix}$ to the error term ε_i .

Example – Sparrow Size

- (Tarsus,Mass) \sim 1

Example – Sparrow Size

- (Tarsus,Mass)~1

$$(y_i, z_i) = b_0 + \varepsilon_i$$

$$\begin{pmatrix} y_1 & z_1 \\ y_2 & z_2 \\ \dots & \dots \\ y_i & z_i \end{pmatrix}$$

$$\begin{pmatrix} \beta_{0y} \\ \beta_{0z} \end{pmatrix}$$

$$\begin{pmatrix} \varepsilon_{1,y} & \varepsilon_{1,z} \\ \varepsilon_{2,y} & \varepsilon_{2,z} \\ \dots & \dots \\ \varepsilon_{i,y} & \varepsilon_{i,z} \end{pmatrix}$$

Example – Sparrow Size

- (Tarsus,Mass)~1

$$(y_i, z_i) = b_0 + \varepsilon_i$$

↓ ↓ ↓

Mean of tarsus

$$\begin{pmatrix} y_1 & z_1 \\ y_2 & z_2 \\ \dots & \dots \\ y_i & z_i \end{pmatrix}$$
$$\begin{pmatrix} \beta_{0y} \\ \beta_{0z} \end{pmatrix}$$
$$\begin{pmatrix} \varepsilon_{1,y} & \varepsilon_{1,z} \\ \varepsilon_{2,y} & \varepsilon_{2,z} \\ \dots & \dots \\ \varepsilon_{i,y} & \varepsilon_{i,z} \end{pmatrix}$$

Example – Sparrow Size

- (Tarsus,Mass)~1

$$(y_i, z_i) = b_0 + \varepsilon_i$$

The diagram illustrates the decomposition of observed data points (y_i, z_i) into a mean vector and error vectors. A large black arrow points from the equation $(y_i, z_i) = b_0 + \varepsilon_i$ down to a matrix containing the data points y_1, z_1 ; y_2, z_2 ; \dots ; y_i, z_i . Another black arrow points from the same equation down to a vector containing the error terms $\varepsilon_{1,y}, \varepsilon_{1,z}$; $\varepsilon_{2,y}, \varepsilon_{2,z}$; \dots ; $\varepsilon_{i,y}, \varepsilon_{i,z}$. A red arrow points from the error vector to the term ε_i in the equation.

$$\begin{pmatrix} y_1 & z_1 \\ y_2 & z_2 \\ \dots & \dots \\ y_i & z_i \end{pmatrix}$$
$$\begin{pmatrix} \beta_{0y} \\ \beta_{0z} \end{pmatrix}$$
$$\begin{pmatrix} \varepsilon_{1,y} & \varepsilon_{1,z} \\ \varepsilon_{2,y} & \varepsilon_{2,z} \\ \dots & \dots \\ \varepsilon_{i,y} & \varepsilon_{i,z} \end{pmatrix}$$

Mean of tarsus

Mean of mass

Example – Sparrow Size

- (Tarsus,Mass)~1

$$(y_i, z_i) = b_0 + \varepsilon_i$$

↓

↓

↓

Mean of tarsus

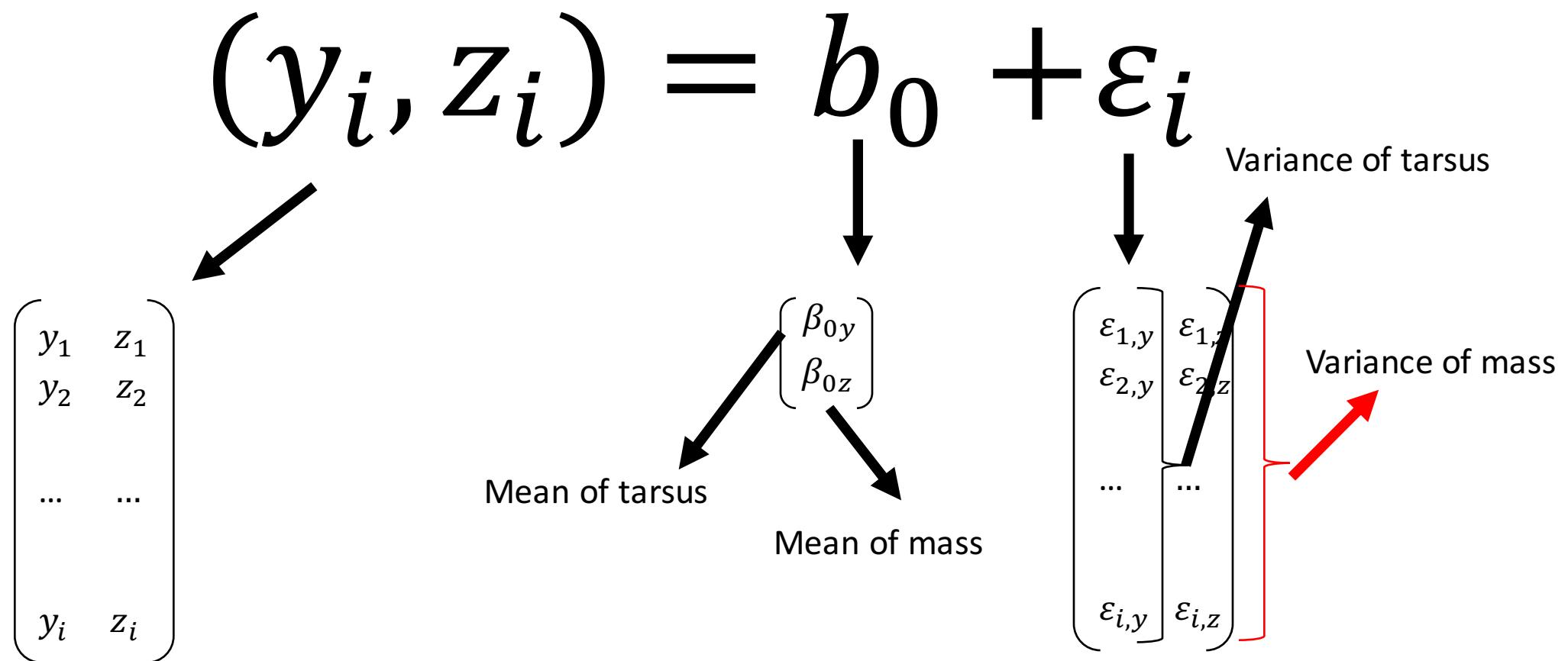
Mean of mass

Variance of tarsus

The diagram illustrates the decomposition of observed data points (y_i, z_i) into a mean component and error components. A large bracket on the left groups the data points $y_1, z_1; y_2, z_2; \dots; y_i, z_i$. An arrow points from this bracket to the term b_0 in the equation. Another arrow points from the equation to a bracket on the right grouping the error terms $\varepsilon_{1,y}, \varepsilon_{1,z}; \varepsilon_{2,y}, \varepsilon_{2,z}; \dots; \varepsilon_{i,y}, \varepsilon_{i,z}$. A red arrow points from the right bracket to the variance term. Labels "Mean of tarsus" and "Mean of mass" are placed between the mean vector and the error terms.

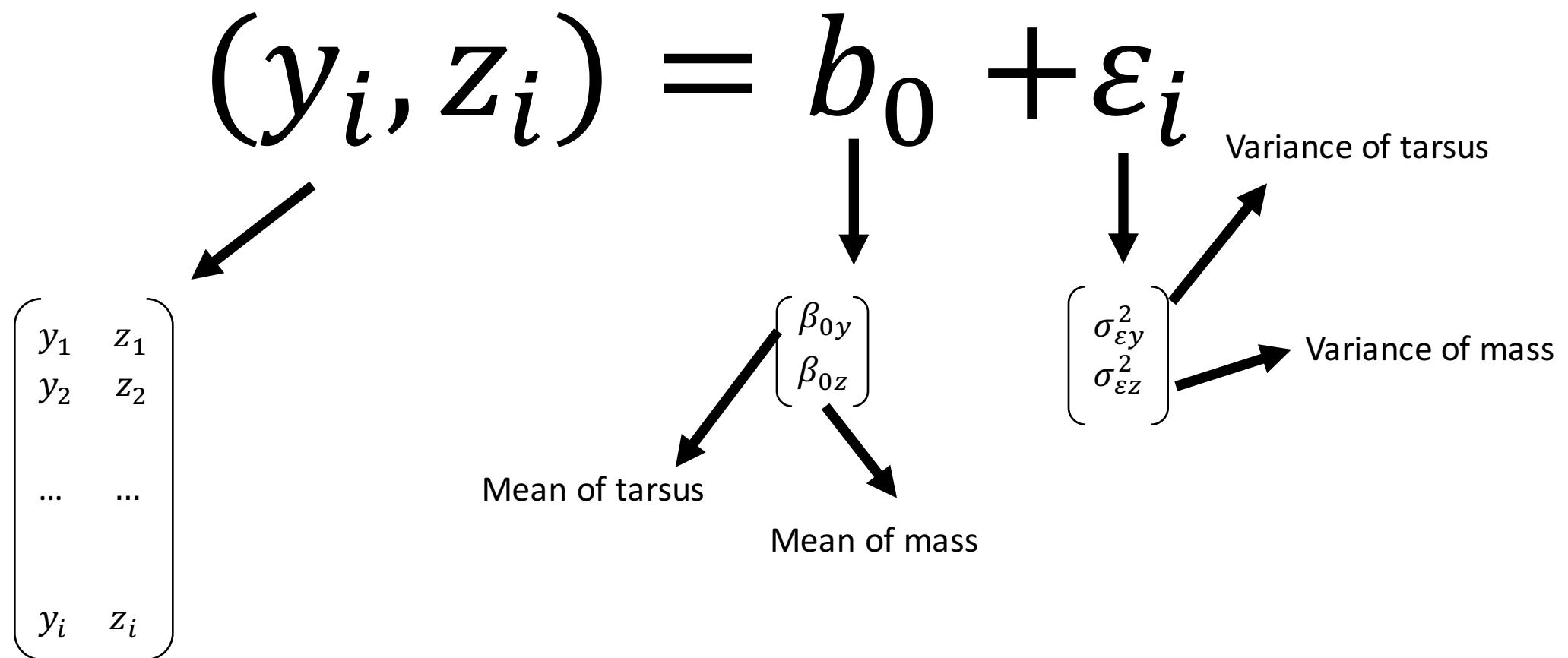
Example – Sparrow Size

- (Tarsus,Mass)~1

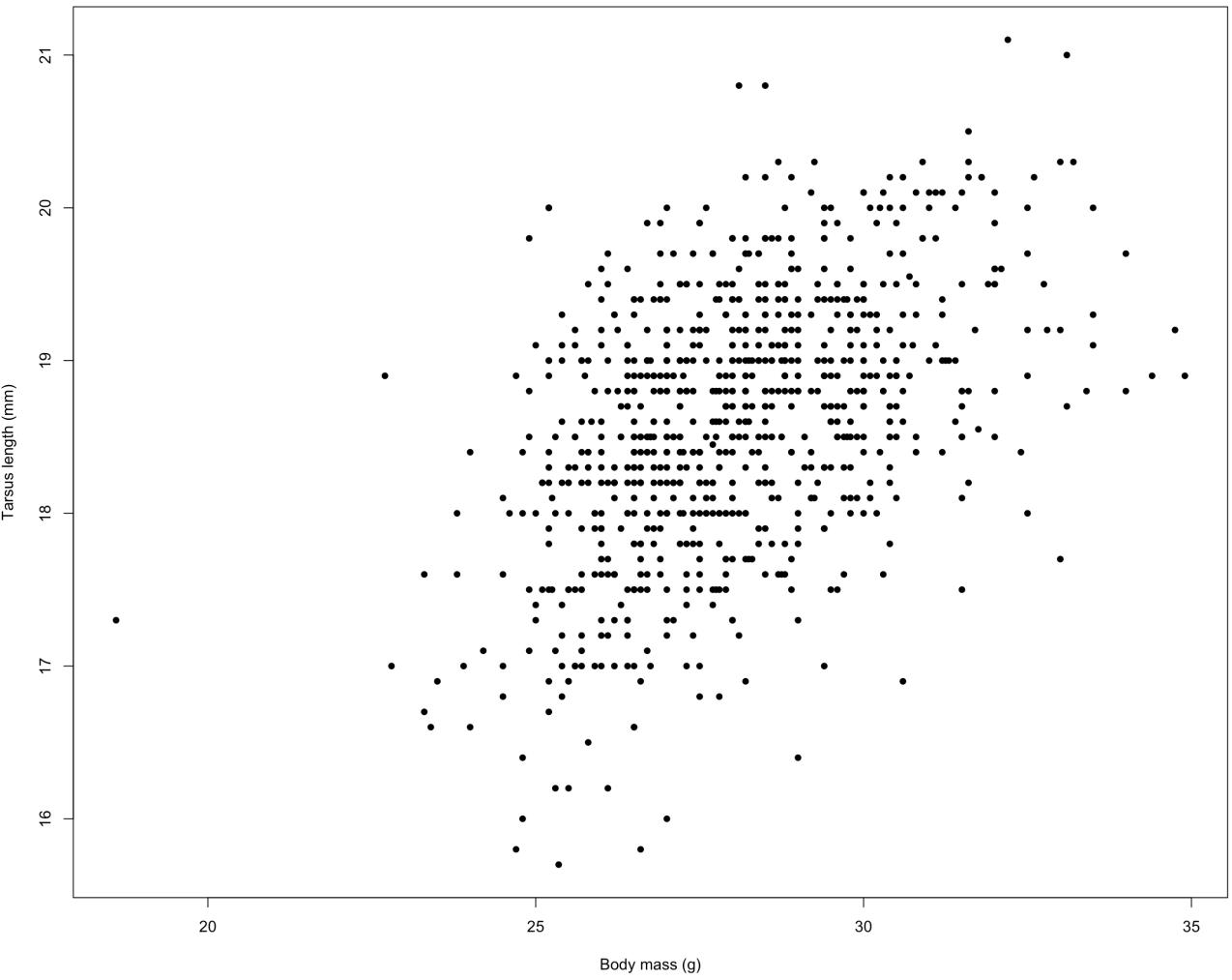


Example – Sparrow Size

- (Tarsus,Mass)~1

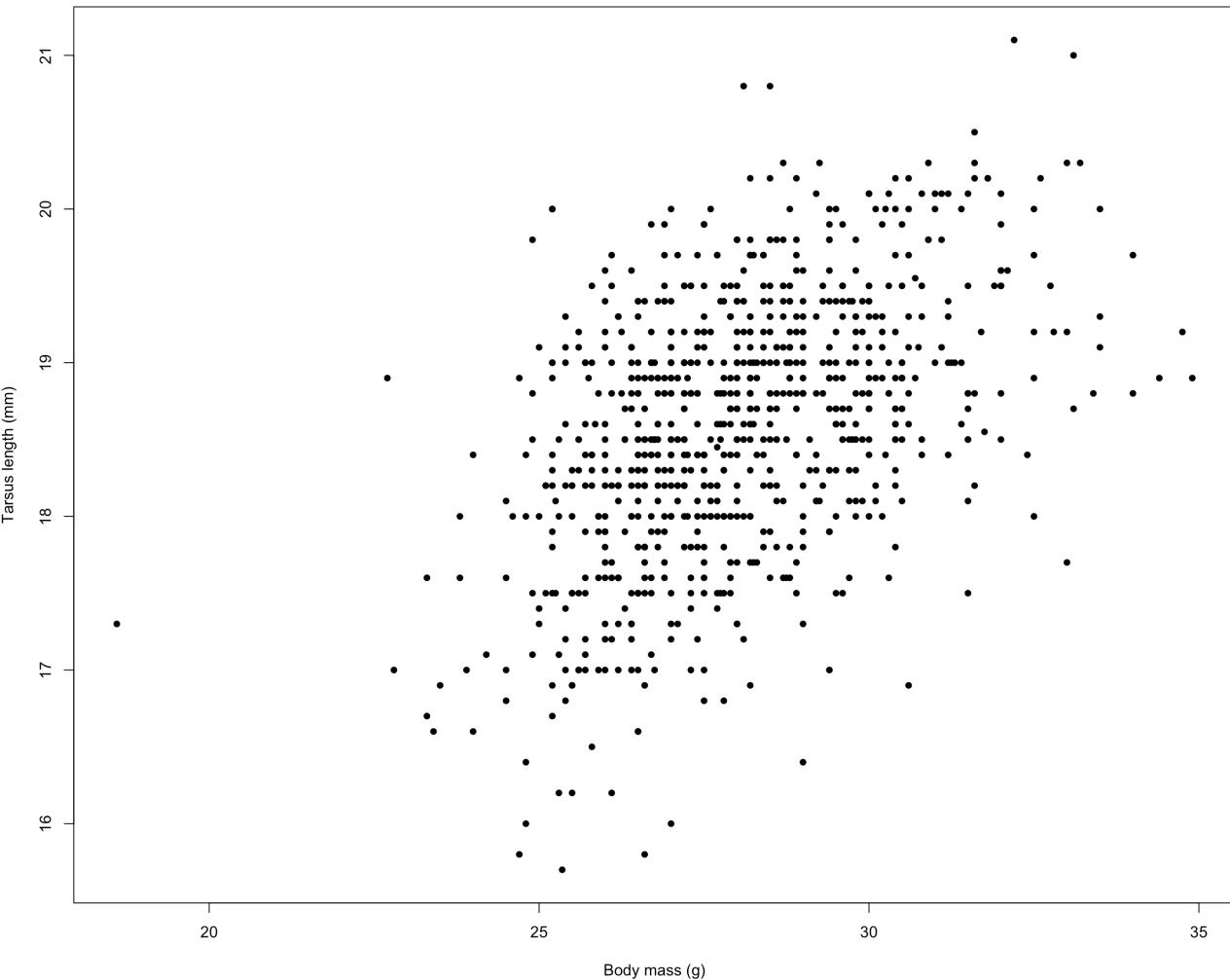


Example – Sparrow Size



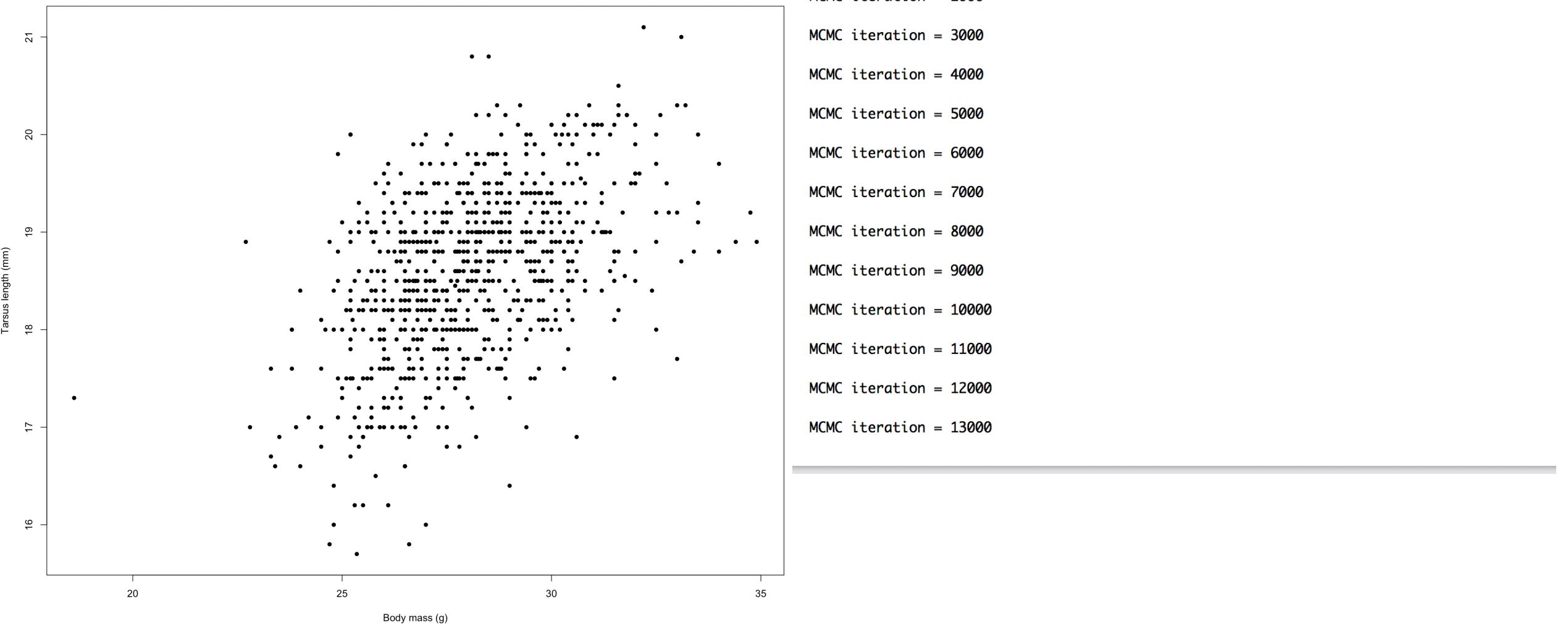
Example – Sparrow Size

```
> mean(dat$Tarsus)    > var(dat$Tarsus)  
[1] 18.60054           [1] 0.7251402  
> mean(dat$Mass)      > var(dat$Mass)  
[1] 28.06075           [1] 4.060524  
[1]
```



Example – Sparrow Size

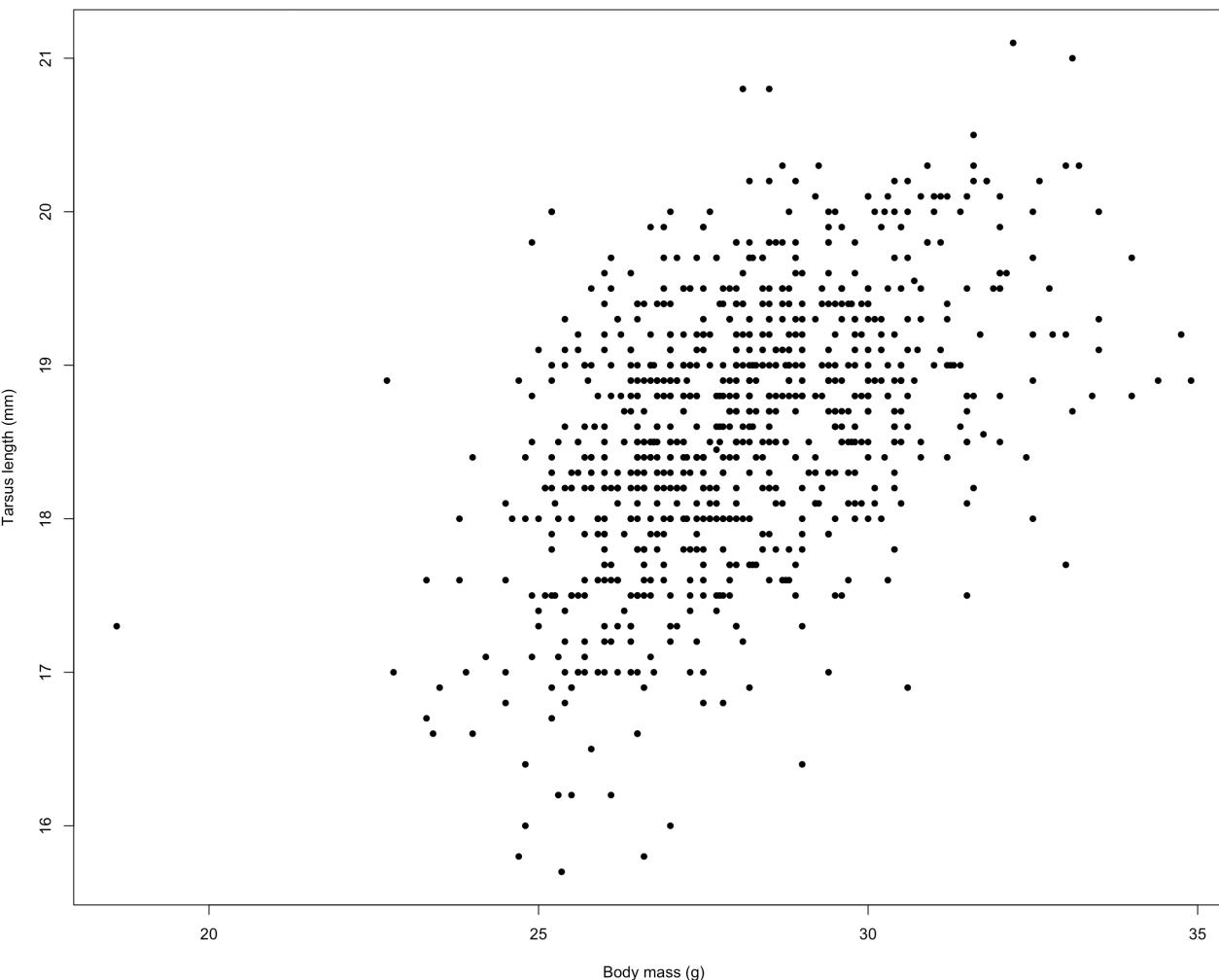
```
> mean(dat$Tarsus)      > var(dat$Tarsus)          > m<-MCMCglmm(cbind(Tarsus, Mass)~trait-1, rcov=~us(trait):units, family=c("gaussian","gaussian"),data=dat)
[1] 18.60054              [1] 0.7251402
> mean(dat$Mass)        > var(dat$Mass)          MCMC iteration = 0
[1] 28.06075              [1] 4.060524
[1]
```



Example – Sparrow Size

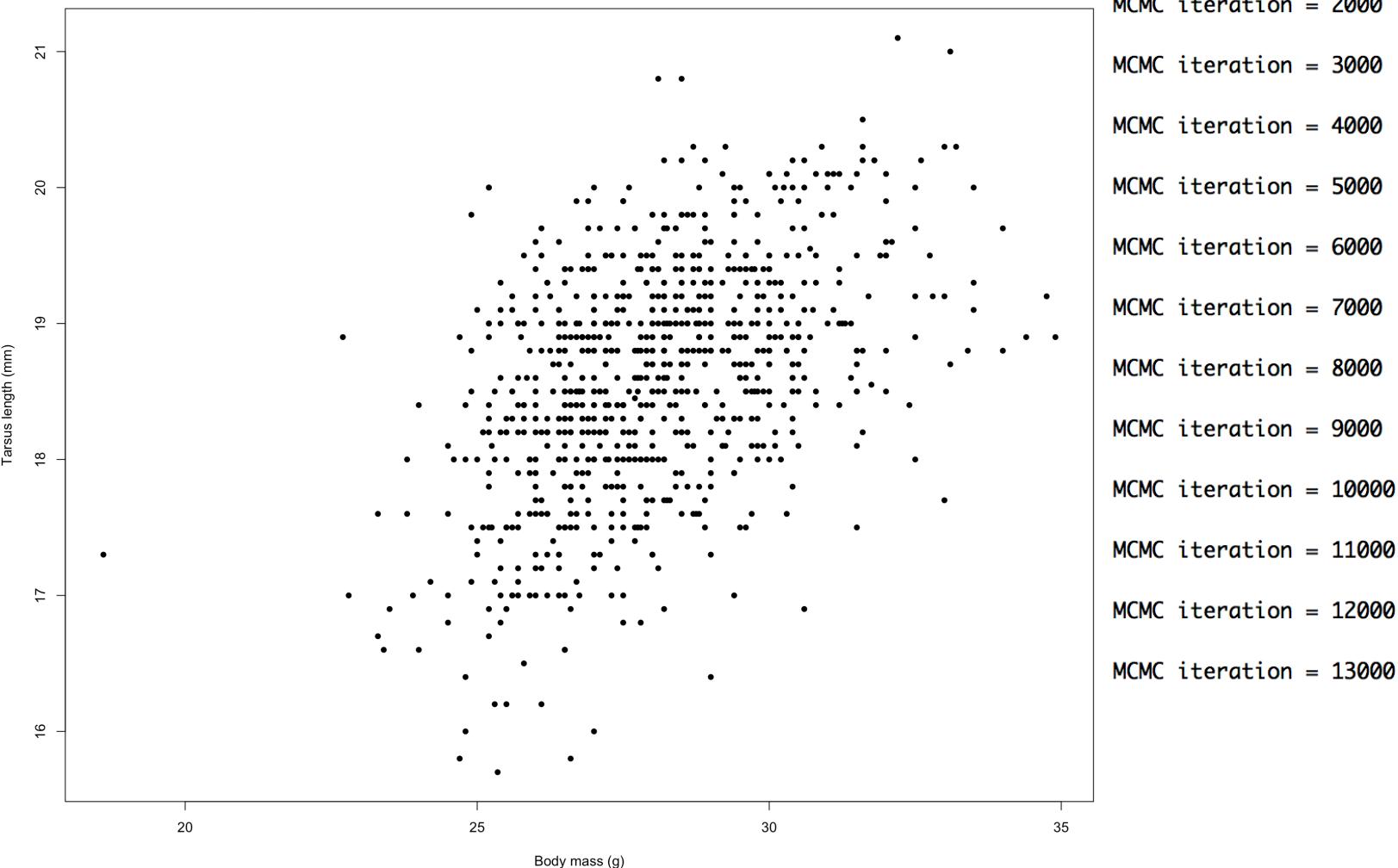
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> mean(dat$Tarsus)    > var(dat$Tarsus)      > m<-MCMCglmm(c(Tarsus, Mass)~trait-1, rcov=~idh(trait):units, family=c("gaussian","gaussian"),data=dat)
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MCMC iteration = 0
MCMC iteration = 1000
MCMC iteration = 2000
MCMC iteration = 3000
MCMC iteration = 4000
MCMC iteration = 5000
MCMC iteration = 6000
MCMC iteration = 7000
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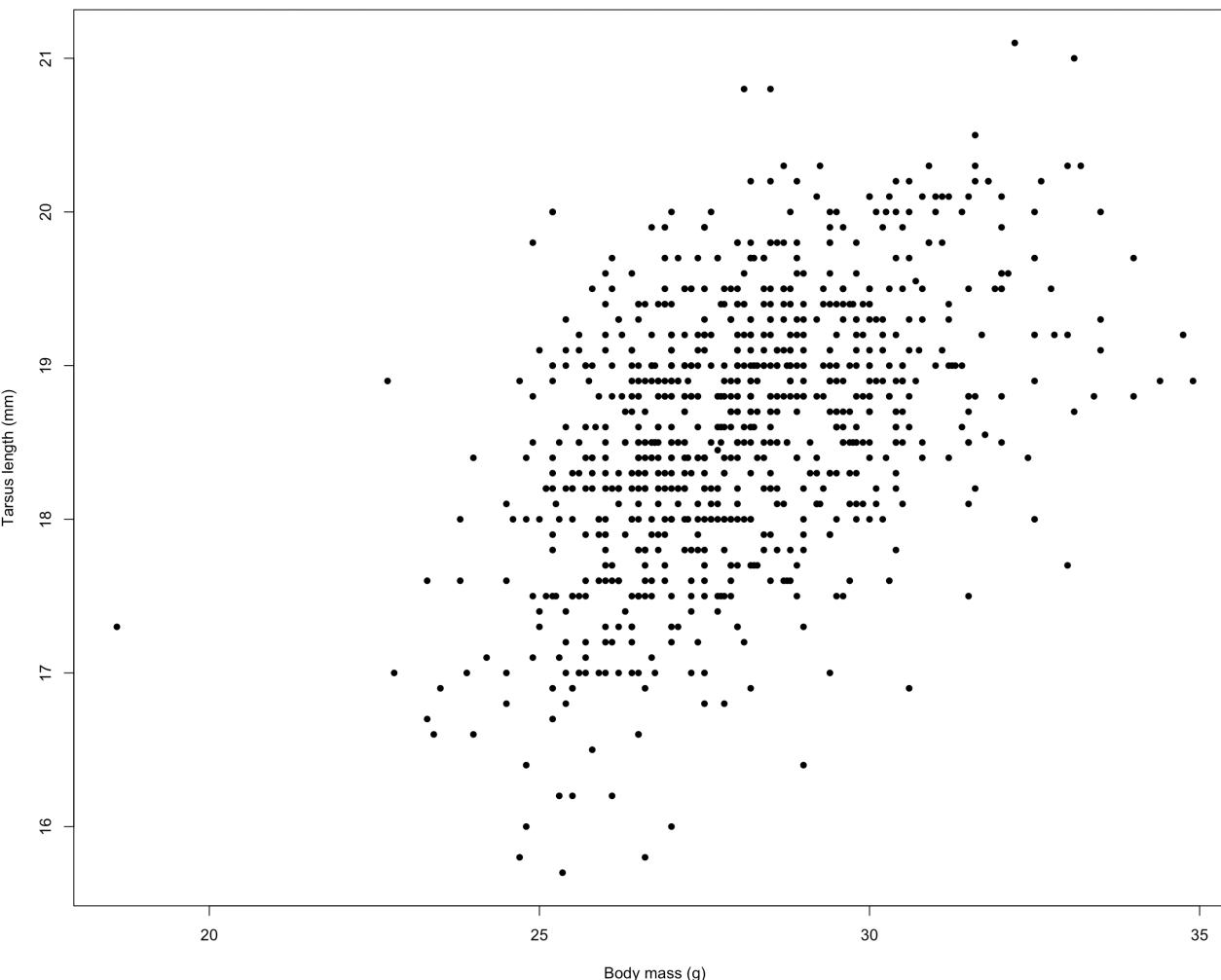
MCMC iteration = 10000

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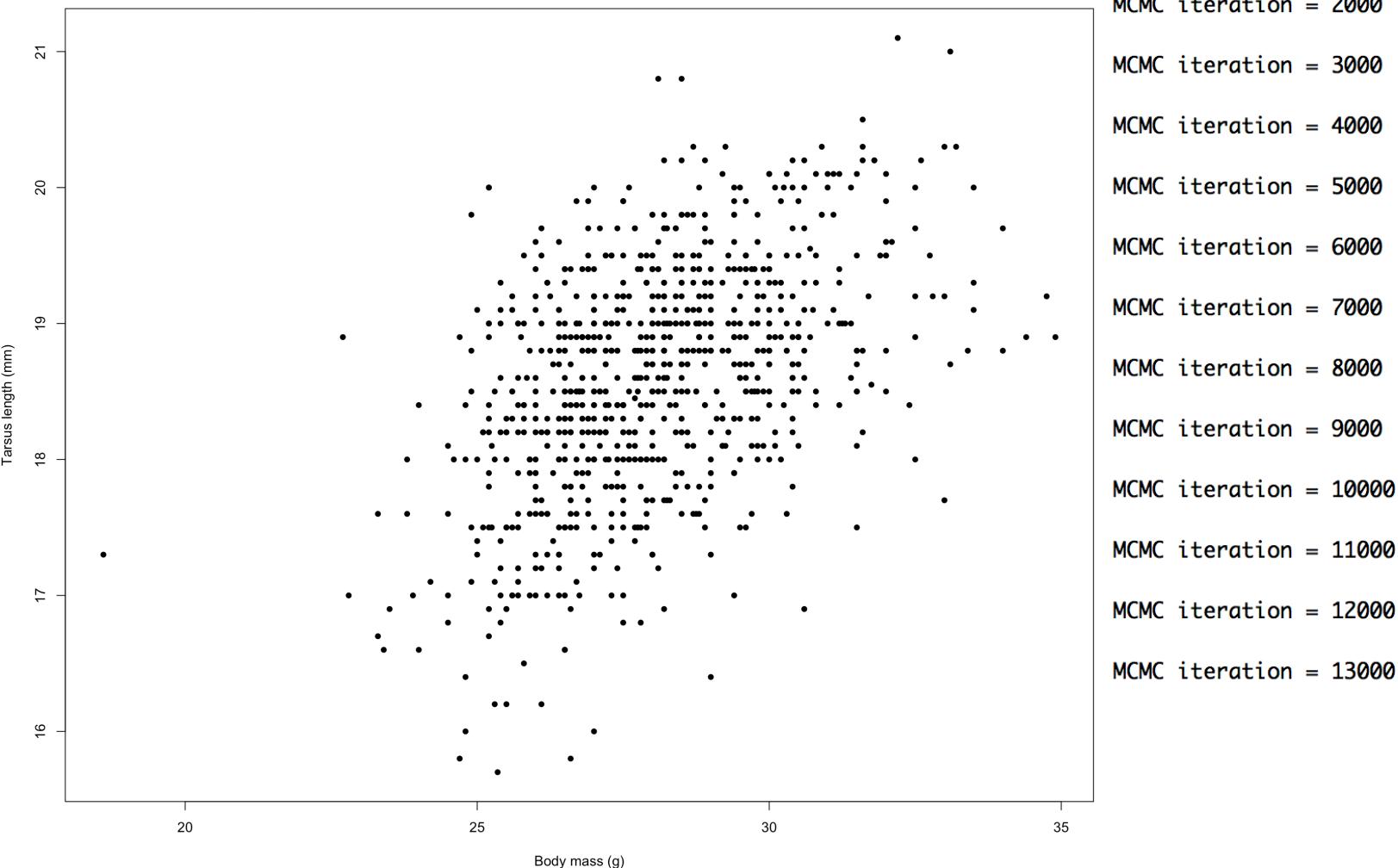
MCMC iteration = 13000

Structure of the residuals



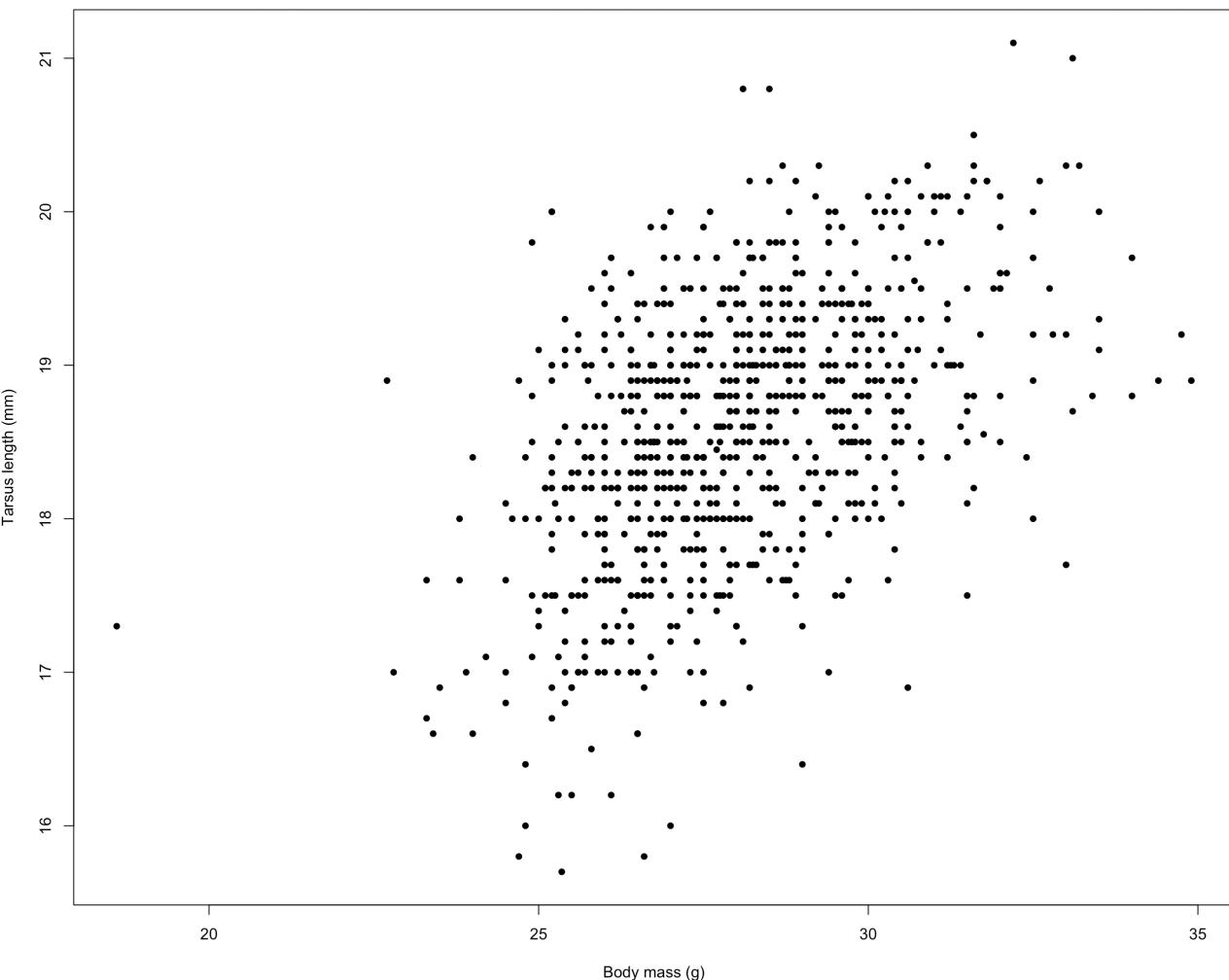
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[1] 18.60054           [1] 0.7251402        > summary(m)
[1] 28.06075           > var(dat$Mass)       Iterations = 3001:12991
[1] 4.060524          .                         Thinning interval = 10
[1] 28.06075           .                         Sample size = 1000
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```



```
Iterations = 3001:12991
Thinning interval = 10
Sample size = 1000
```

DIC: 5660.597

R-structure: ~idh(trait):units

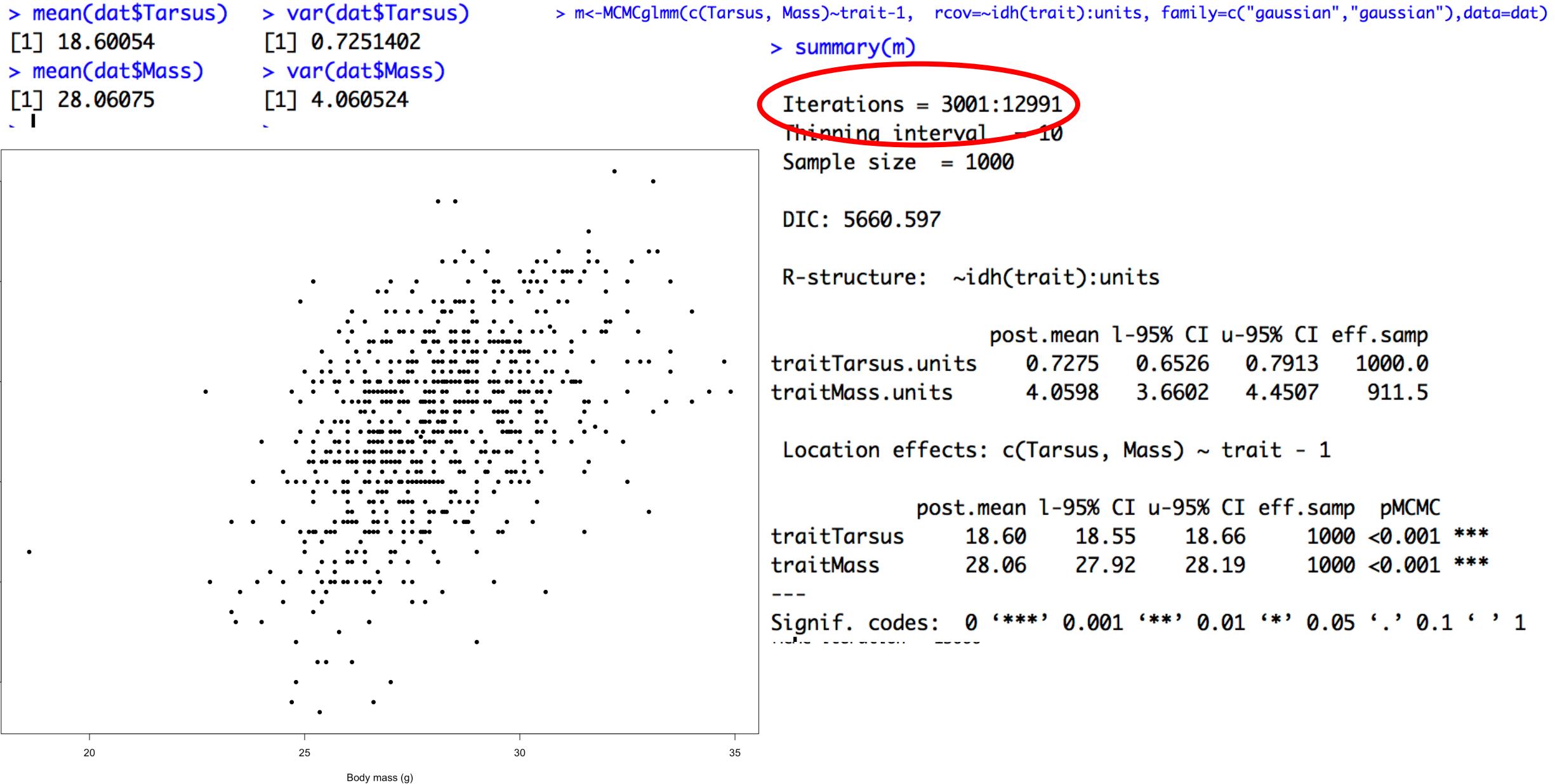
	post.mean	l-95% CI	u-95% CI	eff.samp
traitTarsus.units	0.7275	0.6526	0.7913	1000.0
traitMass.units	4.0598	3.6602	4.4507	911.5

Location effects: c(Tarsus, Mass) ~ trait - 1

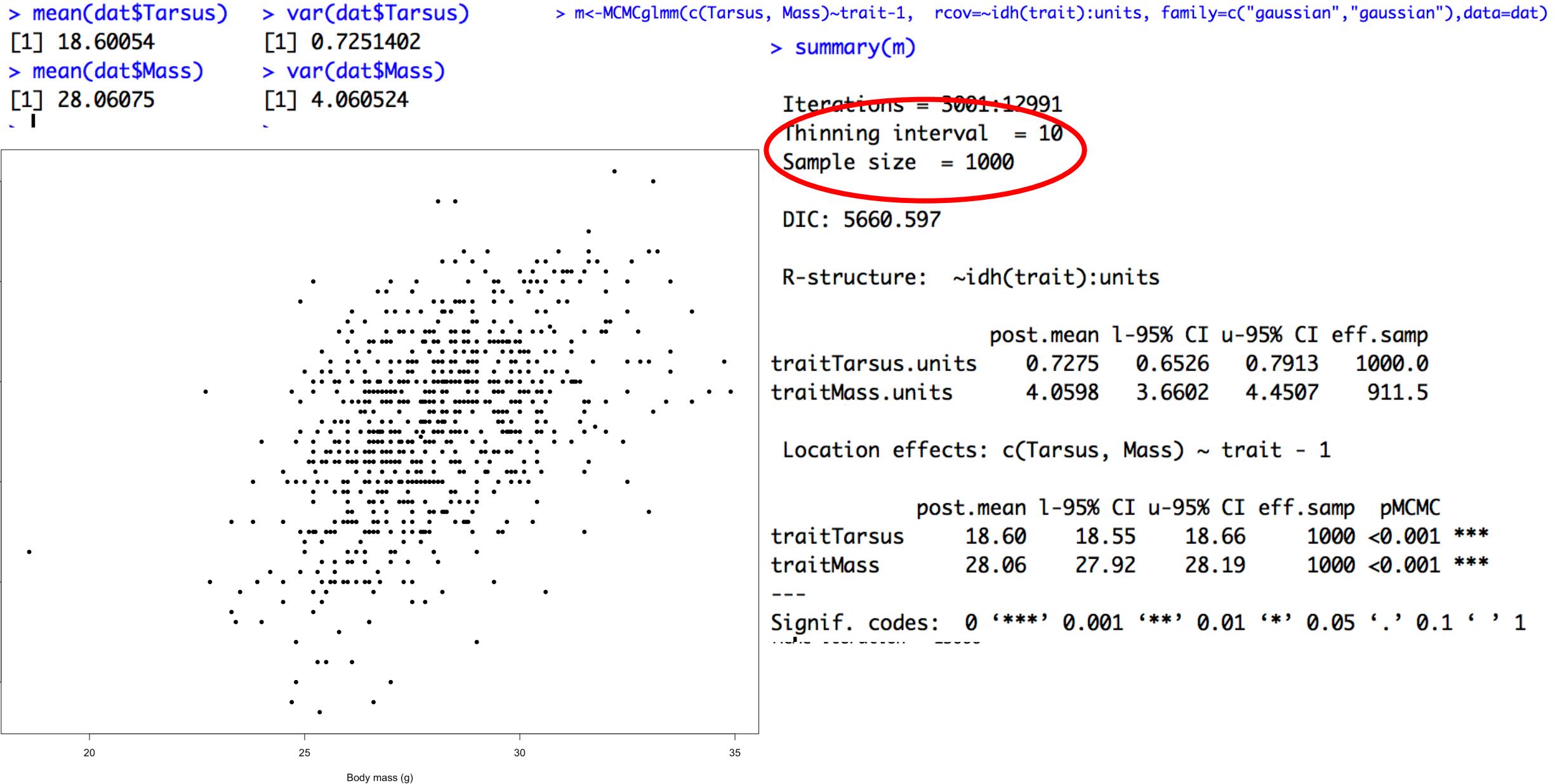
	post.mean	l-95% CI	u-95% CI	eff.samp	pMCMC
traitTarsus	18.60	18.55	18.66	1000	<0.001 ***
traitMass	28.06	27.92	28.19	1000	<0.001 ***

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Example – Sparrow Size

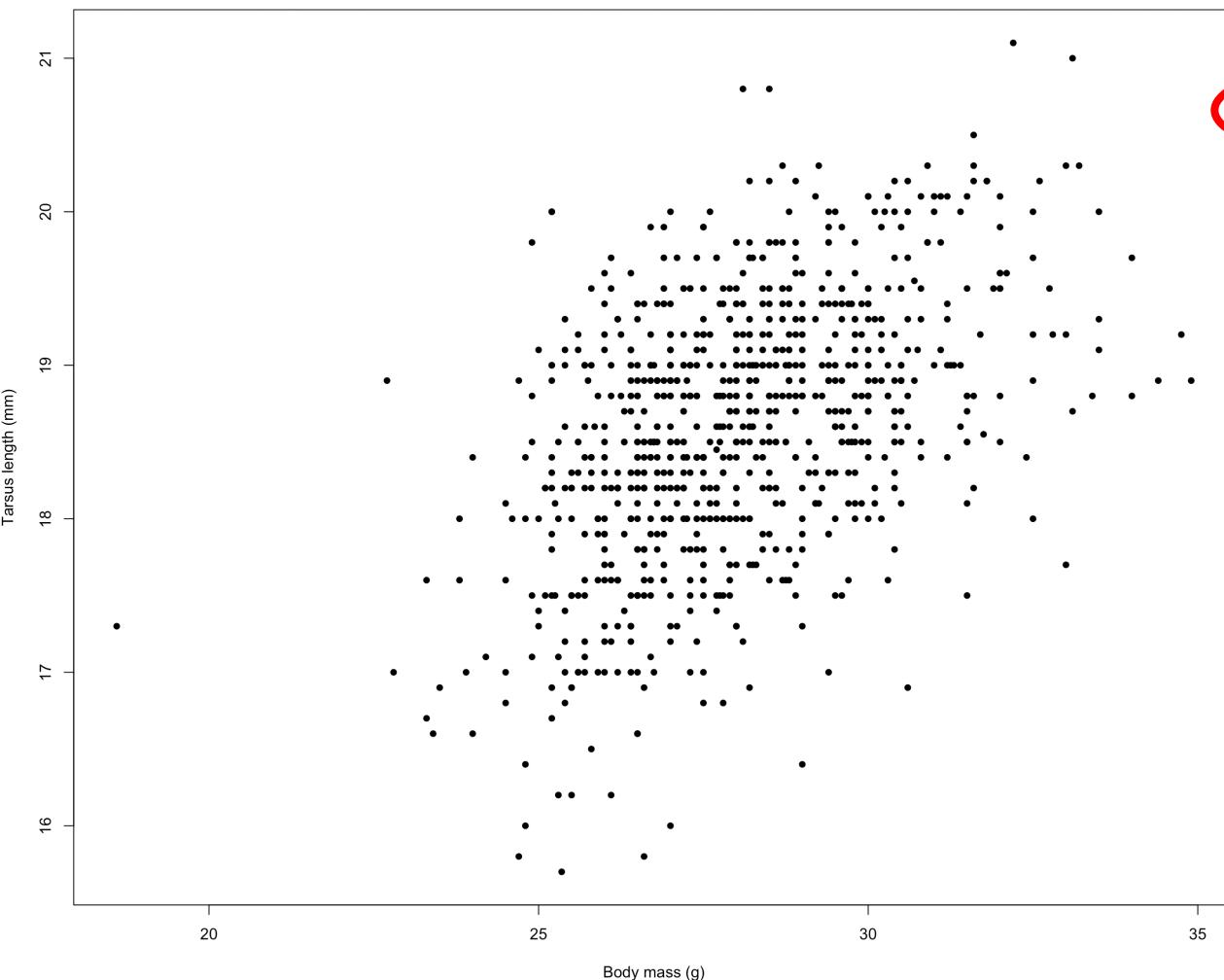


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DIC: 5660.597

Bayesian equivalent to AIC

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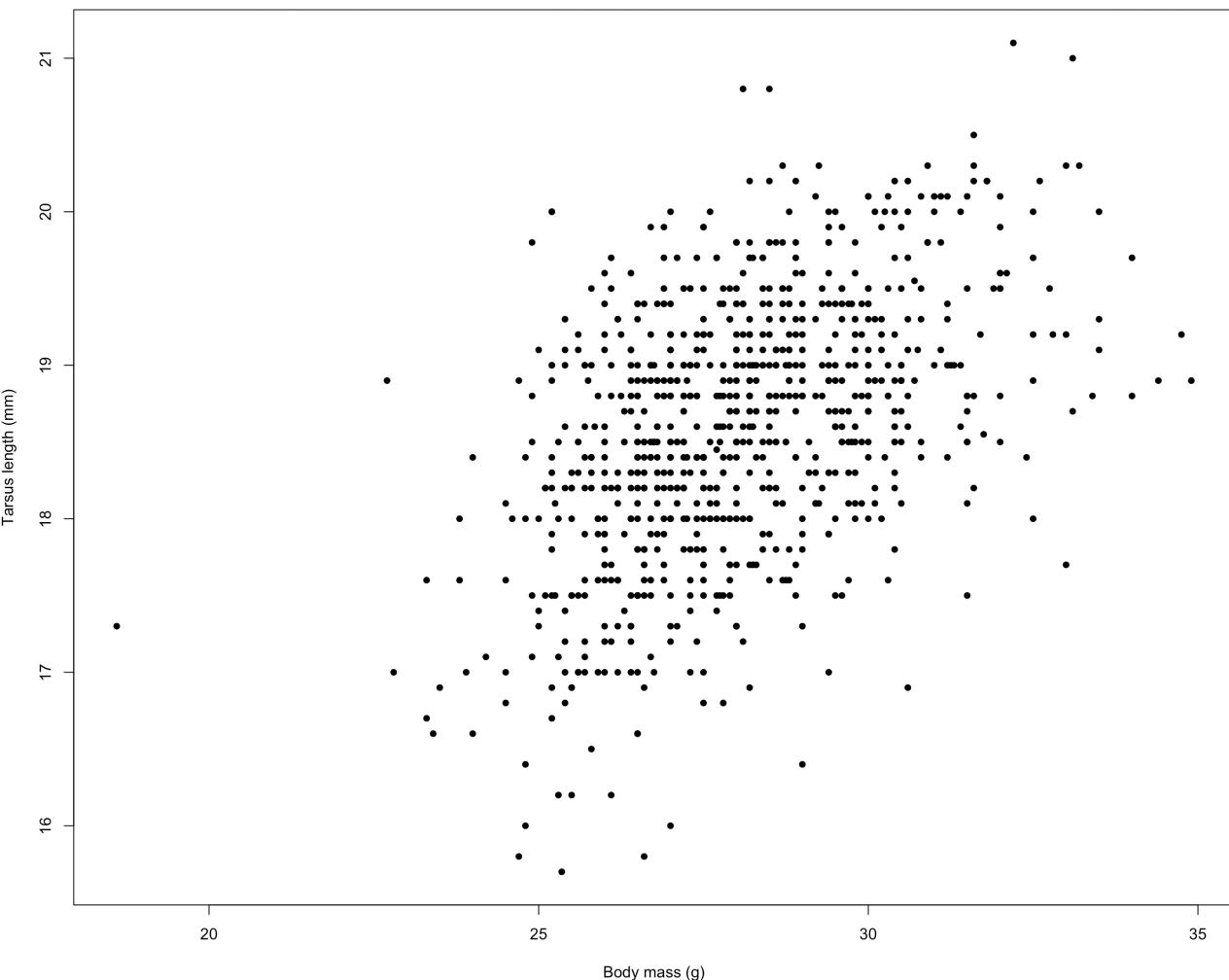
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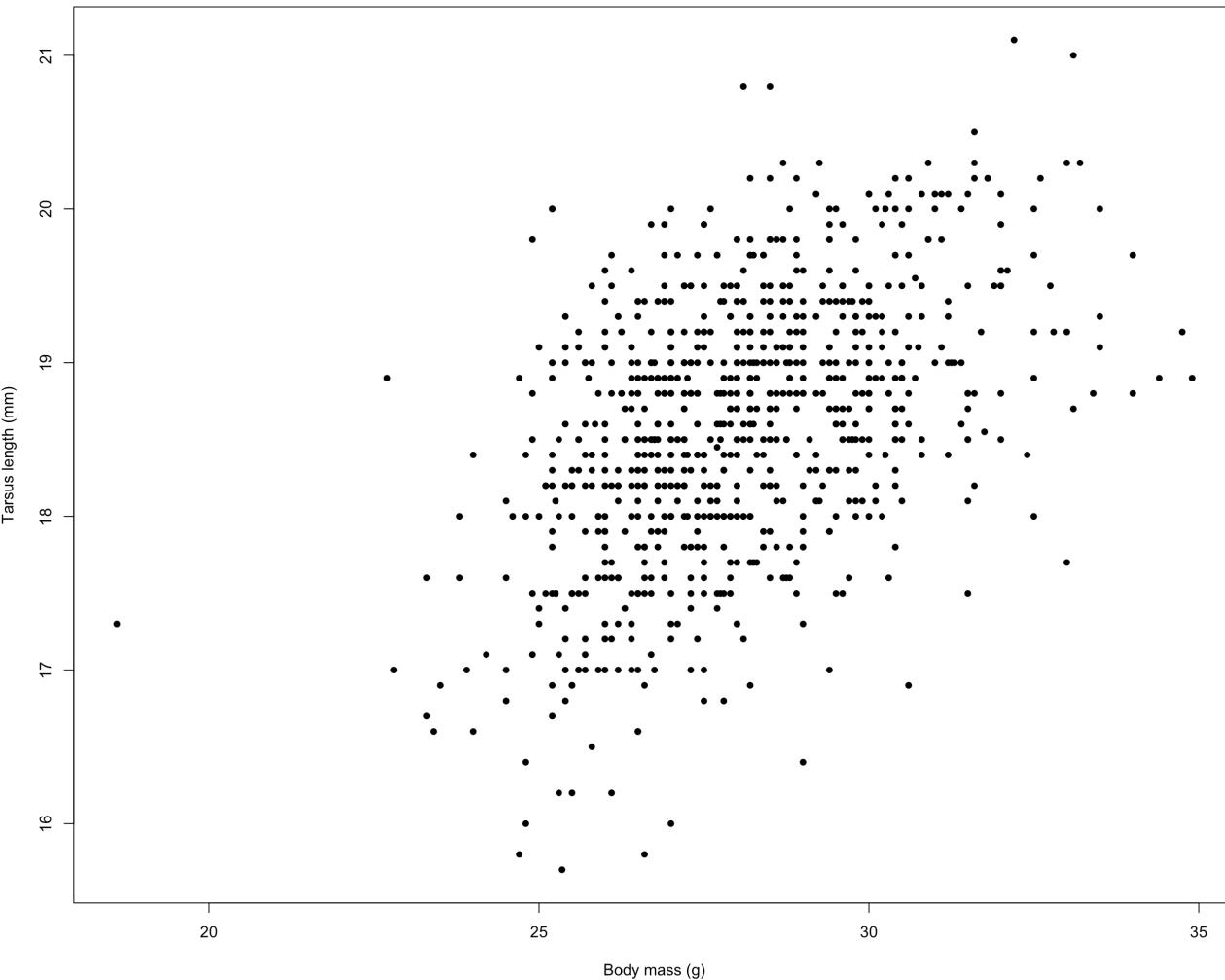
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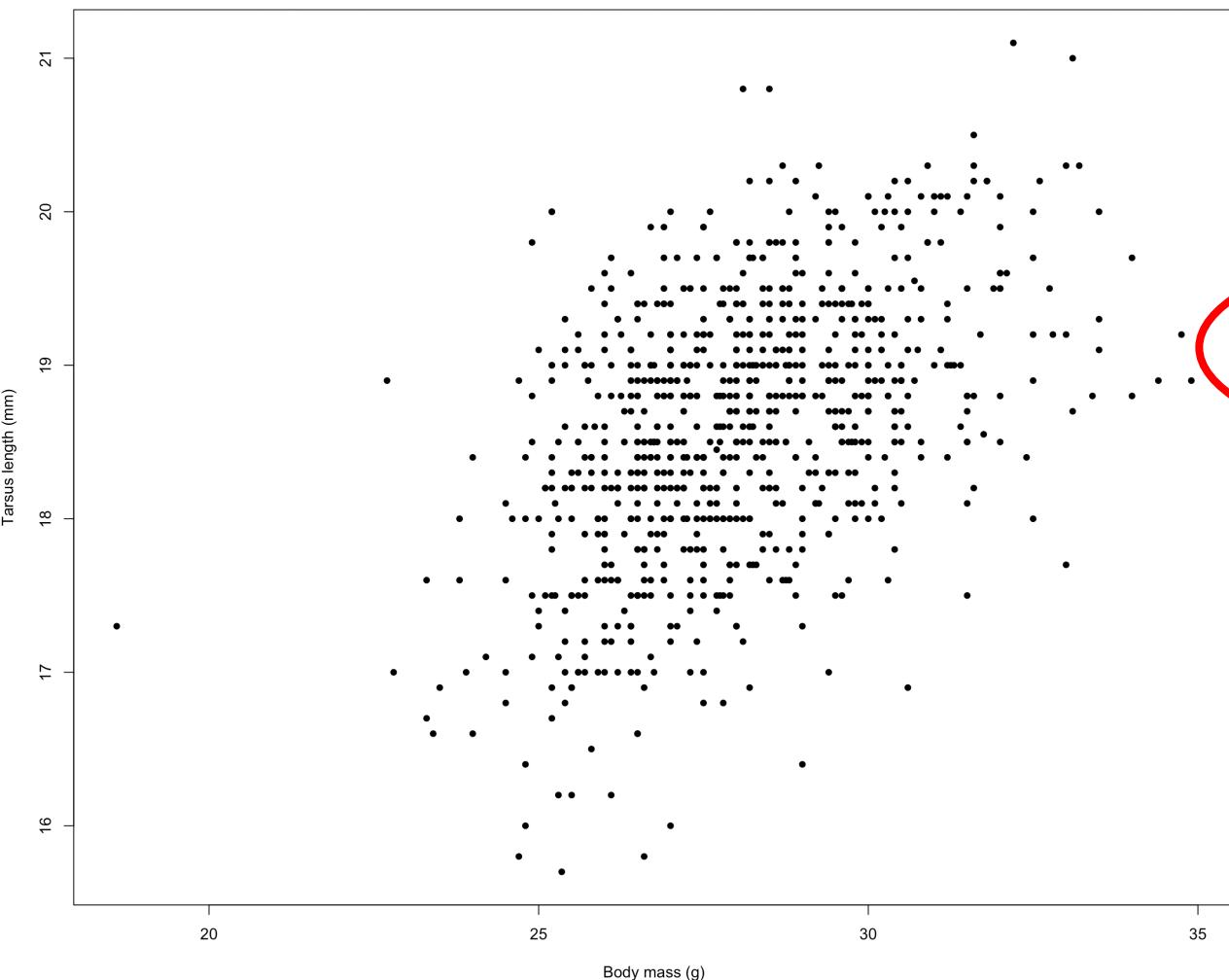
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> mean(dat$Tarsus)
```

```
[1] 18.60054
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```
> mean(dat$Mass)
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```
[1] 28.06075
```

```
.
```

```
> var(dat$Tarsus)
```

```
[1] 0.7251402
```

```
> var(dat$Mass)
```

```
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```

```
.
```

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```

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DIC: 5660.597

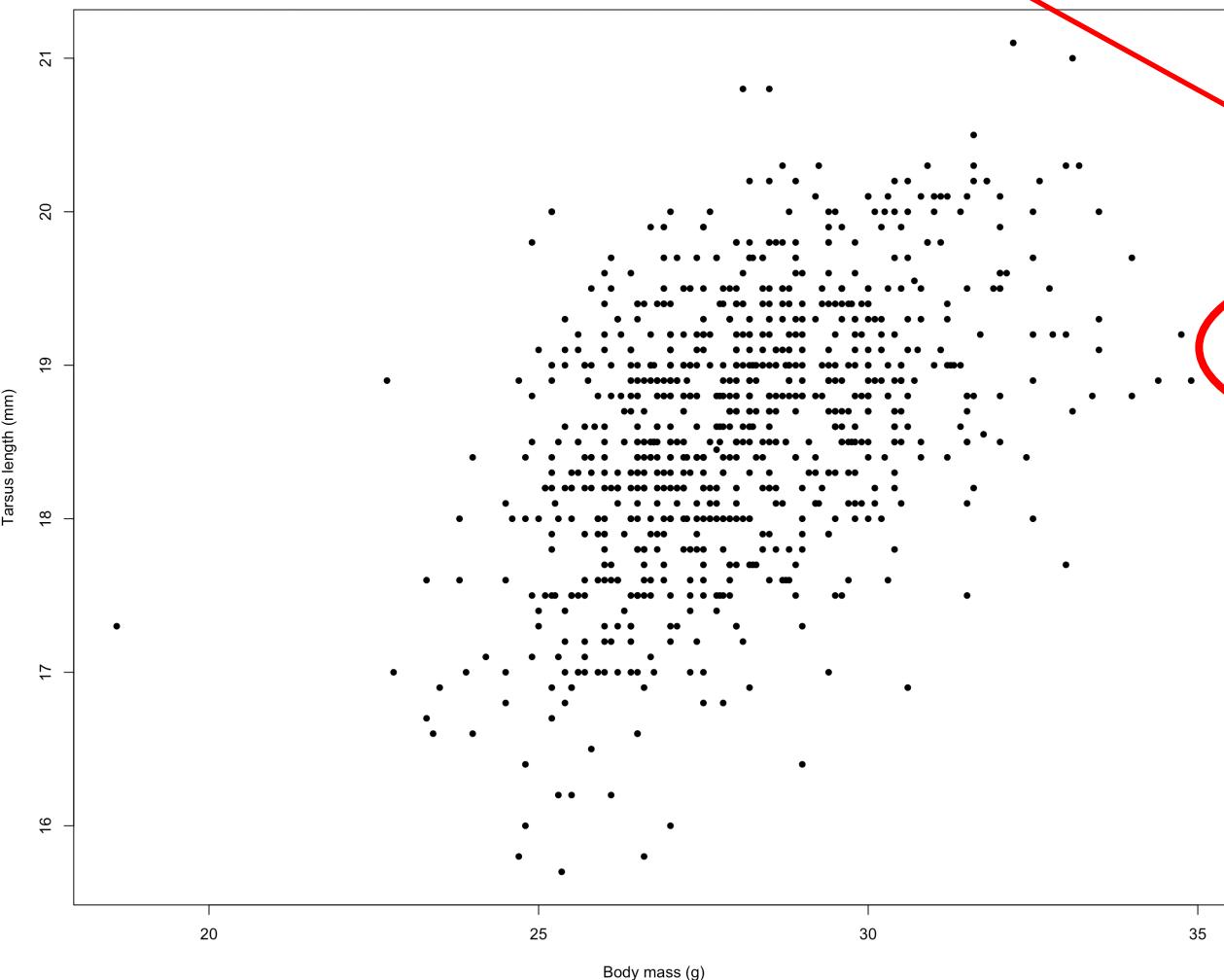
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DIC: 5660.597

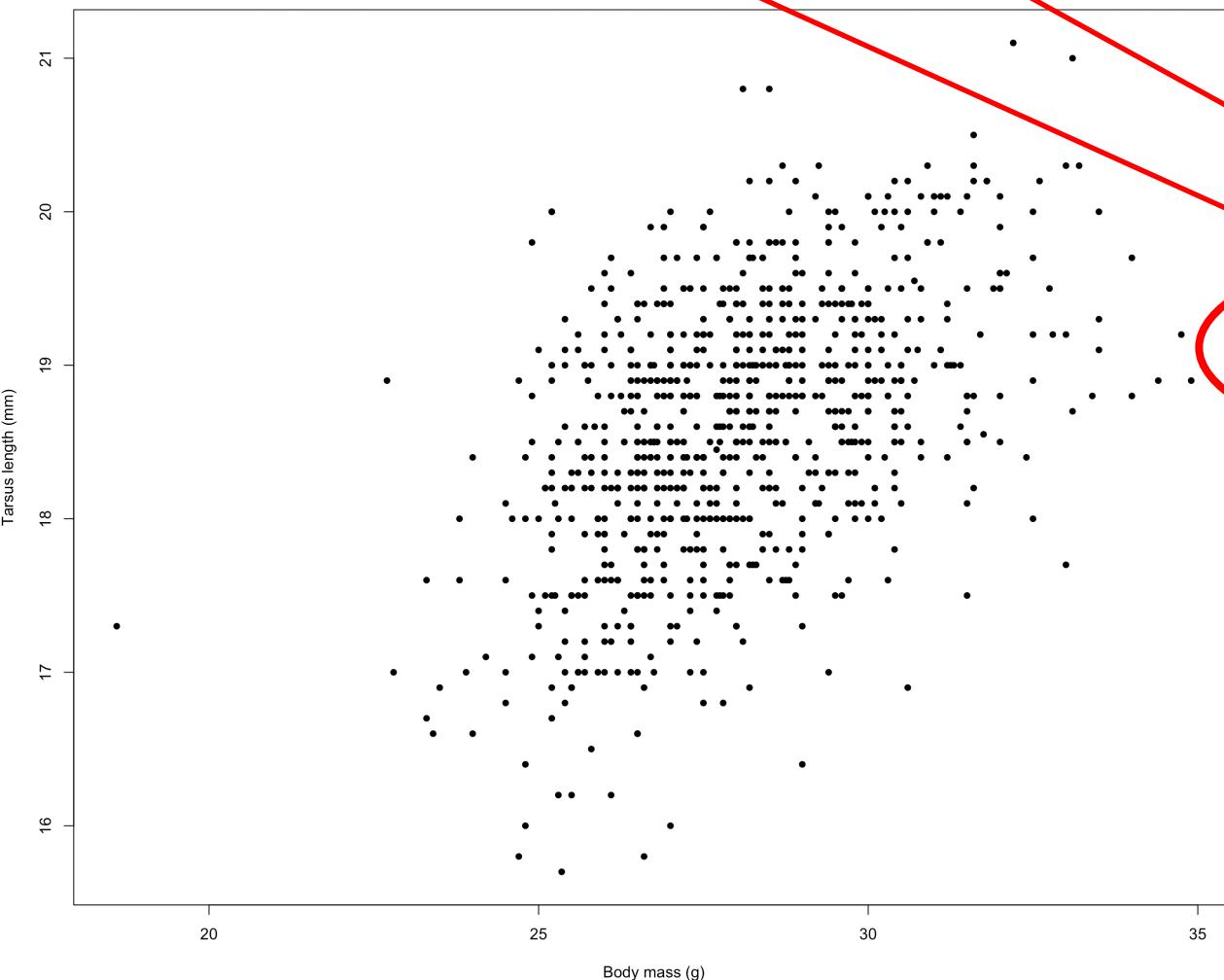
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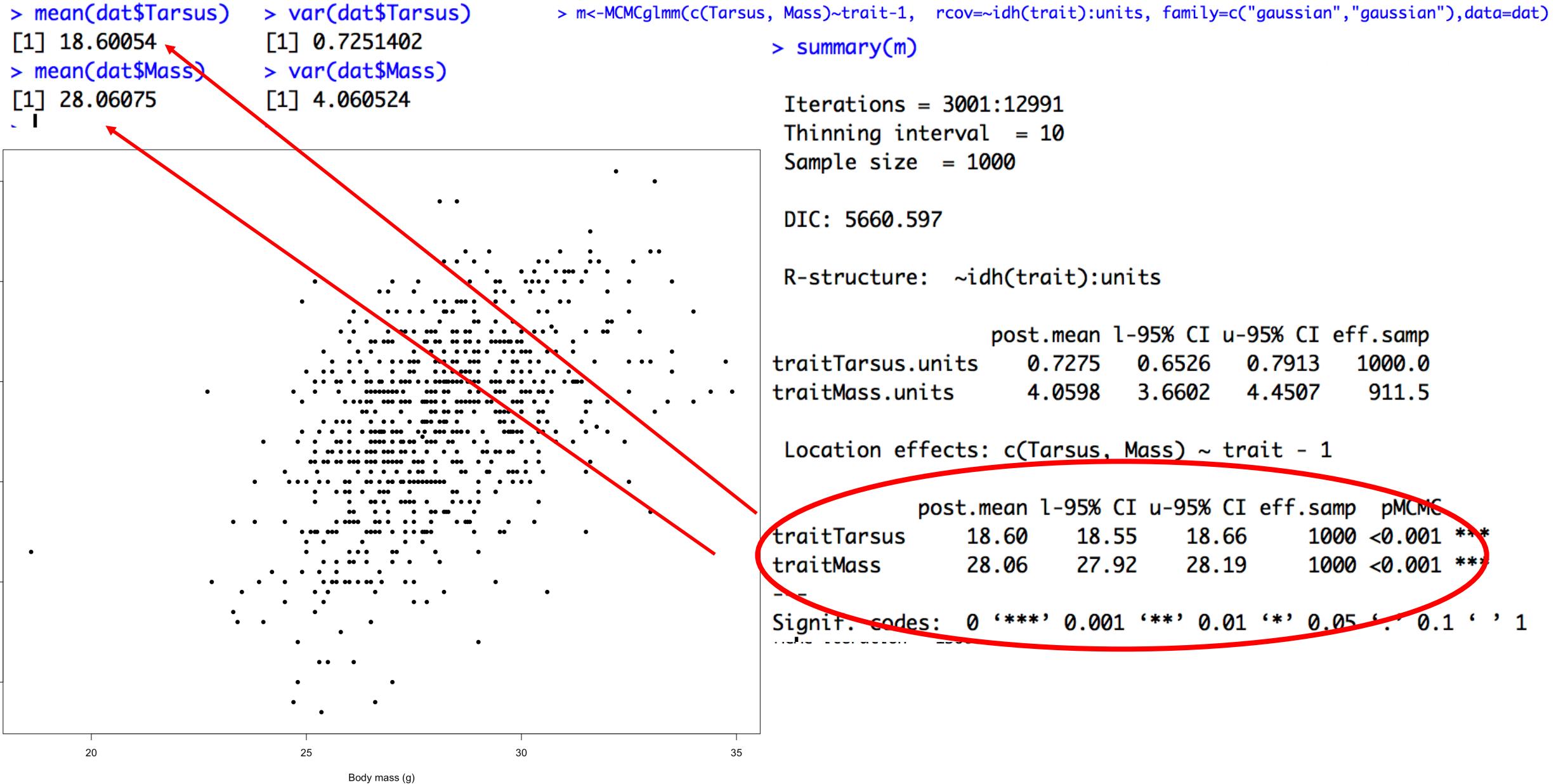
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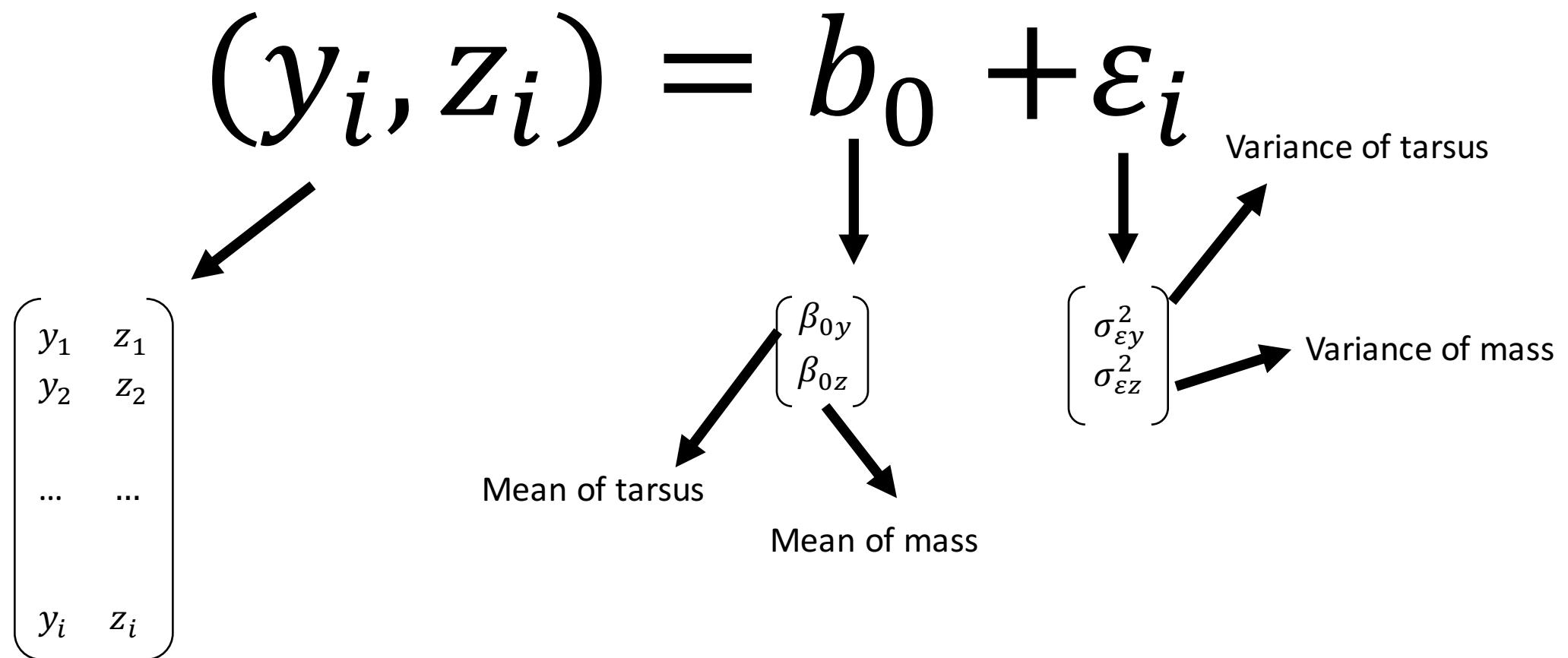


Example – Sparrow Size



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- (Tarsus,Mass)~1



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↓ ↓ ↓

$\begin{pmatrix} y_1 & z_1 \\ y_2 & z_2 \\ \dots & \dots \\ y_i & z_i \end{pmatrix}$

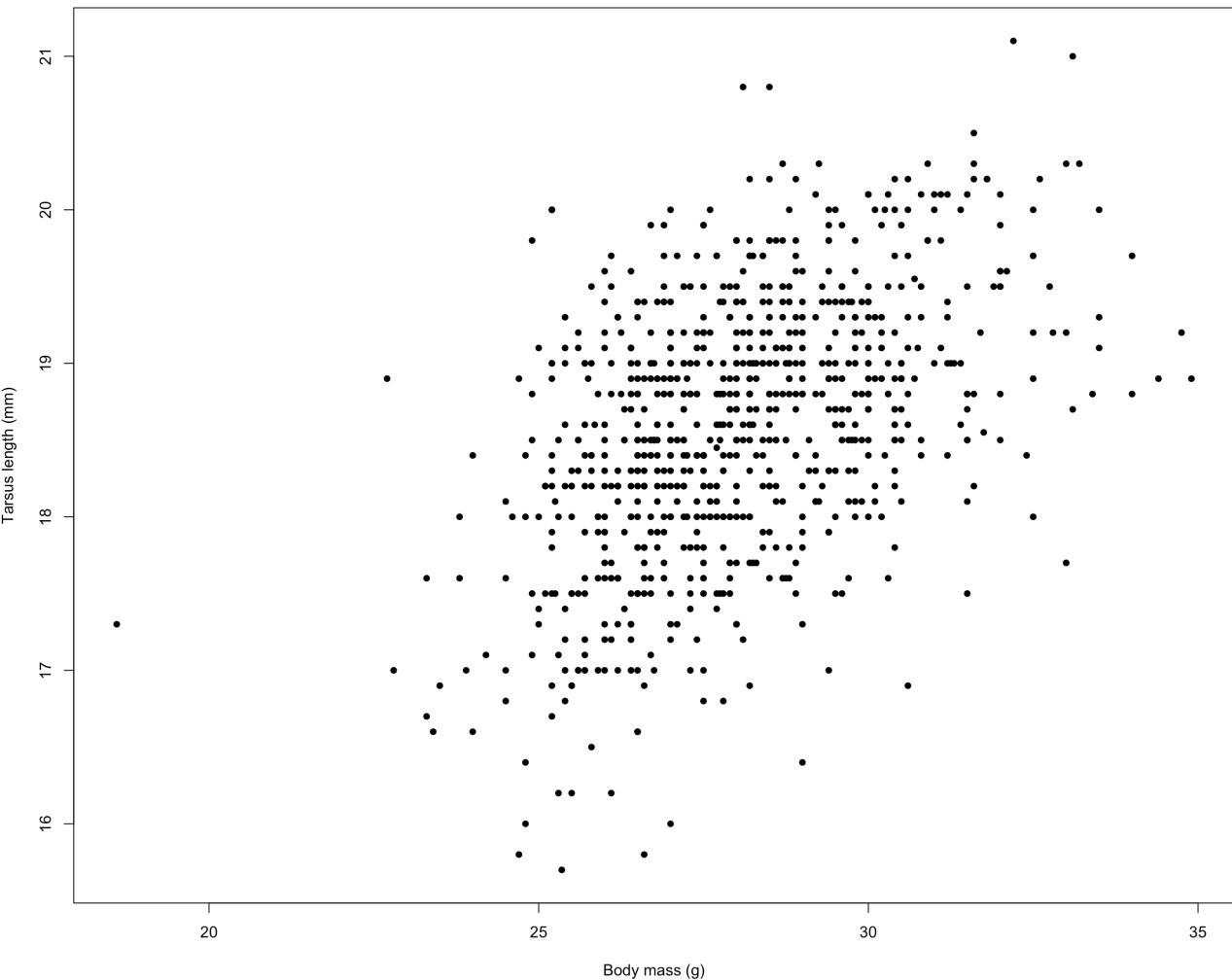
Mean of tarsus Mean of mass

$\begin{pmatrix} \beta_{0y} \\ \beta_{0z} \end{pmatrix}$

$\begin{pmatrix} \sigma_{\varepsilon y}^2 & COV(\varepsilon_y, \varepsilon_z) \\ COV(\varepsilon_z, \varepsilon_y) & \sigma_{\varepsilon z}^2 \end{pmatrix}$

Example – Sparrow Size

```
> mean(dat$Tarsus)    > var(dat$Tarsus)
[1] 18.60054           [1] 0.7251402      > cov(dat$Tarsus,dat$Mass)
> mean(dat$Mass)      > var(dat$Mass)     [1] 0.8068064
[1] 28.06075           [1] 4.060524
[1]
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[1] 28.06075 [1] 4.060524
>
> m<-MCMCglmm(c(Tarsus, Mass)~trait-1, rcov=~us(trait):units, family=c("gaussian","gaussian"),data=dat, verbose=FALSE)
> summary(m)
```

Example – Sparrow Size

```
> mean(dat$Tarsus)    > var(dat$Tarsus)
[1] 18.60054           [1] 0.7251402      > cov(dat$Tarsus,dat$Mass)
> mean(dat$Mass)      > var(dat$Mass)     [1] 0.8068064
[1] 28.06075          [1] 4.060524
> m<-MCMCglmm(c(Tarsus, Mass)~trait-1, rcov=~us(trait):units, family=c("gaussian","gaussian"), data=dat, verbose=FALSE)
> summary(m)
```

UNSTRUCTURED

UnreStricted

Example – Sparrow Size

```
> mean(dat$Tarsus) > var(dat$Tarsus)
[1] 18.60054 [1] 0.7251402 > cov(dat$Tarsus,dat$Mass)
> mean(dat$Mass) > var(dat$Mass) [1] 0.8068064
[1] 28.06075 [1] 4.060524
```

> m<-MCMCglmm(c(Tarsus, Mass)~trait-1, rcov=~us(trait):units, family=c("gaussian","gaussian"), data=dat, verbose=FALSE)

> summary(m)

Iterations = 3001:12991
Thinning interval = 10
Sample size = 1000

DIC: 5453.385

R-structure: ~us(trait):units

	post.mean	l-95% CI	u-95% CI	eff.samp
--	-----------	----------	----------	----------

traitTarsus:traitTarsus.units	0.7303	0.6650	0.8052	1000.0
traitMass:traitTarsus.units	0.8128	0.6786	0.9403	1000.0
traitTarsus:traitMass.units	0.8128	0.6786	0.9403	1000.0
traitMass:traitMass.units	4.0794	3.6691	4.4330	899.3

Location effects: c(Tarsus, Mass) ~ trait - 1

	post.mean	l-95% CI	u-95% CI	eff.samp	pMCMC
--	-----------	----------	----------	----------	-------

traitTarsus	18.60	18.55	18.66	1000	<0.001 ***
traitMass	28.06	27.94	28.20	1170	<0.001 ***

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Example – Sparrow Size

```
> mean(dat$Tarsus) > var(dat$Tarsus)
[1] 18.60054 [1] 0.7251402 > cov(dat$Tarsus,dat$Mass)
> mean(dat$Mass) > var(dat$Mass) [1] 0.8068064
[1] 28.06075 [1] 4.060524
```

```
> m<-MCMCglmm(c(Tarsus, Mass)~trait-1, rcov=~us(trait):units, family=c("gaussian","gaussian"),data=dat, verbose=FALSE)
> summary(m)
```

Iterations = 3001:12991

Thinning interval = 10

Sample size = 1000

DIC: 5453.385

R-structure: ~us(~trait):units

	post.mean	l-95% CI	u-95% CI	eff.samp
traitTarsus:traitTarsus.units	0.7303	0.6650	0.8052	1000.0
traitMass:traitTarsus.units	0.8128	0.6786	0.9403	1000.0
traitTarsus:traitMass.units	0.8128	0.6786	0.9403	1000.0
traitMass:traitMass.units	4.0794	3.6691	4.4330	899.3

Location effects: c(Tarsus, Mass) ~ trait - 1

	post.mean	l-95% CI	u-95% CI	eff.samp	pMCMC
traitTarsus	18.60	18.55	18.66	1000	<0.001 ***
traitMass	28.06	27.94	28.20	1170	<0.001 ***

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1					

Example – Sparrow Size

```
> mean(dat$Tarsus) > var(dat$Tarsus)
[1] 18.60054 [1] 0.7251402 > cov(dat$Tarsus,dat$Mass)
> mean(dat$Mass) > var(dat$Mass) [1] 0.8068064
[1] 28.06075 [1] 4.060524
```



```
> m<-MCMCglmm(c(Tarsus, Mass)~trait-1, rcov=~us(trait):units, family=c("gaussian","gaussian"),data=dat, verbose=FALSE)
> summary(m)
```

Iterations = 3001:12991

Thinning interval = 10

Sample size = 1000

DIC: 5453.385

Variance-Covariance matrix

R-structure: ~us(~trait):units

	post.mean	l-95% CI	u-95% CI	eff.samp
traitTarsus:traitTarsus.units	0.7303	0.6650	0.8052	1000.0
traitMass:traitTarsus.units	0.8128	0.6786	0.9403	1000.0
traitTarsus:traitMass.units	0.8128	0.6786	0.9403	1000.0
traitMass:traitMass.units	4.0794	3.6691	4.4330	899.3

Location effects: c(Tarsus, Mass) ~ trait - 1

	post.mean	l-95% CI	u-95% CI	eff.samp	pMCMC
traitTarsus	18.60	18.55	18.66	1000	<0.001 ***
traitMass	28.06	27.94	28.20	1170	<0.001 ***

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1					

Example – Sparrow Size

```
> mean(dat$Tarsus) > var(dat$Tarsus)
[1] 18.60054 [1] 0.7251402 > cov(dat$Tarsus,dat$Mass)
> mean(dat$Mass) > var(dat$Mass) [1] 0.8068064
[1] 28.06075 [1] 4.060524
```



```
> m<-MCMCglmm(c(Tarsus, Mass)~trait-1, rcov=~us(trait):units, family=c("gaussian","gaussian"),data=dat, verbose=FALSE)
> summary(m)
```

Iterations = 3001:12991

Thinning interval = 10

Sample size = 1000

DIC: 5453.385

R-structure: ~us(~trait+):units

	post.mean	l-95% CI	u-95% CI	eff.samp
traitTarsus:traitTarsus.units	0.7303	0.6650	0.8052	1000.0
traitMass:traitTarsus.units	0.8128	0.6786	0.9403	1000.0
traitTarsus:traitMass.units	0.8128	0.6786	0.9403	1000.0
traitMass:traitMass.units	4.0794	3.6691	4.4330	899.3

Location effects: c(Tarsus, Mass) ~ trait - 1

	post.mean	l-95% CI	u-95% CI	eff.samp	pMCMC
traitTarsus	18.60	18.55	18.66	1000	<0.001 ***
traitMass	28.06	27.94	28.20	1170	<0.001 ***

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1					

Variance-Covariance matrix

$$\begin{pmatrix} \sigma_{\varepsilon_y}^2 & COV(\varepsilon_y, \varepsilon_z) \\ COV(\varepsilon_z, \varepsilon_y) & \sigma_{\varepsilon_z}^2 \end{pmatrix}$$

Example – Sparrow Size

```
> mean(dat$Tarsus) > var(dat$Tarsus)
[1] 18.60054 [1] 0.7251402 > cov(dat$Tarsus,dat$Mass)
> mean(dat$Mass) > var(dat$Mass) [1] 0.8068064
[1] 28.06075 [1] 4.060524
```



```
> m<-MCMCglmm(c(Tarsus, Mass)~trait-1, rcov=~us(trait):units, family=c("gaussian","gaussian"),data=dat, verbose=FALSE)
> summary(m)
```

Iterations = 3001:12991

Thinning interval = 10

Sample size = 1000

DIC: 5453.385

R-structure: ~us(+trait):units

	post.mean	l-95% CI	u-95% CI	eff.samp
traitTarsus:traitTarsus.units	0.7303	0.6650	0.8052	1000.0
traitMass:traitTarsus.units	0.8128	0.6786	0.9403	1000.0
traitTarsus:traitMass.units	0.8128	0.6786	0.9403	1000.0
traitMass:traitMass.units	4.0794	3.6691	4.4330	899.3

Location effects: c(Tarsus, Mass) ~ trait - 1

	post.mean	l-95% CI	u-95% CI	eff.samp	pMCMC
traitTarsus	18.60	18.55	18.66	1000	<0.001 ***
traitMass	28.06	27.94	28.20	1170	<0.001 ***

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1					

Variance-Covariance matrix

$$\begin{pmatrix} \sigma_{\varepsilon_y}^2 & COV(\varepsilon_y, \varepsilon_z) \\ COV(\varepsilon_z, \varepsilon_y) & \sigma_{\varepsilon_z}^2 \end{pmatrix}$$

$$\begin{pmatrix} 0.73 (0.67-0.81) & 0.81 (0.68-0.94) \\ 0.81 (0.68-0.94) & 4.08 (3.67-4.43) \end{pmatrix}$$

Example – Sparrow Size - extensions

- (Tarsus,Mass)~1, random = BirdID

$$(y_{i,j}, z_{i,j}) = b_0 + \alpha_j + \varepsilon_i$$

Diagram illustrating the components of the equation:

- A black arrow points from the term b_0 to a matrix $\begin{pmatrix} y_1 & z_1 \\ y_2 & z_2 \\ \dots & \dots \\ y_i & z_i \end{pmatrix}$.
- A black arrow points from the term α_j to a vector $\begin{pmatrix} \beta_{0y} \\ \beta_{0z} \end{pmatrix}$, labeled "Mean of tarsus" below it.
- A red arrow points from the term ε_i to a matrix $\begin{pmatrix} \sigma_{\alpha y}^2 & \text{COV}(\varepsilon_y, \varepsilon_z) \\ \text{COV}(\varepsilon_z, \varepsilon_y) & \sigma_{\alpha z}^2 \end{pmatrix}$.

Example – Sparrow Size

```
> m<-MCMCglmm(c(Tarsus, Mass)~trait-1, random=~idh(trait):BirdID, rcov=~us(trait):uni:s, family=c("gaussian","gaussian"),data=dat, verbose=FALSE)
```

```
> summary(m)
```

Iterations = 3001:12991
Thinning interval = 10
Sample size = 1000

DIC: 3783.797

G-structure: ~idh(trait):BirdID

	post.mean	l-95% CI	u-95% CI	eff.samp
traitTarsus.BirdID	0.6477	0.5381	0.7674	1000
traitMass.BirdID	2.7315	2.1217	3.2869	1000

R-structure: ~us(trait):units

	post.mean	l-95% CI	u-95% CI	eff.samp
traitTarsus:traitTarsus.units	0.10717	0.09512	0.11923	1106
traitMass:traitTarsus.units	0.01168	-0.02326	0.04541	1000
traitTarsus:traitMass.units	0.01168	-0.02326	0.04541	1000
traitMass:traitMass.units	1.58148	1.40069	1.77900	1000

Location effects: c(Tarsus, Mass) ~ trait - 1

	post.mean	l-95% CI	u-95% CI	eff.samp	pMCMC
traitTarsus	18.59	18.50	18.68	1034.3	<0.001 ***
traitMass	28.16	27.96	28.37	908.1	<0.001 ***

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

```
> summary(m)
```

Iterations = 3001:12991
Thinning interval = 10
Sample size = 1000

DIC: 3783.797

G-structure: ~idh(trait):BirdID

	post.mean	l-95% CI	u-95% CI	eff.samp
traitTarsus.BirdID	0.6477	0.5381	0.7674	1000
traitMass.BirdID	2.7315	2.1217	3.2869	1000

R-structure: ~us(trait):units

	post.mean	l-95% CI	u-95% CI	eff.samp
traitTarsus:traitTarsus.units	0.10717	0.09512	0.11923	1106
traitMass:traitTarsus.units	0.01168	-0.02326	0.04541	1000
traitTarsus:traitMass.units	0.01168	-0.02326	0.04541	1000
traitMass:traitMass.units	1.58148	1.40069	1.77900	1000

Location effects: c(Tarsus, Mass) ~ trait - 1

	post.mean	l-95% CI	u-95% CI	eff.samp	pMCMC
traitTarsus	18.59	18.50	18.68	1034.3	<0.001 ***
traitMass	28.16	27.96	28.37	908.1	<0.001 ***

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Example – Sparrow Size - extensions

- (Tarsus,Mass)~1, random = BirdID

$$(y_{i,j}, z_{i,j}) = b_0 + \alpha_j + \varepsilon_i$$

Diagram illustrating the components of the equation:

- An arrow points from the term $(y_{i,j}, z_{i,j})$ to a matrix:
$$\begin{pmatrix} y_1 & z_1 \\ y_2 & z_2 \\ \dots & \dots \\ y_i & z_i \end{pmatrix}$$
- An arrow points from the term b_0 to a vector:
$$\begin{pmatrix} \beta_{0y} \\ \beta_{0z} \end{pmatrix}$$

labeled "Mean of tarsus" and "Mean of mass".

- An arrow points from the term ε_i to a matrix:
$$\begin{pmatrix} \sigma_{\alpha y}^2 & \sigma_{\alpha z}^2 \\ \sigma_{\varepsilon y}^2 & COV(\varepsilon_y, \varepsilon_z) \\ COV(\varepsilon_z, \varepsilon_y) & \sigma_{\varepsilon z}^2 \end{pmatrix}$$

Example – Sparrow Size - extensions

- (Tarsus,Mass)~1, random = BirdID

$$(y_{i,j}, z_{i,j}) = b_0 + \alpha_j + \varepsilon_i$$

↓

Mean of tarsus

Mean of mass

↓

$\begin{pmatrix} y_1 & z_1 \\ y_2 & z_2 \\ \dots & \dots \\ y_i & z_i \end{pmatrix}$

$\begin{pmatrix} \beta_{0y} \\ \beta_{0z} \end{pmatrix}$

$\begin{pmatrix} \sigma_{\alpha y}^2 & COV(\alpha_y, \alpha_z) \\ COV(\alpha_y, \alpha_z) & \sigma_{\alpha z}^2 \end{pmatrix}$

$\begin{pmatrix} \sigma_{\varepsilon y}^2 & COV(\varepsilon_y, \varepsilon_z) \\ COV(\varepsilon_z, \varepsilon_y) & \sigma_{\varepsilon z}^2 \end{pmatrix}$

Example – Sparrow Size

- Hypothesis:
- Sparrows that get a lot of parental care grow to become larger adults

Example – Sparrow Size

```
> m<-MCMCglmm(c(Tarsus, Mass)~trait-1, random=~us(trait):BirdID, rcov=~us(trait):units, family=c("gaussian","gaussian"),data=dat, verbose=FALSE)
```

> summary(m)

Iterations = 3001:12991
Thinning interval = 10
Sample size = 1000

DIC: 3740.01

G-structure: ~us(trait):BirdID

	post.mean	l-95% CI	u-95% CI	eff.samp
traitTarsus:traitTarsus.BirdID	0.6545	0.5457	0.7688	1000
traitMass:traitTarsus.BirdID	0.9069	0.7146	1.1309	1000
traitTarsus:traitMass.BirdID	0.9069	0.7146	1.1309	1000
traitMass:traitMass.BirdID	2.7366	2.2478	3.3672	1000

R-structure: ~us(trait):units

	post.mean	l-95% CI	u-95% CI	eff.samp
traitTarsus:traitTarsus.units	0.106649	0.09488	0.11921	1116.0
traitMass:traitTarsus.units	-0.009273	-0.04226	0.03019	993.3
traitTarsus:traitMass.units	-0.009273	-0.04226	0.03019	993.3
traitMass:traitMass.units	1.584112	1.39463	1.78875	1000.0

Location effects: c(Tarsus, Mass) ~ trait - 1

	post.mean	l-95% CI	u-95% CI	eff.samp	pMCMC
traitTarsus	18.59	18.50	18.69	1105	<0.001 ***
traitMass	28.15	27.94	28.33	1123	<0.001 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1					

```
> summary(m)
```

Iterations = 3001:12991
Thinning interval = 10
Sample size = 1000

DIC: 3740.01

G-structure: ~us(trait):BirdID

	post.mean	l-95% CI	u-95% CI	eff.samp
traitTarsus:traitTarsus.BirdID	0.6545	0.5457	0.7688	1000
traitMass:traitTarsus.BirdID	0.9069	0.7146	1.1309	1000
traitTarsus:traitMass.BirdID	0.9069	0.7146	1.1309	1000
traitMass:traitMass.BirdID	2.7366	2.2478	3.3672	1000

R-structure: ~us(trait):units

	post.mean	l-95% CI	u-95% CI	eff.samp
traitTarsus:traitTarsus.units	0.106649	0.09488	0.11921	1116.0
traitMass:traitTarsus.units	-0.009273	-0.04226	0.03019	993.3
traitTarsus:traitMass.units	-0.009273	-0.04226	0.03019	993.3
traitMass:traitMass.units	1.584112	1.39463	1.78875	1000.0

Location effects: c(Tarsus, Mass) ~ trait - 1

	post.mean	l-95% CI	u-95% CI	eff.samp	pMCMC
traitTarsus	18.59	18.50	18.69	1105	<0.001 ***
traitMass	28.15	27.94	28.33	1123	<0.001 ***

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

```

> mReduced<-MCMCglmm(c(Tarsus, Mass)~trait-1, random=~us(trait):BirdID, rcov=~idh(trait):units, family=c("gaussian","gaussian"),data=dat, verbose=FALSE)
> m<-MCMCglmm(c(Tarsus, Mass)~trait-1, random=~us(trait):BirdID, rcov=~us(trait):units, family=c("gaussian","gaussian"),data=dat, verbose=FALSE)

```

$$\begin{pmatrix} \sigma_{\alpha y}^2 & COV(\alpha_y, \alpha_z) \\ COV(\alpha_y, \alpha_z) & \sigma_{\alpha z}^2 \end{pmatrix} \begin{pmatrix} \sigma_{\varepsilon y}^2 & COV(\varepsilon_y, \varepsilon_z) \\ COV(\varepsilon_z, \varepsilon_y) & \sigma_{\varepsilon z}^2 \end{pmatrix}$$

$$\begin{pmatrix} \sigma_{\alpha y}^2 & COV(\alpha_y, \alpha_z) \\ COV(\alpha_y, \alpha_z) & \sigma_{\alpha z}^2 \end{pmatrix} \begin{pmatrix} \sigma_{\varepsilon y}^2 & 0 \\ 0 & \sigma_{\varepsilon z}^2 \end{pmatrix}$$

```

> mReduced<-MCMCglmm(c(Tarsus, Mass)~trait-1, random=~us(trait):BirdID, rcov=~idh(trait):units, family=c("gaussian","gaussian"),data=dat, verbose=FALSE)
> m<-MCMCglmm(c(Tarsus, Mass)~trait-1, random=~us(trait):BirdID, rcov=~us(trait):units, family=c("gaussian","gaussian"),data=dat, verbose=FALSE)

```

```

> mReduced$DIC
[1] 3739.497
> m$DIC
[1] 3740.01
>

```

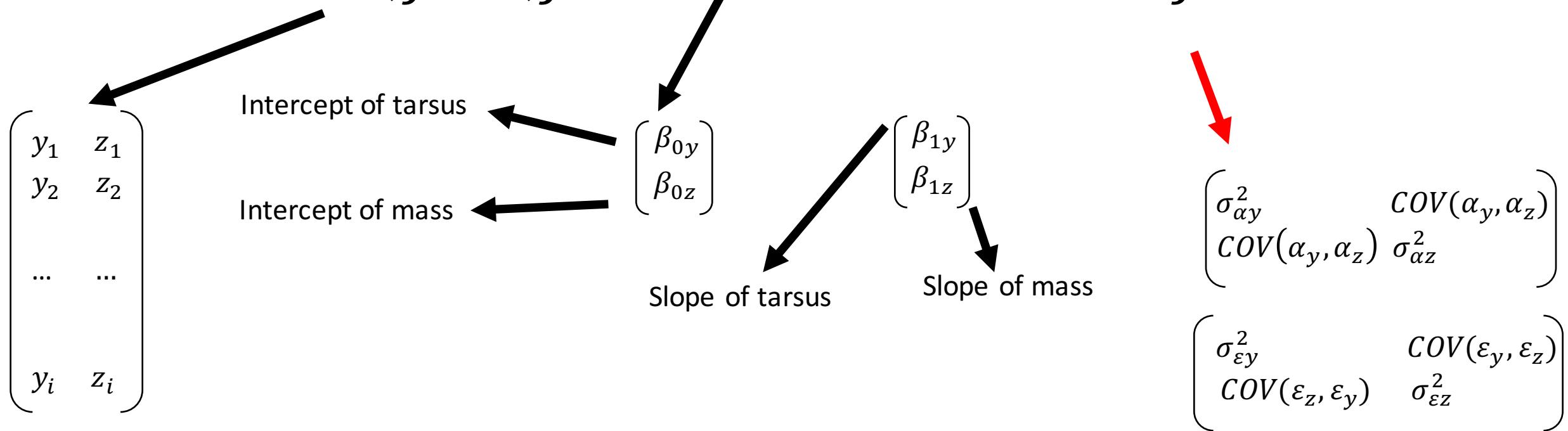
$$\begin{pmatrix} \sigma_{\alpha y}^2 & COV(\alpha_y, \alpha_z) \\ COV(\alpha_y, \alpha_z) & \sigma_{\alpha z}^2 \end{pmatrix} \begin{pmatrix} \sigma_{\varepsilon y}^2 & COV(\varepsilon_y, \varepsilon_z) \\ COV(\varepsilon_z, \varepsilon_y) & \sigma_{\varepsilon z}^2 \end{pmatrix}$$

$$\begin{pmatrix} \sigma_{\alpha y}^2 & COV(\alpha_y, \alpha_z) \\ COV(\alpha_y, \alpha_z) & \sigma_{\alpha z}^2 \end{pmatrix} \begin{pmatrix} \sigma_{\varepsilon y}^2 & 0 \\ 0 & \sigma_{\varepsilon z}^2 \end{pmatrix}$$

Example – Sparrow Size - extensions

- $(\text{Tarsus}, \text{Mass}) \sim \text{Sex}$, random = BirdID

$$(y_{i,j}, z_{i,j}) = b_0 + b_0 X_1 + \alpha_j + \varepsilon_i$$



More extensions

- GLMMs – mixed models with different error distributions
 - Poisson
 - Binomial
 - Mixed!

More extensions

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 - Binomial
- Multivariate models (with more than 2 responses)

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- GLMMs with relatedness matrix as random effect (= animal models)

More extensions

- GLMMs – mixed models with different error distributions
 - Poisson
 - Binomial
- Multivariate models (with more than 2 responses)
- GAM models with exotic link functions
- GLMMs with relatedness matrix as random effect (= animal models)
- GLMMS with phylogeny as random effect

More extensions

- GLMMs – mixed models with different error distributions
 - Poisson
 - Binomial
- Multivariate models (with more than 2 responses)
- GAM models with exotic link functions
- GLMMs with relatedness matrix as random effect (= animal models)
- GLMMS with phylogeny as random effect
- GLMMS for meta-analysis (phylogeny or other random effects)

EVEN! more extensions

- ZIP – Zero-inflated models
- ZAP – Zero altered models
- ZAT – Zero-truncated models

HO – bivariate models and others

- Use this time to keep us with other HO's
- Only do bivariate HO once you feel comfortable with the other HO's