article

Richel Bilderbeek

July 6, 2017

Questions:

- Why use the *absolute* deviation from cage mean body mass, as in figure 2?
- How would it look like if the signed deviation is used?

Experiment

```
traits_filename <- "Bolnick_traits.txt"

if (!file.exists(traits_filename)) {
  stop("File '", traits_filename,
    "' not found. Set the correct working directory")
}

traits <- read.csv(traits_filename, sep = " ")
print(names(traits))
```

```
##  [1] "sampleID"    "fishID"      "origin"      "enclosure"   "transplant"
##  [6] "date_in"     "pre_mass"    "pre_length"  "post_mass"   "post_length"
## [11] "pw"          "bd"          "gw"          "grn"         "grl"
## [16] "sex"         "survived"
```

```
knitr::kable(head(traits))
```

sampleID	fishID	origin	enclosure	transplant	date_in	pre_mass	pre_length	post_mass	post_length	p
118	118	Stream	S2	Stream	06/03/11	1.75	4.9	NA	NA	N
12	12	Stream	L8	Lake	06/02/11	1.13	4.6	NA	NA	N
122	122	Lake	S2	Stream	06/03/11	2.37	5.6	NA	NA	N
123	123	Lake	S3	Stream	06/03/11	1.71	5.2	NA	NA	N
124	124	Lake	S4	Stream	06/03/11	2.45	5.4	NA	NA	N
127	127	Lake	S7	Stream	06/03/11	0.85	4.0	NA	NA	N

```
calc_history <- function(origin, transplant) {
  from <- ifelse(origin == "Stream", "s", "l")
  to <- ifelse(transplant == "Stream", "s", "l")
  return(paste0(from, to))
}
traits$history <- rep(NA, nrow(traits))
#dplyr::tally(traits$origin)
traits$history <- as.factor(mapply(calc_history, traits$origin, traits$transplant))

# Calculate mean body size per enclosure
enclosure <- traits %>% group_by(enclosure) %>%
```

```
        summarise(mean_pre=mean(pre_mass), mean_post=mean(post_mass))

fig2 <- merge(
  x = subset(traits, select = c("enclosure", "origin", "transplant", "history", "pre_mass", "post_mass"
  y = enclosure, by = "enclosure", all = TRUE)
fig2$delta_pre <- fig2$pre_mass - fig2$mean_pre
fig2$delta_post <- fig2$post_mass - fig2$mean_post
fig2$survived <- as.double(fig2$survived)

print(names(fig2))

## [1] "enclosure"  "origin"     "transplant" "history"    "pre_mass"
## [6] "post_mass"  "survived"   "mean_pre"   "mean_post"  "delta_pre"
## [11] "delta_post"

knitr::kable(head(fig2))
```

enclosure	origin	transplant	history	pre_mass	post_mass	survived	mean_pre	mean_post	delta_pre	de
L1	Stream	Lake	sl	1.78	1.61	1	1.256667	NA	0.5233333	
L1	Lake	Lake	ll	1.00	NA	0	1.256667	NA	-0.2566667	
L1	Lake	Lake	ll	0.99	NA	0	1.256667	NA	-0.2666667	
L10	Lake	Lake	ll	1.71	NA	0	1.663333	NA	0.0466667	
L10	Stream	Lake	sl	2.06	1.90	1	1.663333	NA	0.3966667	
L10	Stream	Lake	sl	1.22	NA	0	1.663333	NA	-0.4433333	

At the beginning

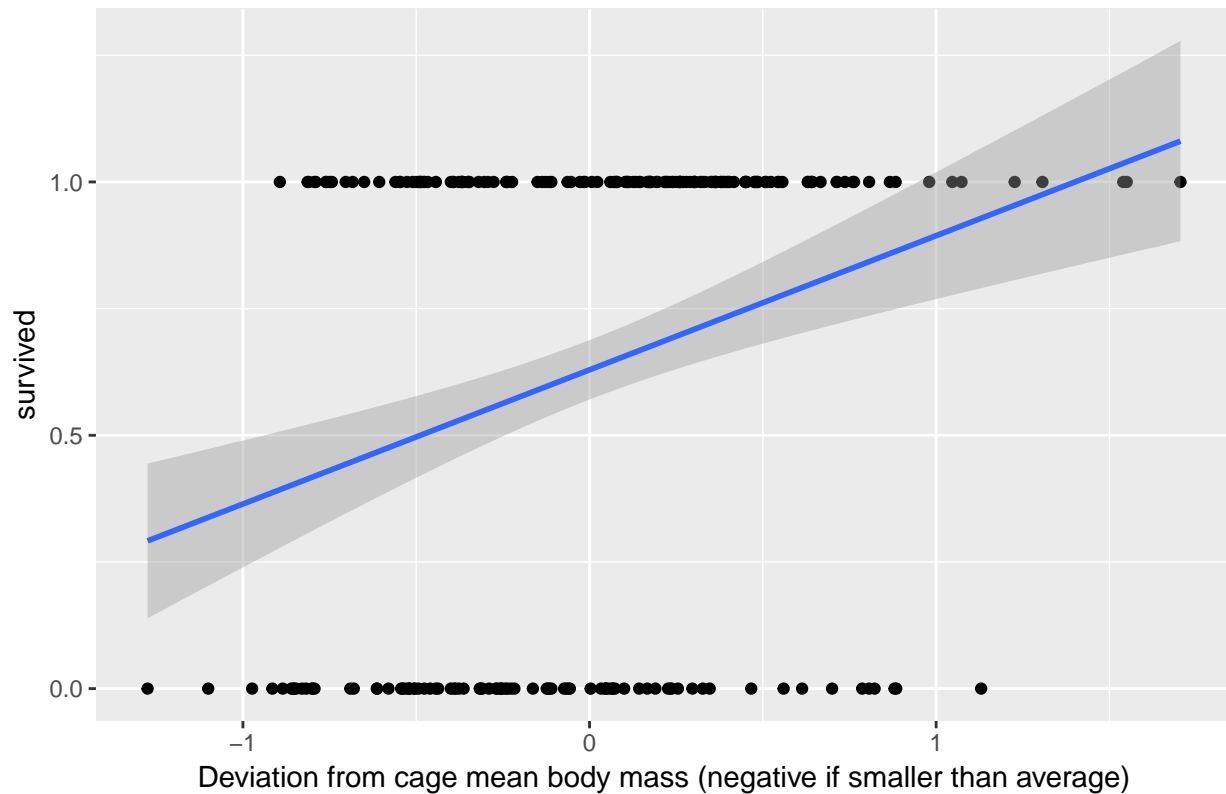Use the deviation of body weight from average at the *beginning* of the experiment

Use real value, lumped:

```
ggplot2::ggplot(
  data = na.omit(subset(fig2, select = c("delta_pre", "survived"))),
  ggplot2::aes(x = delta_pre, y = survived)
) + ggplot2::geom_point() + ggplot2::geom_smooth(method = "glm") +
    ggplot2::scale_x_continuous("Deviation from cage mean body mass (negative if smaller than average)"
    ggplot2::ggtitle("The effect of having a lower or higher pre-mass on survival")
```
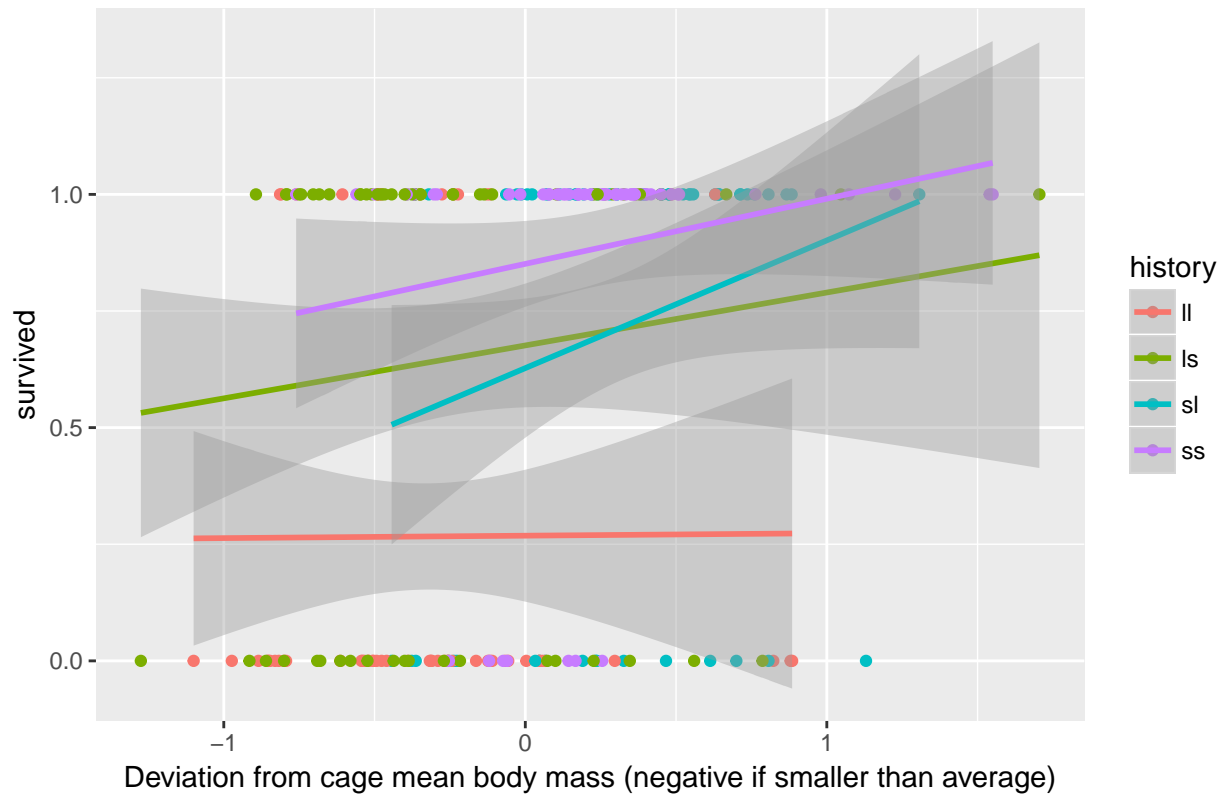
The effect of having a lower or higher pre−mass on survival

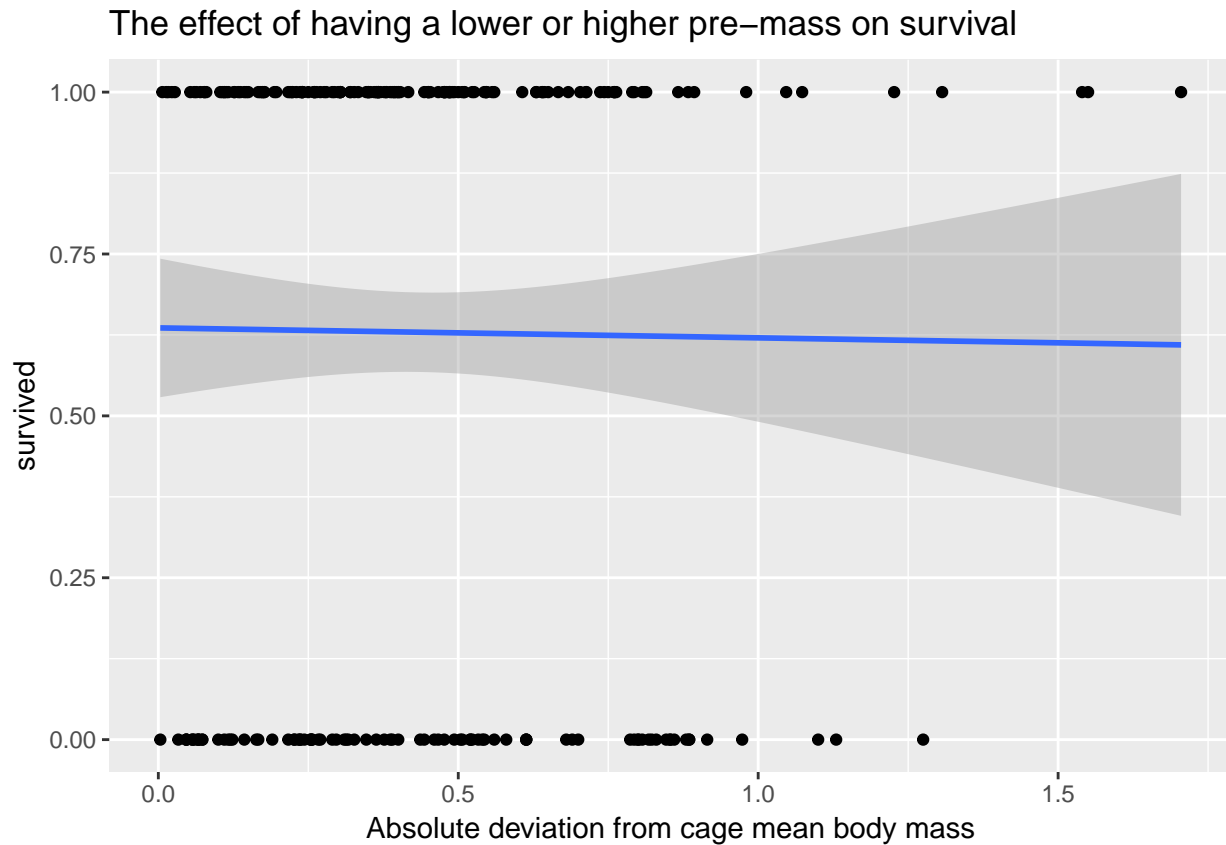Use real value, seperated by history:

```
ggplot2::ggplot(
  data = na.omit(subset(fig2, select = c("delta_pre", "survived", "history"))),
  ggplot2::aes(x = delta_pre, y = survived, color = history)
) + ggplot2::geom_point() + ggplot2::geom_smooth(method = "glm") +
    ggplot2::scale_x_continuous("Deviation from cage mean body mass (negative if smaller than average)")
    ggplot2::ggtitle("The effect of having a lower or higher pre-mass on survival")
```

The effect of having a lower or higher pre−mass on survival

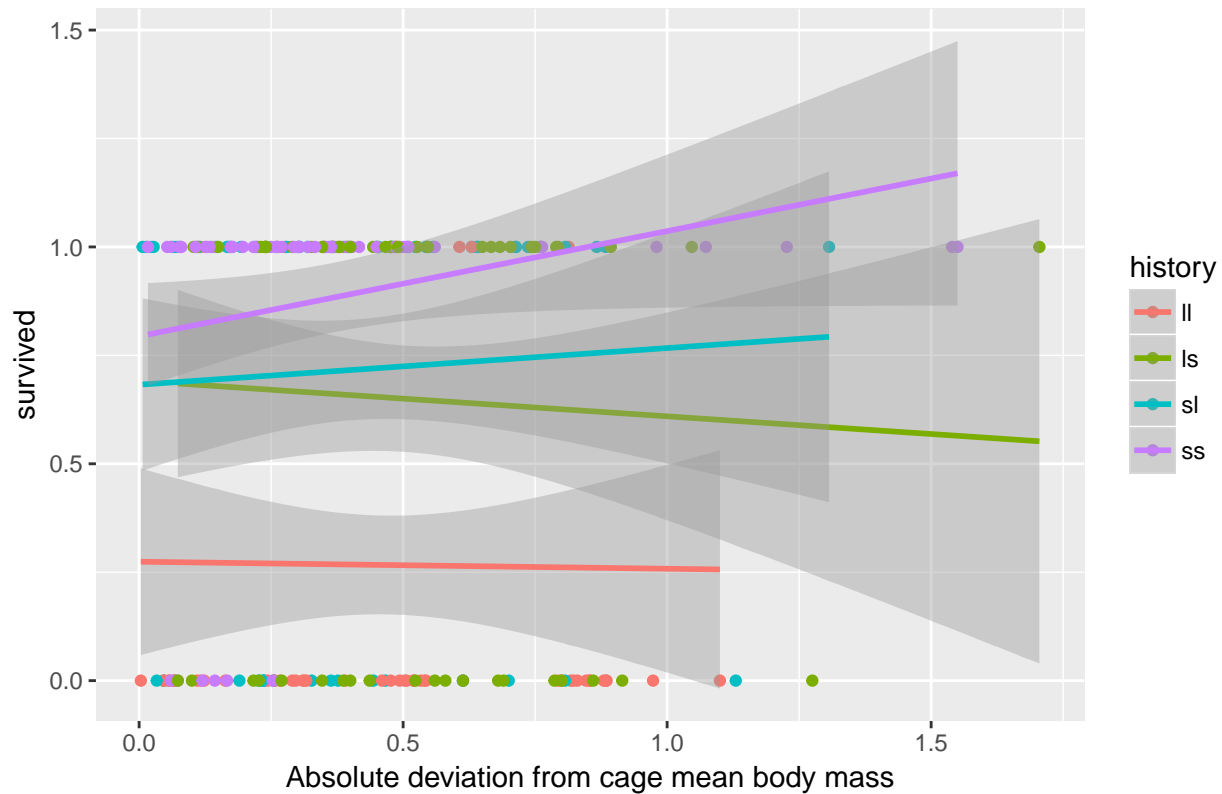Use absolute value, lumped:

```
ggplot2::ggplot(
  data = na.omit(subset(fig2, select = c("delta_pre", "survived"))),
  ggplot2::aes(x = abs(delta_pre), y = survived)
) + ggplot2::geom_point() + ggplot2::geom_smooth(method = "glm") +
    ggplot2::scale_x_continuous("Absolute deviation from cage mean body mass") +
    ggplot2::ggtitle("The effect of having a lower or higher pre-mass on survival")
```

Use absolute value, seperated by history:

```
ggplot2::ggplot(
  data = na.omit(subset(fig2, select = c("delta_pre", "survived", "history"))),
  ggplot2::aes(x = abs(delta_pre), y = survived, color = history)
) + ggplot2::geom_point() +
    #ggplot2::geom_smooth() +
    #ggplot2::geom_smooth(method = "lm") +
    ggplot2::geom_smooth(method = "glm") +
    ggplot2::scale_x_continuous("Absolute deviation from cage mean body mass") +
    ggplot2::ggtitle("The effect of having a lower or higher pre-mass on survival")
```

The effect of having a lower or higher pre−mass on survival

Use absolute value, seperated by history, outliers removed:

```
fig2_no_outliers <- filter(fig2, abs(delta_pre) < 1.2)
ggplot2::ggplot(
  data = na.omit(subset(fig2_no_outliers, select = c("delta_pre", "survived", "history"))),
  ggplot2::aes(x = abs(delta_pre), y = survived, color = history)
) + ggplot2::geom_point() +
    ggplot2::geom_smooth(method = "glm") +
    ggplot2::scale_x_continuous("Absolute deviation from cage mean body mass") +
    ggplot2::ggtitle("The effect of having a lower or higher pre-mass on survival,\nwith outliers remove
```

The effect of having a lower or higher pre−mass on survival,
with outliers removed