

Bolnick, Daniel I., and William E. Stutz. ‘Frequency dependence limits divergent evolution by favouring rare immigrants over residents.’ *Nature* (2017).

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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 | delta_post |
|-----------|--------|------------|---------|----------|-----------|----------|----------|-----------|------------|------------|
| L1 | Stream | Lake | sl | 1.78 | 1.61 | 1 | 1.256667 | NA | 0.5233333 | -0.1366667 |
| L1 | Lake | Lake | ll | 1.00 | NA | 0 | 1.256667 | NA | -0.2566667 | NA |
| L1 | Lake | Lake | ll | 0.99 | NA | 0 | 1.256667 | NA | -0.2666667 | NA |
| L10 | Lake | Lake | ll | 1.71 | NA | 0 | 1.663333 | NA | 0.0466667 | NA |
| L10 | Stream | Lake | sl | 2.06 | 1.90 | 1 | 1.663333 | NA | 0.3966667 | -0.2666667 |
| L10 | Stream | Lake | sl | 1.22 | NA | 0 | 1.663333 | NA | -0.4433333 | NA |

At the beginning

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

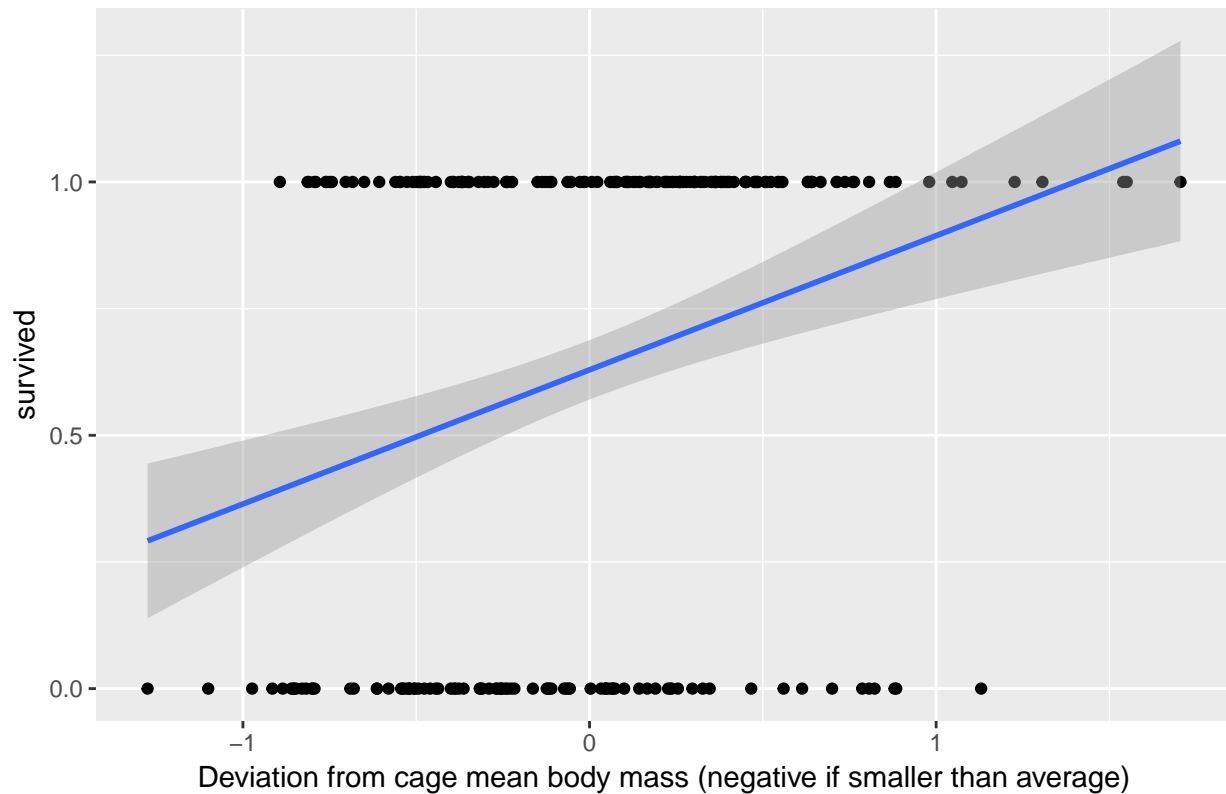
Use real value, lumped:

```

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")

```

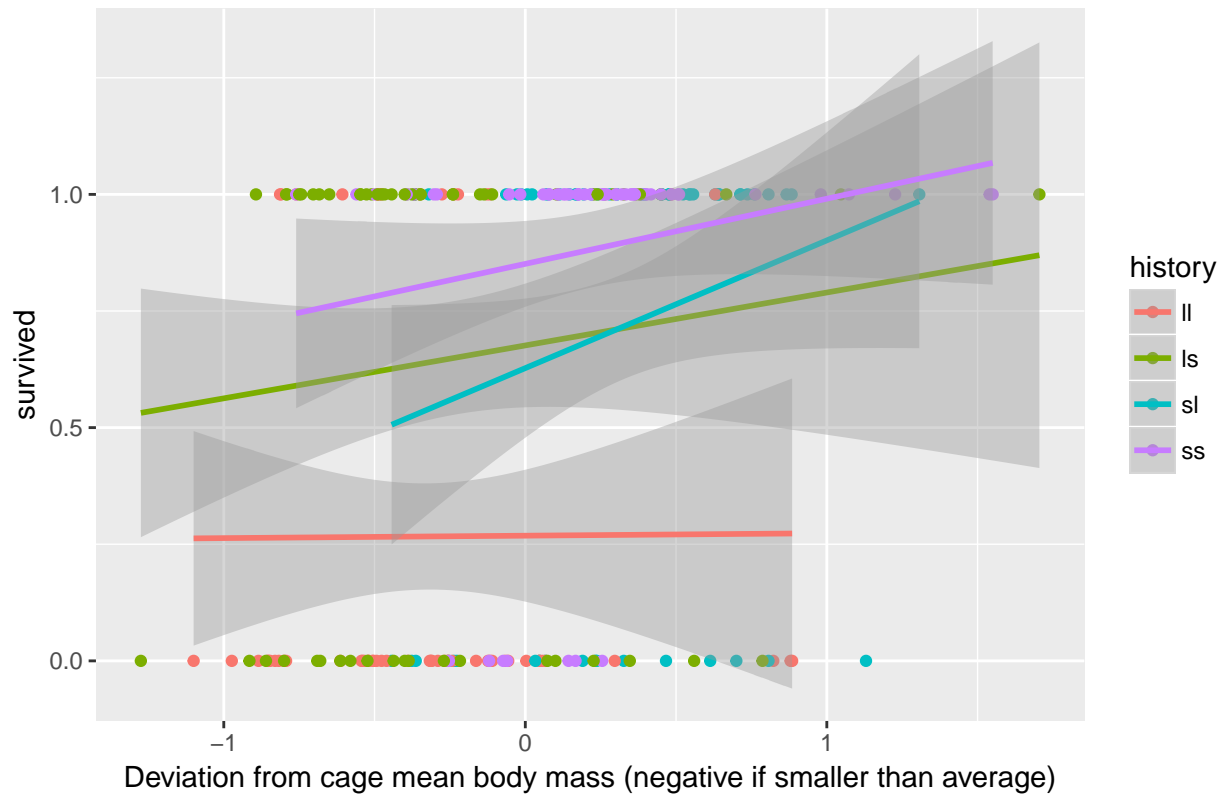
The effect of having a lower or higher pre-mass on survival



Use real value, seperated by history:

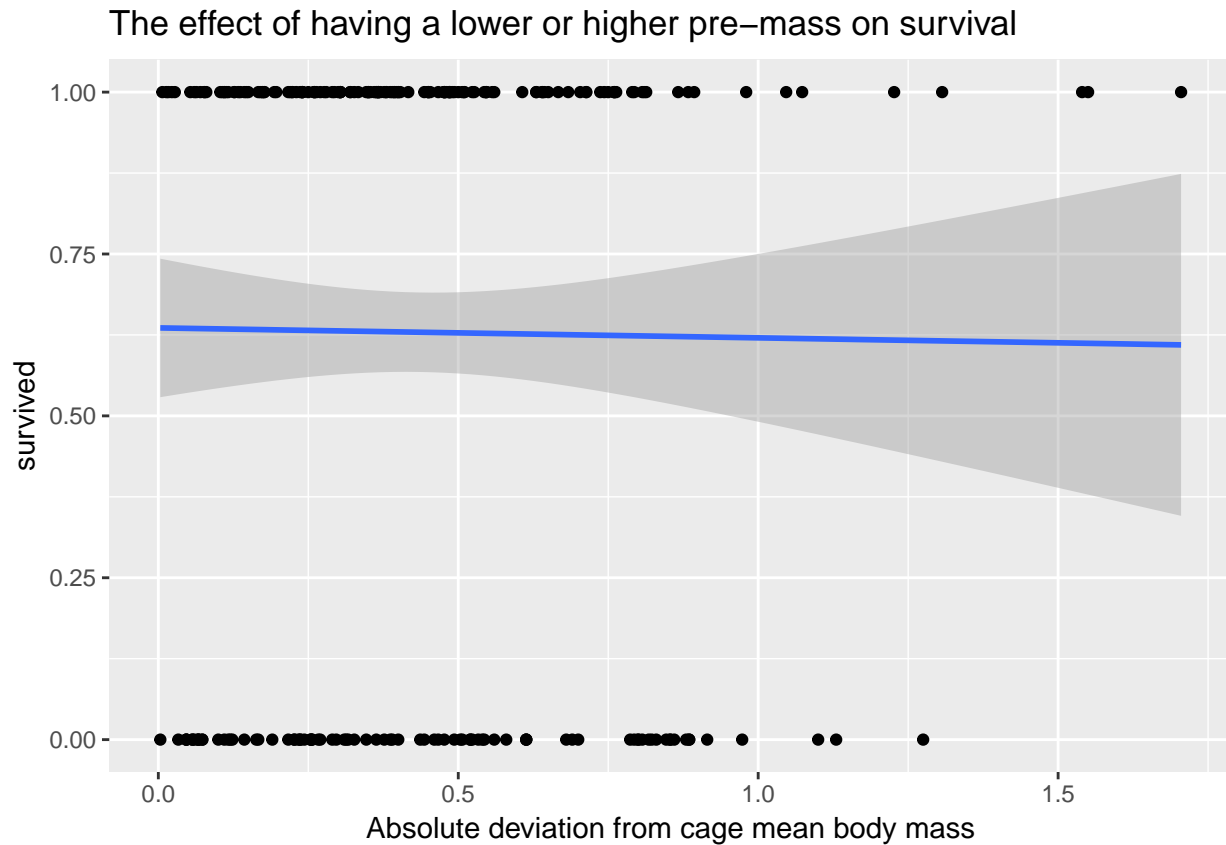
```
ggplot2::ggplot(
  data = na.omit(subset(fig2, select = c("delta_pre", "survived", "history"))),
  ggplot2::aes(x = delta_pre, y = survived, color = history)
) + ggplot2::geom_point() + ggplot2::geom_smooth(method = "glm") +
  ggplot2::scale_x_continuous("Deviation from cage mean body mass (negative 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:

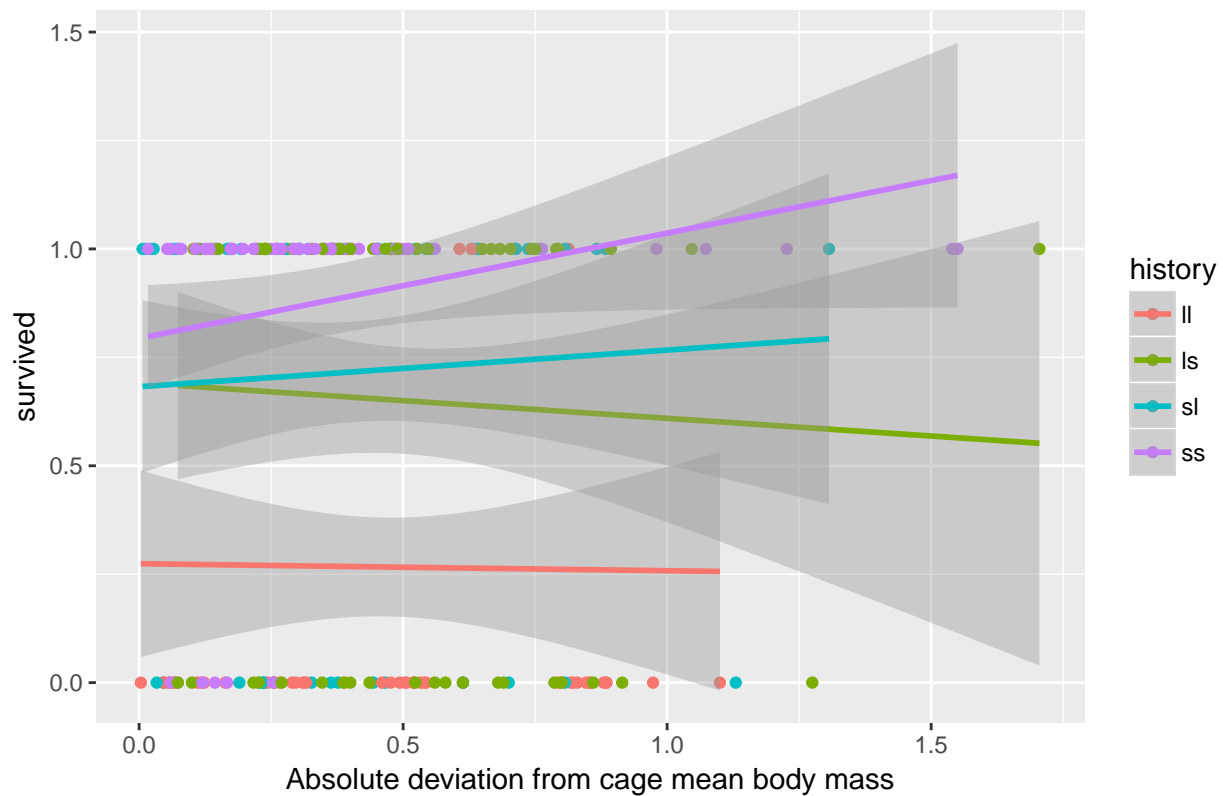
```
ggplot2::ggplot(
  data = na.omit(subset(fig2, select = c("delta_pre", "survived"))),
  ggplot2::aes(x = abs(delta_pre), y = survived)
) + ggplot2::geom_point() + ggplot2::geom_smooth(method = "glm") +
  ggplot2::scale_x_continuous("Absolute deviation from cage mean body mass") +
  ggplot2::ggtitle("The 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 removed")
```

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

