Dialogue

In this document, the dialogue with the AI is described, including all control questions. Of each question, the expected answer is calculated.

```
library(testthat)
```

Expectations

A paper does not typically hold code (like an R markdown document). Hence, in the end, all the constants are copy-pasted into a paper and then left unchecked.

To make it easy to compare the final paper with the constants we've copy-pasted, here are all the constants:

```
total_n_fish <- 300
n_fish_control <- 60
n_fish_transplanted <- 240
origin_values <- c("Lake", "Stream")
transplanted_values <- c("Lake", "Stream", "Control")
lowest_pre_mass <- 0.5
highest_pre_mass <- 3.6
n_survived <- 151
n_died <- 89
n_enclosures <- 80
n_enclosures_with_2_fish <- 3
n_enclosures_with_3_fish <- 74
n_enclosures_with_4_fish <- 3
anomous_enclosures <- c("L20", "L25", "L6", "L7", "S22", "S24")
cage_mass_mean_for_l1 <- 1.256667
cage_mass_stdev_for_l1 <- 0.4532475
cage_mass_mean_deviation_sd_for_l1 <- c(1.1546303, -0.5662836, -0.5883466)

abs_cage_mass_mean_deviation_sd_for_l1 <- abs(cage_mass_mean_deviation_sd_for_l1)

# Check consistency between these variables
expect_equal(
  total_n_fish,
  n_fish_control + n_fish_transplanted
)
expect_equal(
  n_fish_transplanted,
  n_survived + n_died
)
expect_equal(
  n_enclosures,
  n_enclosures_with_2_fish + n_enclosures_with_3_fish + n_enclosures_with_4_fish
)
expect_equal(
  length(anomous_enclosures),
  n_enclosures_with_2_fish + n_enclosures_with_4_fish
)
```

All solutions to the dialog are written here, and tested below, during the dialogue.

D1. Ask an AI to read the dataset

D1.1: describe research paper conclusiom

Ask the AI:

```
I am going to upload data.

The data consist of fish in cages and their survival.

A paper that analysed this data concluded:
'survival is higher for atypically sized individuals within cages'.

How would you suggest to analyse the data?
```

D1.2: read data

- The dialogue starts by uploading the data for the paper at here.

```
t_all <- read.csv("Bolnick_traits.txt", sep = " ")
```

D1.3: first impression

```
I will now walk you through how the data should be understood.

A paper that analysed this data concluded:
'survival is higher for atypically sized individuals within cages'.

Do you already think that this data suggests that?
```

D1.4: show first rows

Ask the AI:

```
Could you show the first rows of the data?
```

Expected:

```
knitr::kable(head(t_all))
```

sampleID	fishID	origin	enclosure	transplant	date_in	pre_mass	pre_length	post_mass	post_length	pth	bd	gw	grn	grl	sex	survived
118	118	Stream	S2	Stream	06/03/11	1.75	4.9	NA	NA	NA	NA	NA	NA	NA	NA	0
12	12	Stream	L8	Lake	06/02/11	1.13	4.6	NA	NA	NA	NA	NA	NA	NA	NA	0
122	122	Lake	S2	Stream	06/03/11	2.37	5.6	NA	NA	NA	NA	NA	NA	NA	NA	0
123	123	Lake	S3	Stream	06/03/11	1.71	5.2	NA	NA	NA	NA	NA	NA	NA	NA	0
124	124	Lake	S4	Stream	06/03/11	2.45	5.4	NA	NA	NA	NA	NA	NA	NA	NA	0
127	127	Lake	S7	Stream	06/03/11	0.85	4.0	NA	NA	NA	NA	NA	NA	NA	NA	0

We select only the relevant data here, so that the analysis can be checked by humans more easily:

```
t <- t_all |> dplyr::select(fishID, origin, enclosure, pre_mass, transplant,  survived) |> dplyr::arran
knitr::kable(head(t))
```

	fishID	origin	enclosure	pre_mass	transplant	survived
27	181	Lake	L1	1.00	Lake	0
28	182	Lake	L1	0.99	Lake	0
149	1	Stream	L1	1.78	Lake	1
16	16	Stream	L10	1.22	Lake	0
36	193	Lake	L10	1.71	Lake	0
164	17	Stream	L10	2.06	Lake	1

D2. Describe the dataset

D2.1: count fish

Ask the AI:

```
The `fishID` column denotes the ID of a fish. How many fish are in this dataset?
```

Expected:

```r
expect_equal(total_n_fish, length(unique(t$fishID)))
```

The expected answer is 300.

D2.2: get the ‘origin’ values

Ask the AI:

```
The `origin` column denotes the location where each fish comes from.
What are the locations the fish come from?
```

Expected:

```r
expect_equal(unique(t$origin), origin_values)
```

The correct answers is Lake, Stream.

D2.3: get the ‘transplant’ values

Ask the AI:

```
The `transplant` column denotes the location where each fish is
transplanted to.
What are the locations the fish are transplanted to?
```

Expected:

```r
expect_equal(unique(t$transplant), transplanted_values)
```

The correct answers is Lake, Stream, Control.

D2.4: remove the controls and count the fish

Ask the AI:

```
Remove the rows for which the `transplant` value is 'Control'.
How many fish are left?
```

Expected:

```r
t_1 <- t |> dplyr::filter(transplant != "Control")
expect_equal(n_fish_transplanted, length(unique(t_1$fishID)))
```

The correct answer is 240.

D2.5: get the range of 'pre_mass'

Ask the AI:

```
The `pre_mass` column denotes the mass of a fish
before the transplantation.
What is the range of the values in this column?
```

Expected:

```r
expect_equal(lowest_pre_mass, min(t_1$pre_mass))
expect_equal(highest_pre_mass, max(t_1$pre_mass))
```

The correct answer is 0.5 to 3.6.

D2.6: count the number of dead fish and fish that survived

Ask the AI:

```
The `survived` column denotes if the fish survived the experiment,
where 0 means it died and 1 means that it survived.
How many fish died? And how many survived?
```

Expected:

```r
expect_equal(n_survived, sum(t_1$survived == TRUE))
expect_equal(n_died, sum(t_1$survived == FALSE))
```

The correct answers are 89 died and 151 survived.

D2.7: count the number of enclosures

Ask the AI:

```
The `enclosure` column denotes the ID of an enclosure.
How many enclosures are in this dataset?
```

Expected:

```r
expect_equal(n_enclosures, length(unique(t_1$enclosure)))
```

The correct answer is 80 enclosures.

D2.8: count the number of fish in each enclosure

Ask the AI:

```
How many fish are in each enclosure?
```

Expected:

```r
n_fish_per_enclosure <- dplyr::count(t_1, enclosure)
expect_equal(n_enclosures_with_2_fish, sum(n_fish_per_enclosure$n == 2))
expect_equal(n_enclosures_with_3_fish, sum(n_fish_per_enclosure$n == 3))
expect_equal(n_enclosures_with_4_fish, sum(n_fish_per_enclosure$n == 4))
knitr::kable(head(n_fish_per_enclosure))
```

enclosure	n
L1	3

enclosure	n
L10	3
L11	3
L12	3
L13	3
L14	3

The correct answer is:

- 3 enclosures have 2 fish
- 74 enclosures have 3 fish
- 3 enclosures have 4 fish

As a note to self, these are the anomalies:

```
expect_equal(anomous_enclosures, n_fish_per_enclosure[n_fish_per_enclosure$n != 3, ]$enclosure)
knitr::kable(n_fish_per_enclosure[n_fish_per_enclosure$n != 3, ])
```

	enclosure	n
13	L20	4
18	L25	2
37	L6	2
38	L7	4
55	S22	4
57	S24	2

Q0. Describe the conclusion

- A conclusion drawn from the data is that the extreme body masses are likelier to survive. Would you agree that the data supports this claim?

D4. Reproduce the results in that paper

D4.1: calculate 'cage_mass_mean'

Ask the AI:

```
To make a better comparison, we are going to standarize
body masses per enclosure.
Add a column to the
data called `cage_mass_mean` which holds the average
`pre_mass` within the enclosure each fish is in.
Could you show me the data for enclosure L1?
```

Expected:

```
cage_mass_mean_per_enclosure <- t_1 |>
  dplyr::select(enclosure, pre_mass) |>
  dplyr::group_by(enclosure) |>
  dplyr::summarise(cage_mass_mean = mean(pre_mass))
t_2 <- merge(t_1, cage_mass_mean_per_enclosure)
knitr::kable(head(t_2))
```

enclosure	fishID	origin	pre_mass	transplant	survived	cage_mass_mean
L1	181	Lake	1.00	Lake	0	1.256667
L1	182	Lake	0.99	Lake	0	1.256667
L1	1	Stream	1.78	Lake	1	1.256667
L10	16	Stream	1.22	Lake	0	1.663333
L10	193	Lake	1.71	Lake	0	1.663333
L10	17	Stream	2.06	Lake	1	1.663333

```
knitr::kable(t_2[t_2$enclosure == "L1", ])
```

enclosure	fishID	origin	pre_mass	transplant	survived	cage_mass_mean
L1	181	Lake	1.00	Lake	0	1.256667
L1	182	Lake	0.99	Lake	0	1.256667
L1	1	Stream	1.78	Lake	1	1.256667

```
expect_equal(
  t_2[t_2$enclosure == "L1", ]$cage_mass_mean,
  rep(cage_mass_mean_for_l1, 3),
  tolerance = 1.0e-6
)
```

For enclose L1, the expected `cage_mass_mean` for each of the fish is 1.256667.

D4.2: calculate 'cage_mass_stdev'

Ask the AI:

```
To make a better comparison, we are going to standarize
body masses per enclosure. Add a column to the
data called `cage_mass_stdev` which is the standard
deviation of the `pre_mass` distribution of each enclosure
each fish is in.
Could you show me the data for enclosure L1?
```

Expected:

```
cage_mass_stdev_per_enclosure <- t_2 |>
  dplyr::select(enclosure, pre_mass) |>
  dplyr::group_by(enclosure) |>
  dplyr::summarise(cage_mass_stdev = sd(pre_mass))
t_3 <- merge(t_2, cage_mass_stdev_per_enclosure)
knitr::kable(head(t_3))
```

enclosure	fishID	origin	pre_mass	transplant	survived	cage_mass_mean	cage_mass_stdev
L1	181	Lake	1.00	Lake	0	1.256667	0.4532475
L1	182	Lake	0.99	Lake	0	1.256667	0.4532475
L1	1	Stream	1.78	Lake	1	1.256667	0.4532475
L10	16	Stream	1.22	Lake	0	1.663333	0.4219400
L10	193	Lake	1.71	Lake	0	1.663333	0.4219400
L10	17	Stream	2.06	Lake	1	1.663333	0.4219400

```
knitr::kable(t_3[t_3$enclosure == "L1", ])
```

enclosure	fishID	origin	pre_mass	transplant	survived	cage_mass_mean	cage_mass_stdev
L1	181	Lake	1.00	Lake	0	1.256667	0.4532475
L1	182	Lake	0.99	Lake	0	1.256667	0.4532475
L1	1	Stream	1.78	Lake	1	1.256667	0.4532475

```
expect_equal(
  t_3[t_3$enclosure == "L1", ]$cage_mass_stdev,
  rep(cage_mass_stdev_for_l1, 3),
  tolerance = 1.0e-6
)
```

D4.3: calculate 'cage_mass_mean_deviation_sd'

Ask the AI:

```
To make a better comparison, we are going to standarize
body masses per enclosure. Add a column to the
data called `cage_mass_mean_deviation_sd`.
Its values are calculated per fish.
Each fish its `cage_mass_mean_deviation_sd`
equals the absolute difference between its `pre_mass`
and its enclosure's `cage_mass_mean`,
divided by the `cage_mass_stdev` of its enclosure.
Could you show me the data for enclosure L1?
```

Expected:

```
cage_mass_mean_deviation_sd_per_fish <- t_3 |>
  dplyr::select(fishID, pre_mass, cage_mass_mean, cage_mass_stdev) |>
  dplyr::group_by(fishID) |>
  dplyr::mutate(
    cage_mass_mean_deviation_sd =
      abs(pre_mass - cage_mass_mean) / cage_mass_stdev
  ) |>
  dplyr::select(fishID, cage_mass_mean_deviation_sd)
expect_equal(
  nrow(cage_mass_mean_deviation_sd_per_fish),
  n_fish_transplanted
)

expect_equal(
  nrow(t_3),
  n_fish_transplanted
)
t_4 <- merge(t_3, cage_mass_mean_deviation_sd_per_fish)
expect_equal(
  nrow(t_4),
  n_fish_transplanted
)

knitr::kable(head(t_4))
```

fishID	enclosure	origin	pre_mass	transplant	survived	cage_mass_mean	cage_mass_stdev	cage_mass_mean_deviation_sd
1	L1	Stream	1.78	Lake	1	1.256667	0.4532475	1.1546303
2	L2	Stream	0.65	Lake	1	1.016667	0.5589574	0.6559832
3	L2	Stream	1.66	Lake	1	1.016667	0.5589574	1.1509524
4	L3	Stream	2.26	Lake	1	1.453333	0.8309834	0.9707375
5	L3	Stream	1.50	Lake	0	1.453333	0.8309834	0.0561584
6	L4	Stream	1.89	Lake	1	1.723333	0.9016282	0.1848508

```r
knitr::kable(t_4[t_4$enclosure == "L1", ])
```

	fishID	enclosure	origin	pre_mass	transplant	survived	cage_mass_mean	cage_mass_stdev	cage_mass_mean_deviation_sd
1	1	L1	Stream	1.78	Lake	1	1.256667	0.4532475	1.1546303
181	181	L1	Lake	1.00	Lake	0	1.256667	0.4532475	0.5662836
182	182	L1	Lake	0.99	Lake	0	1.256667	0.4532475	0.5883466

```r
expect_equal(
  t_4[t_4$enclosure == "L1", ]$cage_mass_mean_deviation_sd,
  abs_cage_mass_mean_deviation_sd_for_l1,
  tolerance = 1.0e-6
)
```

The values of `cage_mass_mean_deviation_sd` for enclosure `L1` are expected to be 1.1546303, 0.5662836, 0.5883466.

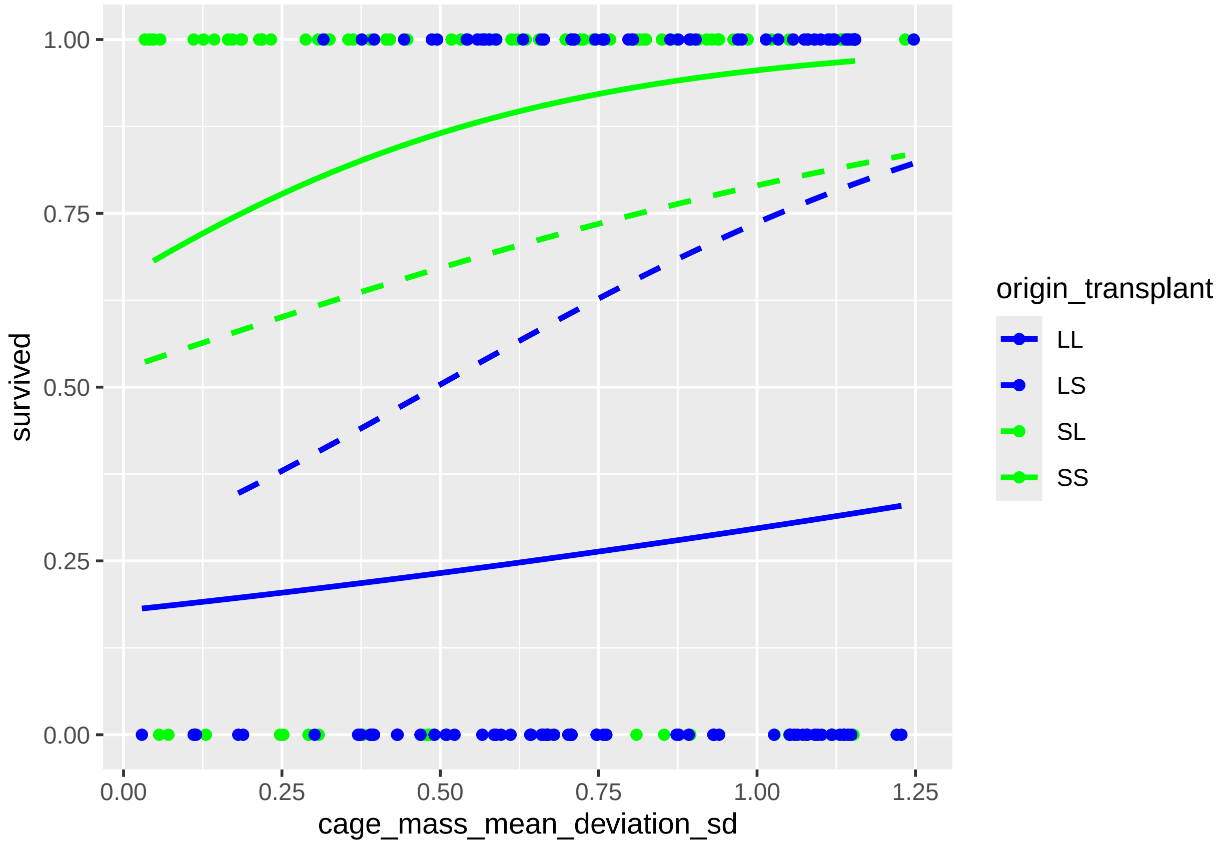
D4.4: reproduce the plot

Ask the AI:

```
Create a scatter plot of this data:
- Each point is a fish.
- Use a blue color for fish
  that have 'Lake' as their origin.
- Use a green color for fish
  that have 'Stream' as their origin.
- On the X axis, put the values of `cage_mass_mean_deviation_sd`
  of each fish
- On the Y axis, put the `survived` of each fish.
- Put the fish in four categories:
  - Fish that have an `origin` of 'Lake' and
    a `transplant` of 'Lake' are in category 'LL'
  - Fish that have an `origin` of 'Lake' and
    a `transplant` of 'Stream' are in category 'LS'
  - Fish that have an `origin` of 'Stream' and
    a `transplant` of 'Lake' are in category 'SL'
  - Fish that have an `origin` of 'Stream' and
    a `transplant` of 'Stream' are in category 'SS'
- Show a trendline for each binomal fit on each of these 4 categories.
  - Use blue lines for categories that originate from a lake
  - Use green lines for categories that originate from a stream
  - Use solid lines for categories 'LL' and 'SS'
  - Use dashed lines for categories 'LS' and 'SL'
```

Expected is the plot in the paper:

```
t_4$origin_transplant <- paste0(
  stringr::str_sub(t_4$origin,1 ,1),
  stringr::str_sub(t_4$transplant,1 ,1)
)
ggplot2::ggplot(
  data = t_4,
  ggplot2::aes(
    x = cage_mass_mean_deviation_sd,
    y = survived,
    color = origin_transplant,
    lty = origin_transplant
  )
) + ggplot2::scale_color_manual(
    values = c("blue", "blue", "green", "green")
  ) +
  ggplot2::scale_linetype_manual(
    values = c("solid", "dashed", "dashed", "solid")
  ) +
  ggplot2::geom_point() +
  ggplot2::geom_smooth(
    method = "glm",
    method.args = list(family = "binomial"),
    se = FALSE
  )
#> `geom_smooth()` using formula = 'y ~ x'
```



Q1: Ask if the conclusion is correct

- A conclusion drawn from the data is that the extreme body masses are likelier to survive. Would you agree that the data supports this claim?

D5 Reproduce the results that show a flaw in the reasoning

D5.1 Add relative standarized body mass

Ask the AI:

```
To make a better comparison, we are going to standarize
body masses per enclosure. Add a column to the
data called `cage_mass_mean_deviation_sd_rel`.
Its values are calculated per fish.
Each fish its `cage_mass_mean_deviation_sd_rel`
equals the difference between its `pre_mass`
and its enclosure's `cage_mass_mean`,
divided by the `cage_mass_stdev` of its enclosure.
Could you show me the data for enclosure L1?
```

Expected:

```r
cage_mass_mean_deviation_sd_per_fish_rel <- t_4 |>
  dplyr::select(fishID, pre_mass, cage_mass_mean, cage_mass_stdev) |>
  dplyr::group_by(fishID) |>
  dplyr::mutate(
    cage_mass_mean_deviation_sd_rel =
      (pre_mass - cage_mass_mean) / cage_mass_stdev
  ) |>
  dplyr::select(fishID, cage_mass_mean_deviation_sd_rel)
expect_equal(
  nrow(cage_mass_mean_deviation_sd_per_fish_rel),
  n_fish_transplanted
)

expect_equal(
  nrow(t_4),
  n_fish_transplanted
)
t_5 <- merge(t_4, cage_mass_mean_deviation_sd_per_fish_rel)
expect_equal(
  nrow(t_5),
  n_fish_transplanted
)

knitr::kable(head(t_5))
```

fishID	enclosure	origin	pre_mass	transplant	survived	cage_mass_mean	cage_mass_stdev	cage_mass_mean_deviation	origin_transplant	cage_mass_mean_deviation_sd_
1	L1	Stream	1.78	Lake	1	1.256667	0.4532475	1.1546303	SL	1.1546303
2	L2	Stream	0.65	Lake	1	1.016667	0.5589574	0.6559832	SL	-0.6559832
3	L2	Stream	1.66	Lake	1	1.016667	0.5589574	1.1509524	SL	1.1509524
4	L3	Stream	2.26	Lake	1	1.453333	0.8309834	0.9707375	SL	0.9707375
5	L3	Stream	1.50	Lake	0	1.453333	0.8309834	0.0561584	SL	0.0561584
6	L4	Stream	1.89	Lake	1	1.723333	0.9016282	0.1848508	SL	0.1848508

```
knitr::kable(t_5[t_5$enclosure == "L1", ])
```

	fishID	enclosure	origin	pre_mass	transplant	survived	cage_mass_mean	cage_mass_sd	cage_mass_mean_deviation	origin_transplant	cage_mass_mean_deviation_sd_rel
1	1	L1	Stream	1.78	Lake	1	1.256667	0.4532475	1.1546303	SL	1.1546303
181	181	L1	Lake	1.00	Lake	0	1.256667	0.4532475	0.5662836	LL	-0.5662836
182	182	L1	Lake	0.99	Lake	0	1.256667	0.4532475	0.5883466	LL	-0.5883466

```
expect_equal(
  t_5[t_5$enclosure == "L1", ]$cage_mass_mean_deviation_sd_rel,
  cage_mass_mean_deviation_sd_for_l1,
  tolerance = 1.0e-6
)
```

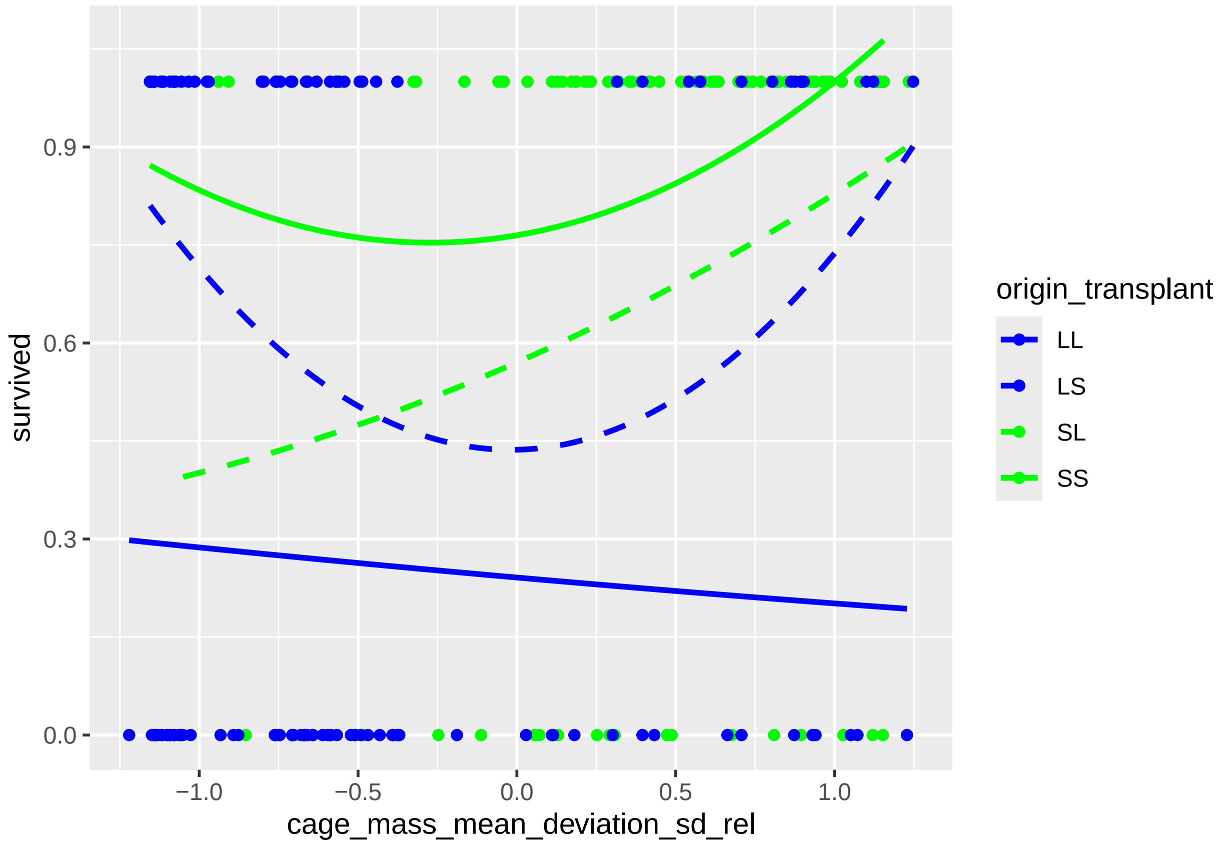
D5.2 Plot relative standarized body mass with same fit

Ask the AI:

```
Create a scatter plot of this data:
- Each point is a fish.
- Use a blue color for fish
  that have 'Lake' as their origin.
- Use a green color for fish
  that have 'Stream' as their origin.
- On the X axis, put the values of `cage_mass_mean_deviation_sd_rel`
  of each fish
- On the Y axis, put the `survived` of each fish.
- Put the fish in four categories:
  - Fish that have an `origin` of 'Lake' and
     a `transplant` of 'Lake' are in category 'LL'
  - Fish that have an `origin` of 'Lake' and
     a `transplant` of 'Stream' are in category 'LS'
  - Fish that have an `origin` of 'Stream' and
     a `transplant` of 'Lake' are in category 'SL'
  - Fish that have an `origin` of 'Stream' and
     a `transplant` of 'Stream' are in category 'SS'
- Show a trendline for each parabolic fit on each of these 4 categories.
   - Use blue lines for categories that originate from a lake
   - Use green lines for categories that originate from a stream
   - Use solid lines for categories 'LL' and 'SS'
   - Use dashed lines for categories 'LS' and 'SL'
```

This should produce this plot:

```
ggplot2::ggplot(
  data = t_5,
  ggplot2::aes(
    x = cage_mass_mean_deviation_sd_rel,
    y = survived,
    color = origin_transplant,
    lty = origin_transplant
  )
) + ggplot2::scale_color_manual(
    values = c("blue", "blue", "green", "green")
  ) +
  ggplot2::scale_linetype_manual(
    values = c("solid", "dashed", "dashed", "solid")
  ) +
  ggplot2::geom_point() +
  ggplot2::geom_smooth(
    method = "lm",
    formula = y ~ x + I(x^2),
    se = FALSE
  )
```



The differences are: - this plot uses relative body masses, instead of absolute - the fit is parabolic, instead of binomial, as the latter is assumed to be monotonically increasing/decreasing. This means that a binomial distribution cannot be used to fit on data that is shaped like a `U` (as is assumed in the original paper: the extreme body masses have the highest fitness)

Q2: Ask if the conclusion is correct

- A conclusion drawn from the data is that the extreme body masses are likelier to survive. Would you agree that the data supports this claim?