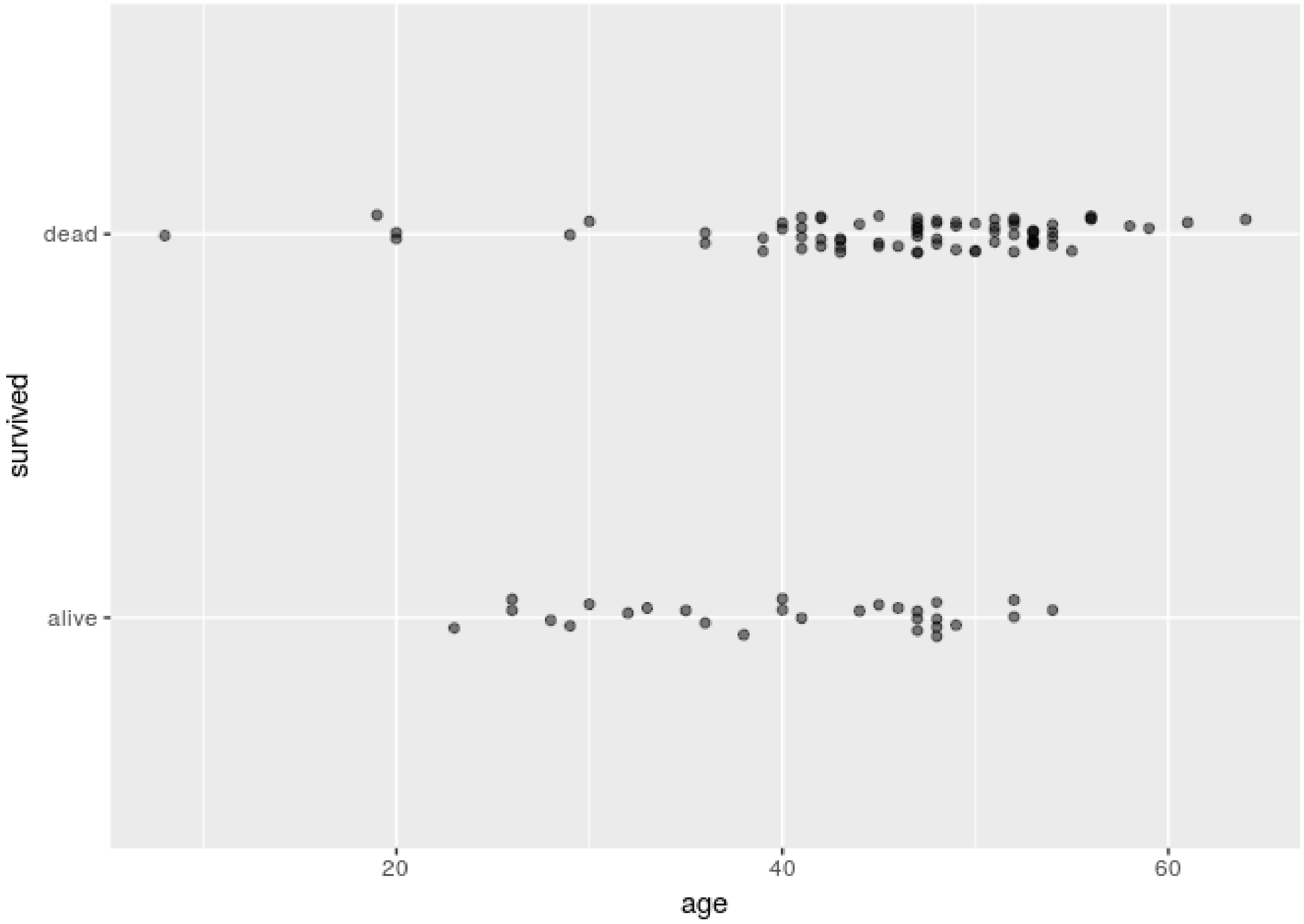
What is logistic regression?

MULTIPLE AND LOGISTIC REGRESSION IN R

Ben Baumer
Instructor

A categorical response variable

```
ggplot(data = heartTr, aes(x = age, y = survived)) +
  geom_jitter(width = 0, height = 0.05, alpha = 0.5)
```

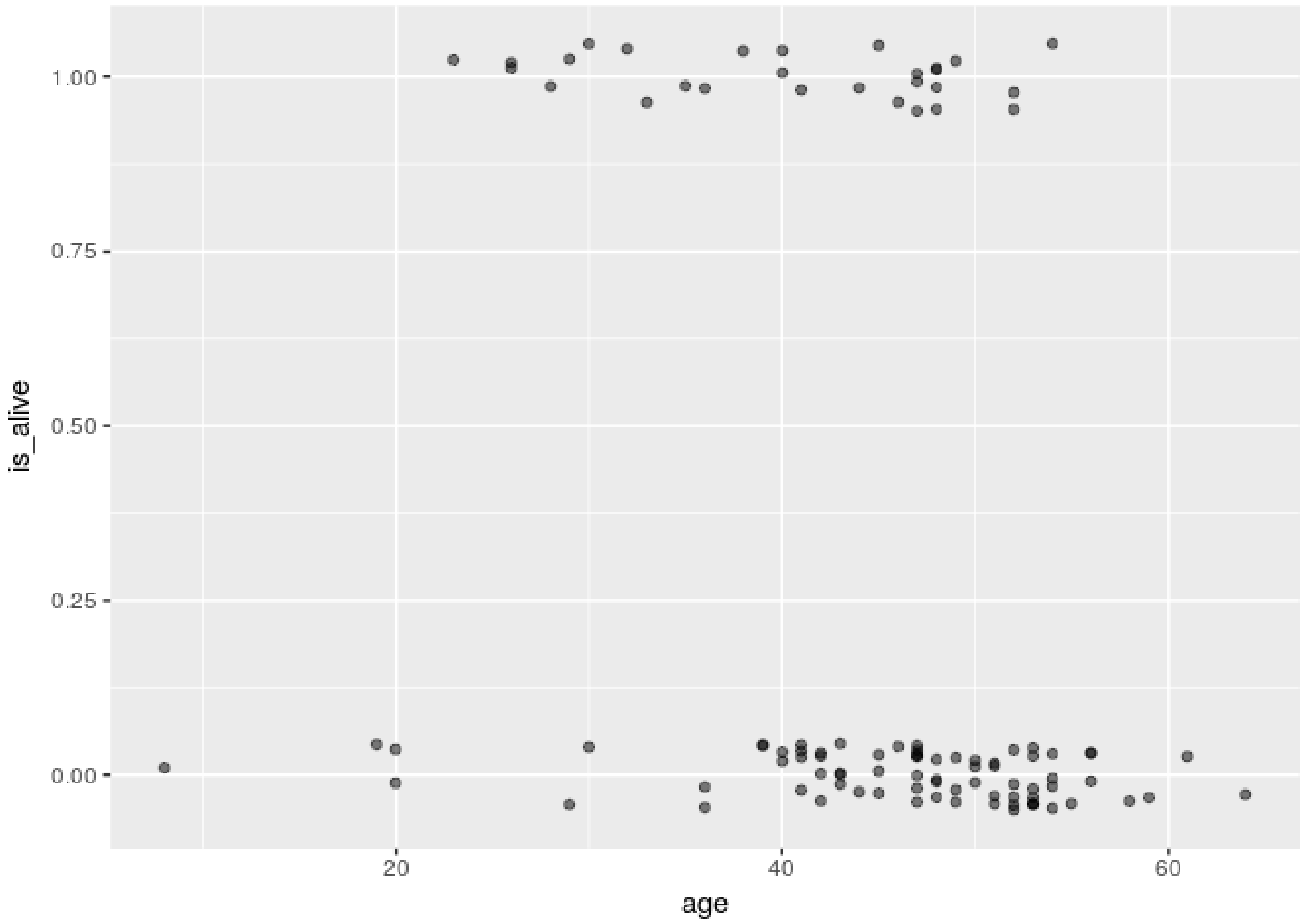


Making a binary variable

```r
heartTr <- heartTr %>%
  mutate(is_alive = ifelse(survived == "alive", 1, 0))
```

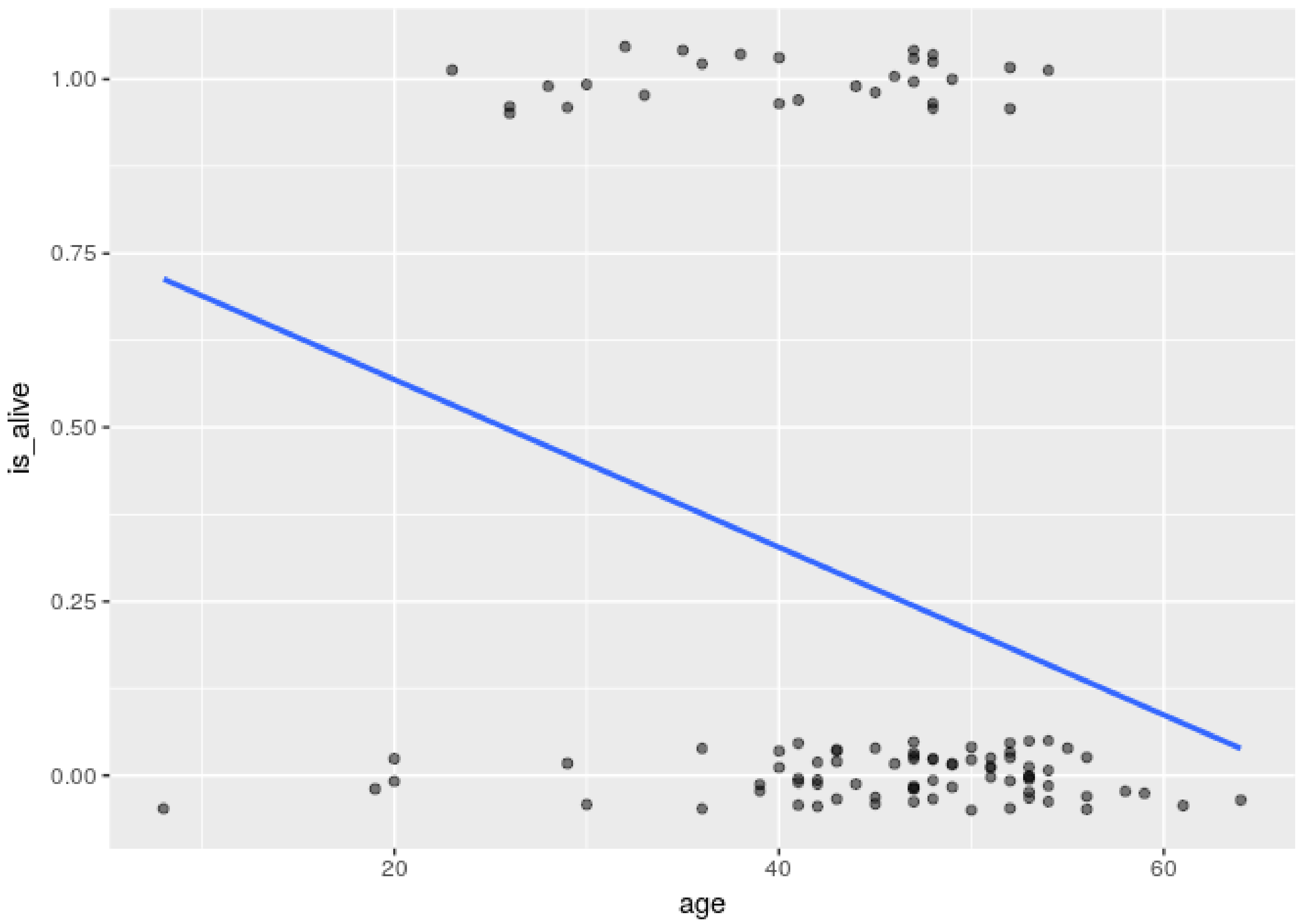
Visualizing a binary response

```
data_space <- ggplot(data = heartTr, aes(x = age, y = is_alive)) +
  geom_jitter(width = 0, height = 0.05, alpha = 0.5)
```



Regression with a binary response

```
data_space +
  geom_smooth(method = "lm", se = FALSE)
```



Limitations of regression

- Could make nonsensical predictions
- Binary response problematic

Generalized linear models

- generalization of multiple regression
  - model non-normal responses
- special case: logistic regression
  - models binary response
  - uses $logit$ link function
  - $logit(p) = \log\left(\frac{p}{1-p}\right) = \beta_0 + \beta_1 \cdot x$

Fitting a GLM

```r
glm(is_alive ~ age, data = heartTr, family = binomial)

binomial()
```

```
    ## Family: binomial
    ## Link function: logit
```

Let's practice!

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Visualizing logistic regression

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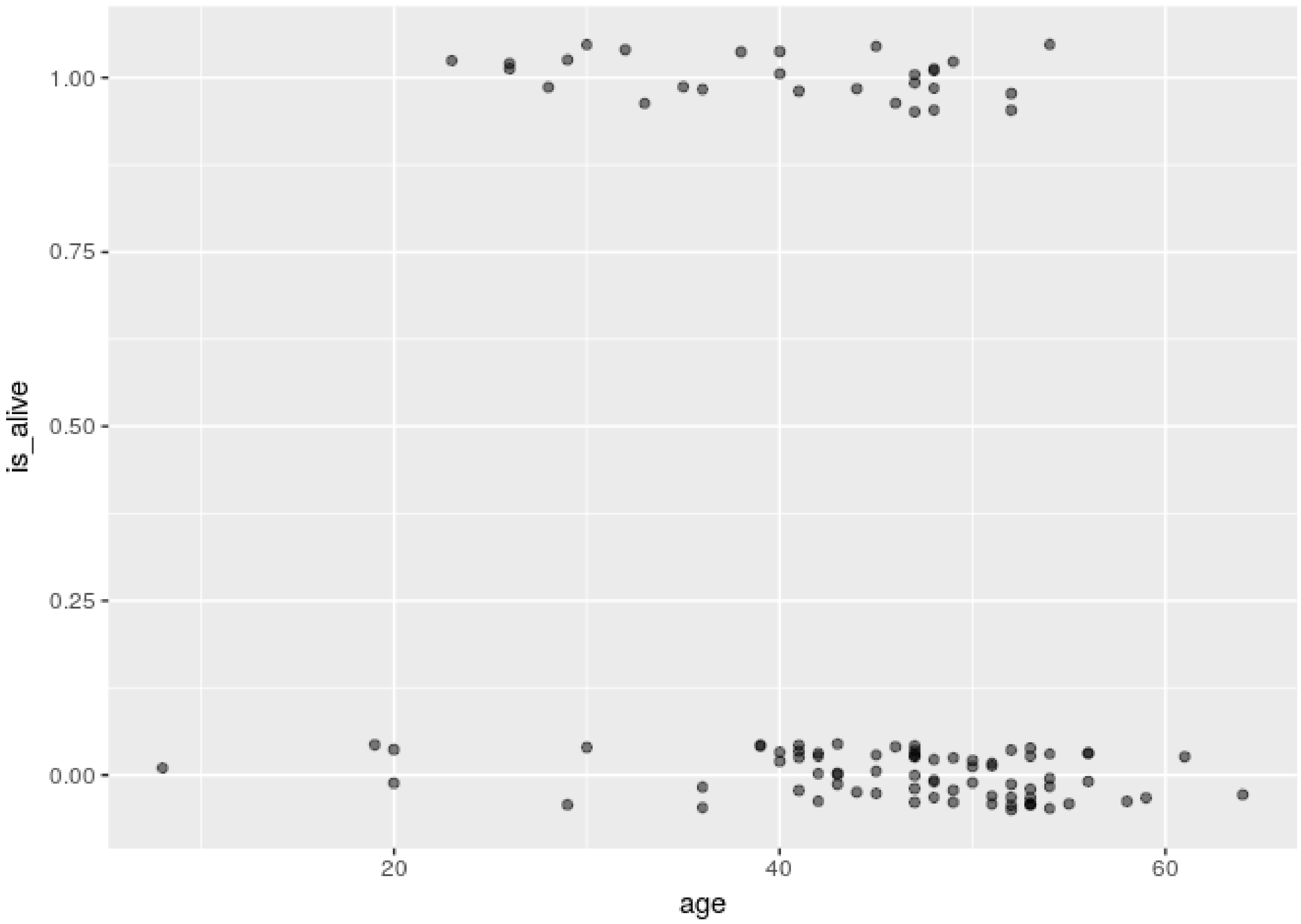
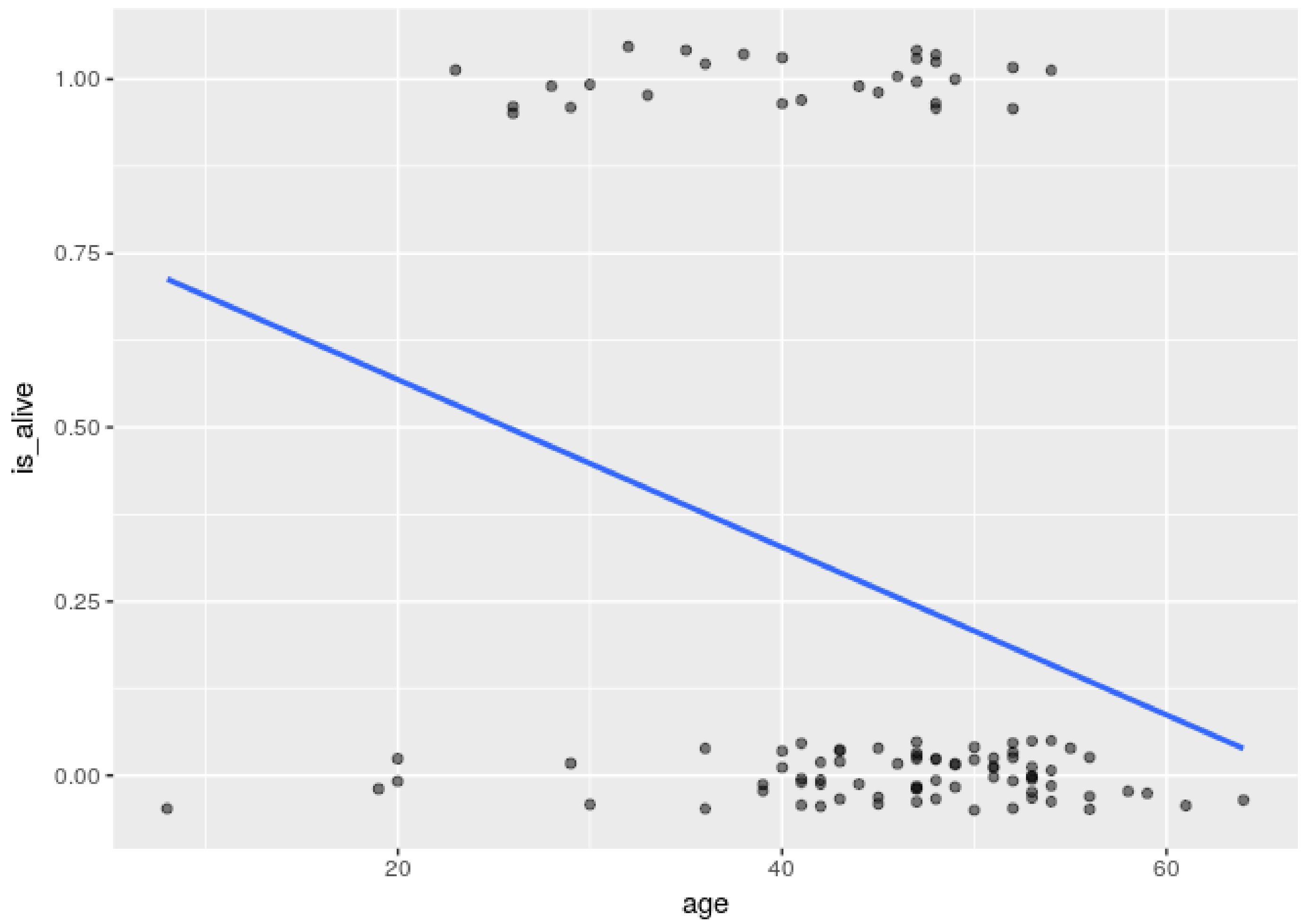
The data space

```
data_space
```



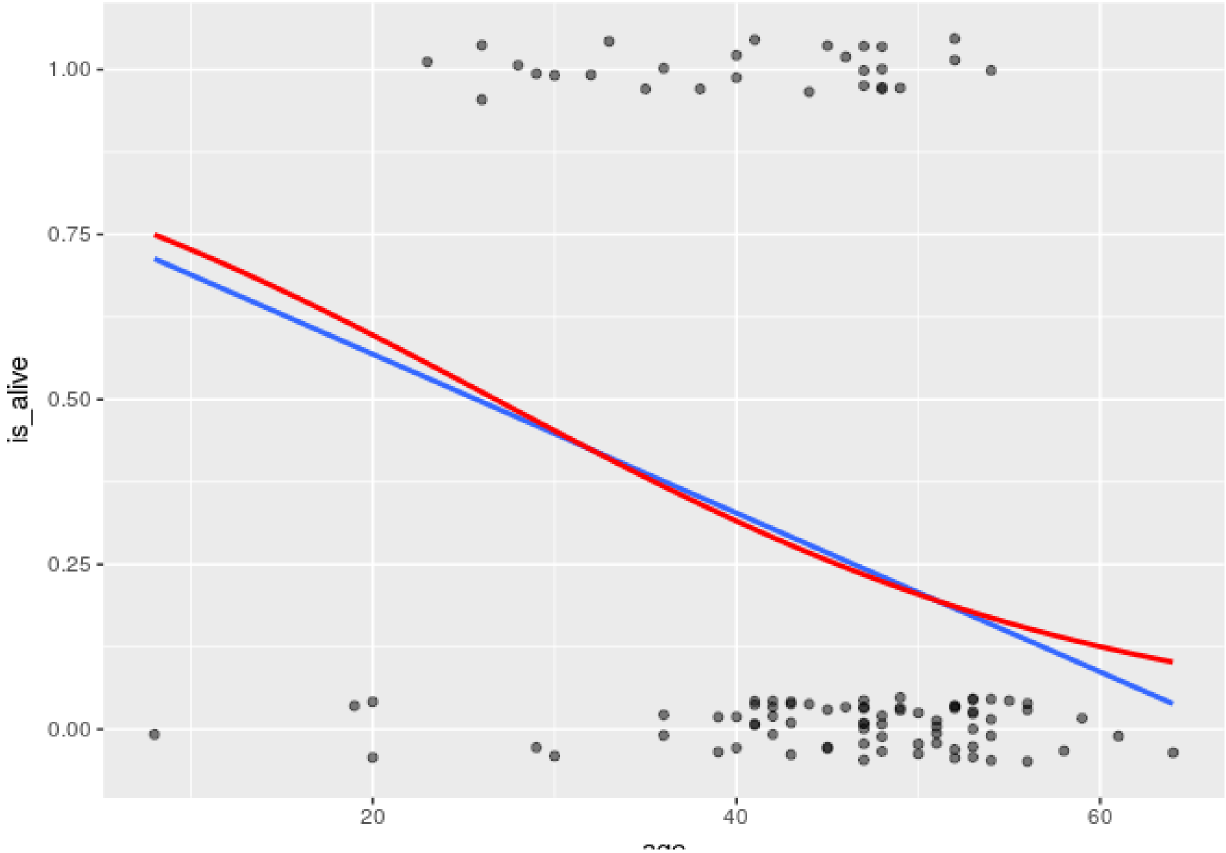
Regression

```
data_space +
  geom_smooth(method = "lm", se = FALSE)
```



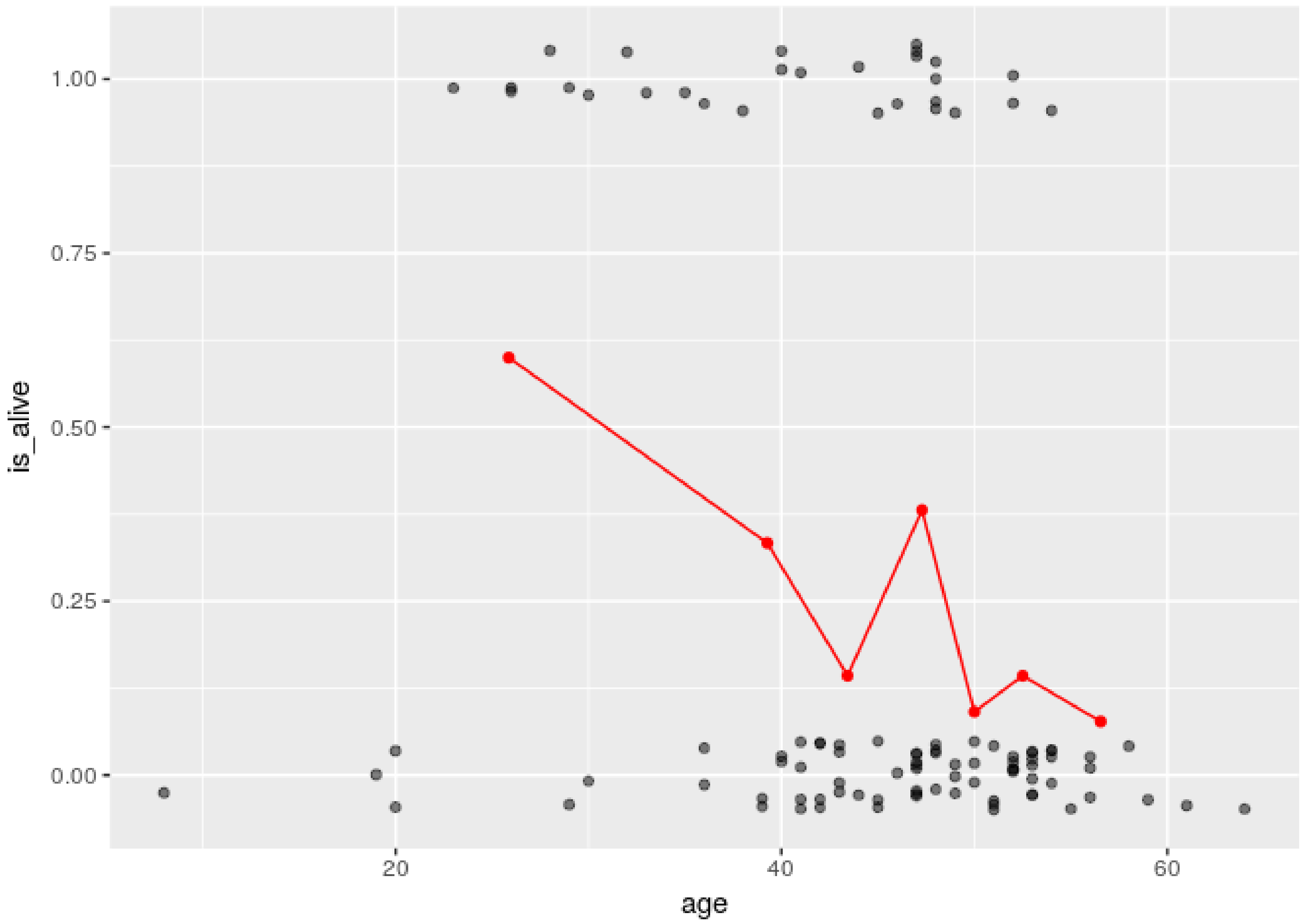
Using geom_smooth()

```
data_space +
  geom_smooth(method = "lm", se = FALSE) +
  geom_smooth(method = "glm", se = FALSE, color = "red",
              method.args = list(family = "binomial"))
```



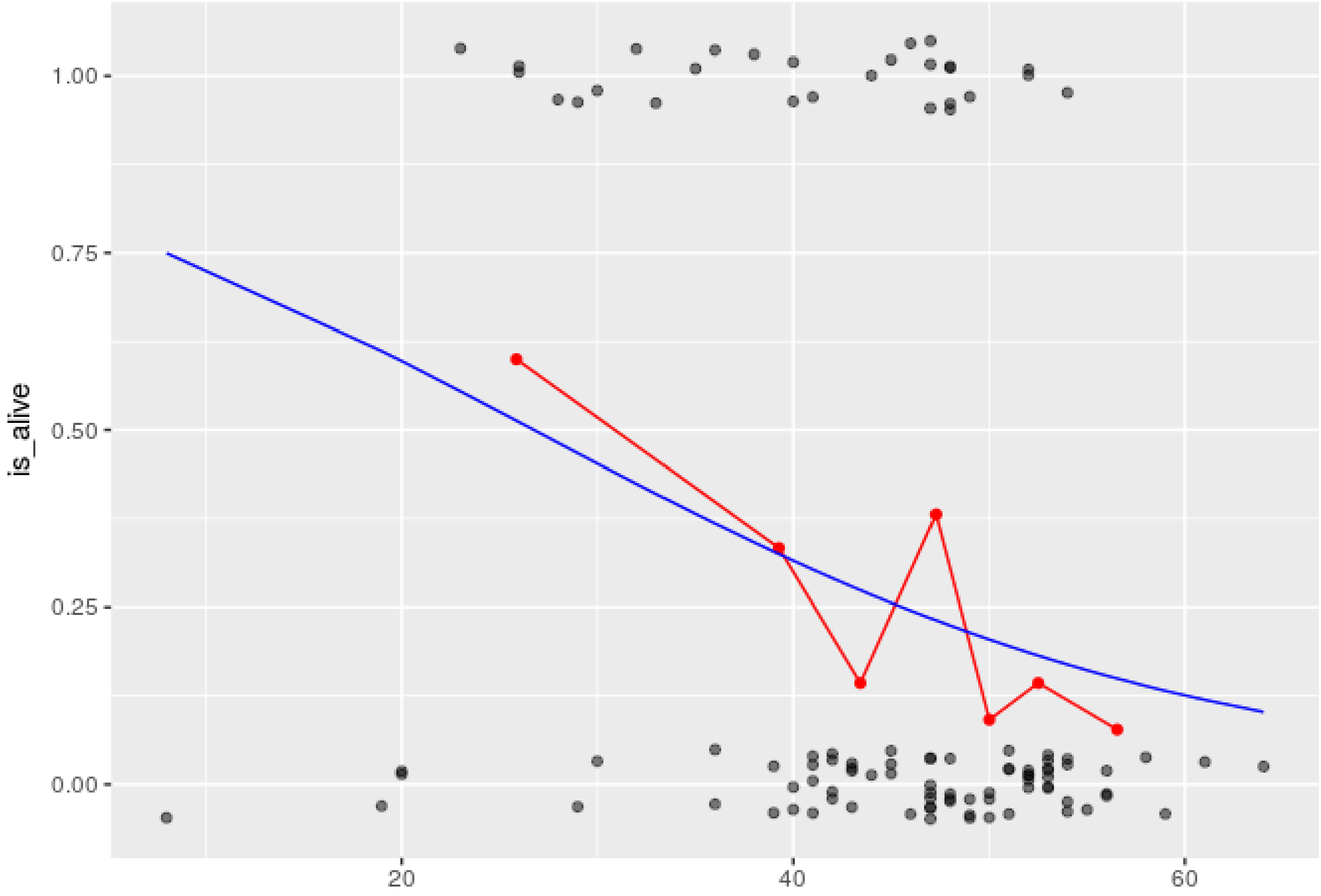
Using bins

```
data_binned_space
```



Adding the model to the binned plot

```
data_binned_space +
  geom_line(data = augment(mod, type.predict = "response"),
            aes(y = .fitted), color = "blue")
```



Let's practice!

MULTIPLE AND LOGISTIC REGRESSION IN R

Three scales approach to interpretation

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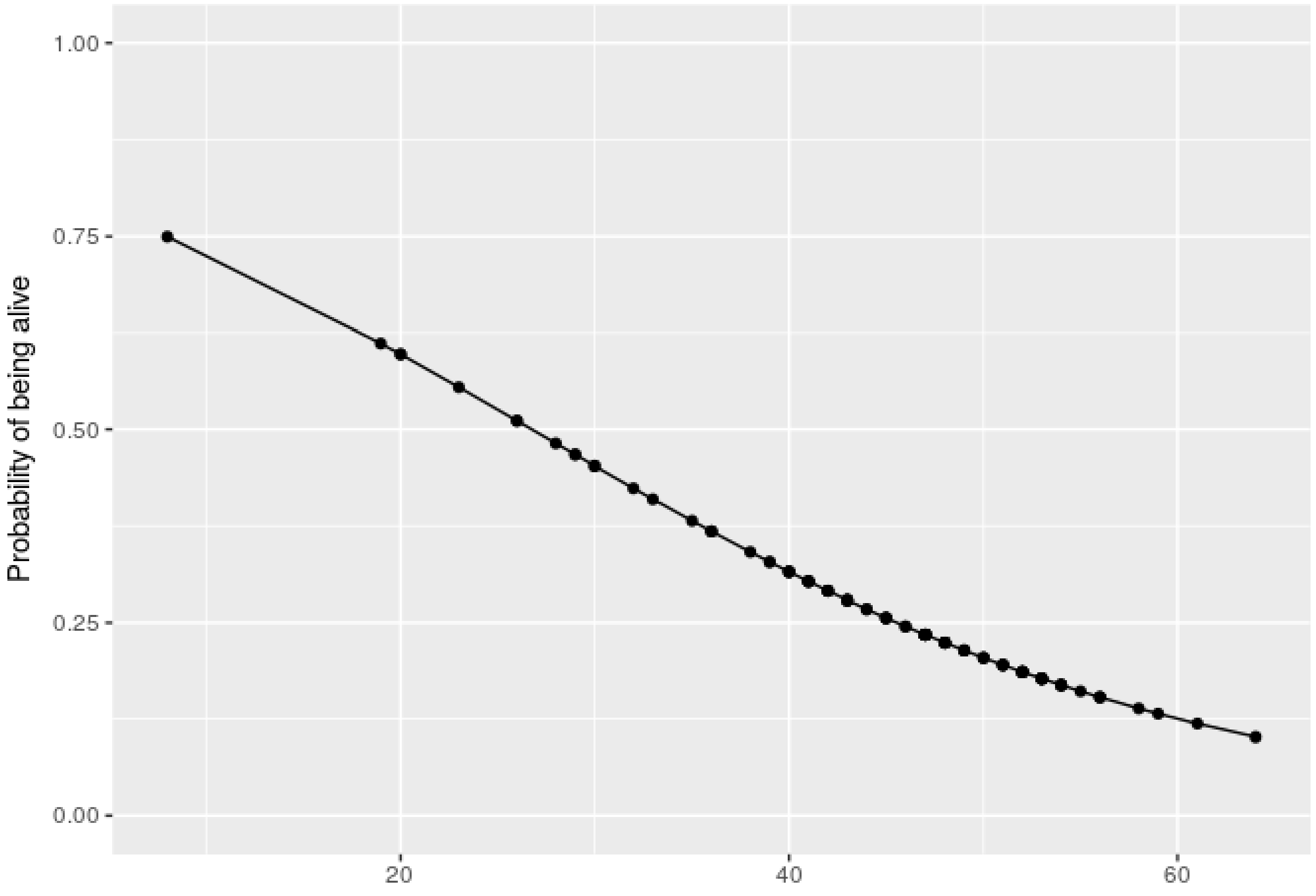
Probability scale

$$\hat{y} = \frac{\exp\left(\hat{\beta}_0 + \hat{\beta}_1 \cdot x\right)}{1 + \exp(\hat{\beta}_0 + \hat{\beta}_1 \cdot x)}$$

```
heartTr_plus <- mod %>%
  augment(type.predict = "response") %>%
  mutate(y_hat = .fitted)
```

Probability scale plot

```
ggplot(heartTr_plus, aes(x = age, y = y_hat)) +
  geom_point() + geom_line() +
  scale_y_continuous("Probability of being alive", limits = c(0, 1))
```



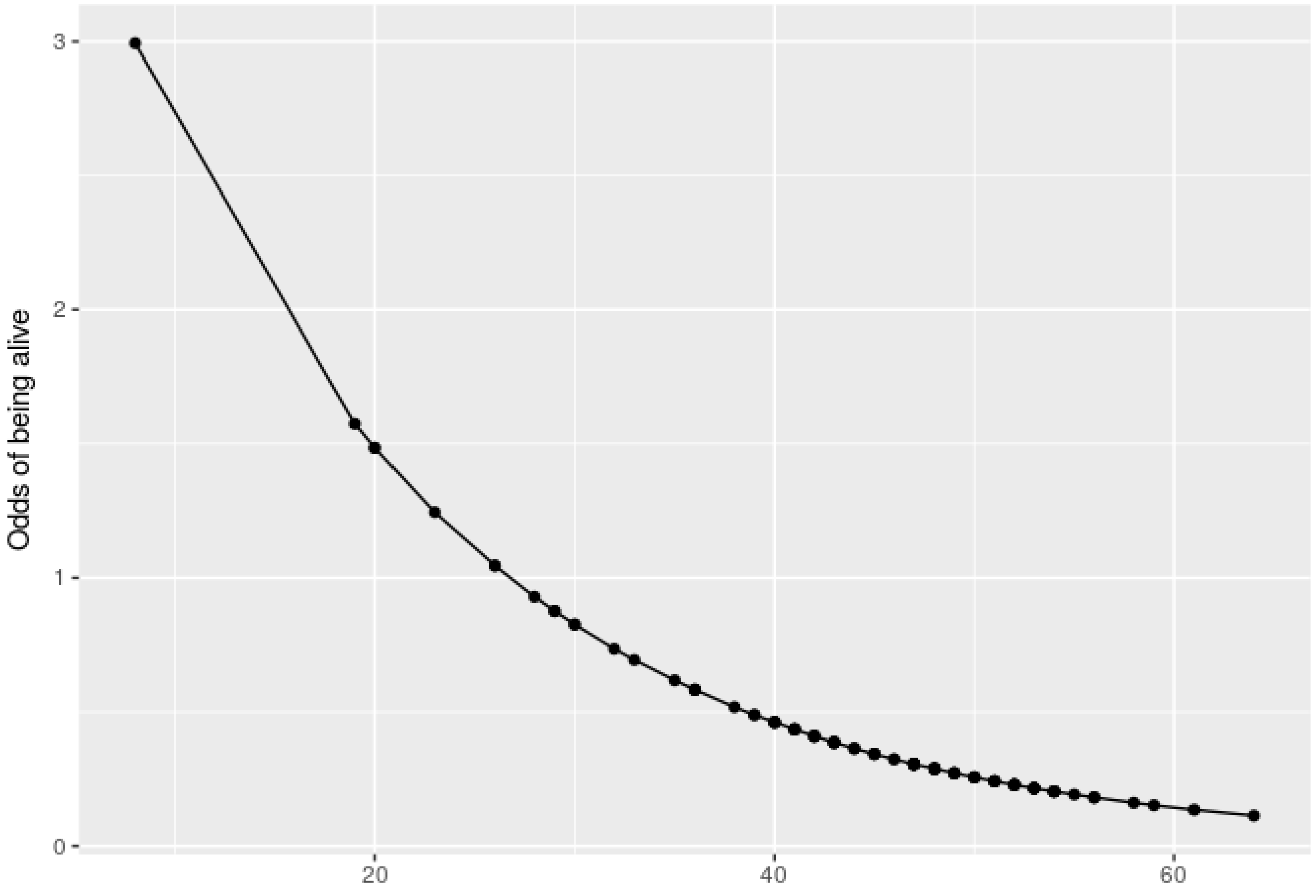
Odds scale

$$odds(\hat{y}) = \frac{\hat{y}}{1 - \hat{y}} = \exp\left(\hat{\beta}_0 + \hat{\beta}_1 \cdot x\right)$$

```
heartTr_plus <- heartTr_plus %>%
  mutate(odds_hat = y_hat / (1 - y_hat))
```

Odds scale plot

```
ggplot(heartTr_plus, aes(x = age, y = odds_hat)) +
  geom_point() + geom_line() +
  scale_y_continuous("Odds of being alive")
```



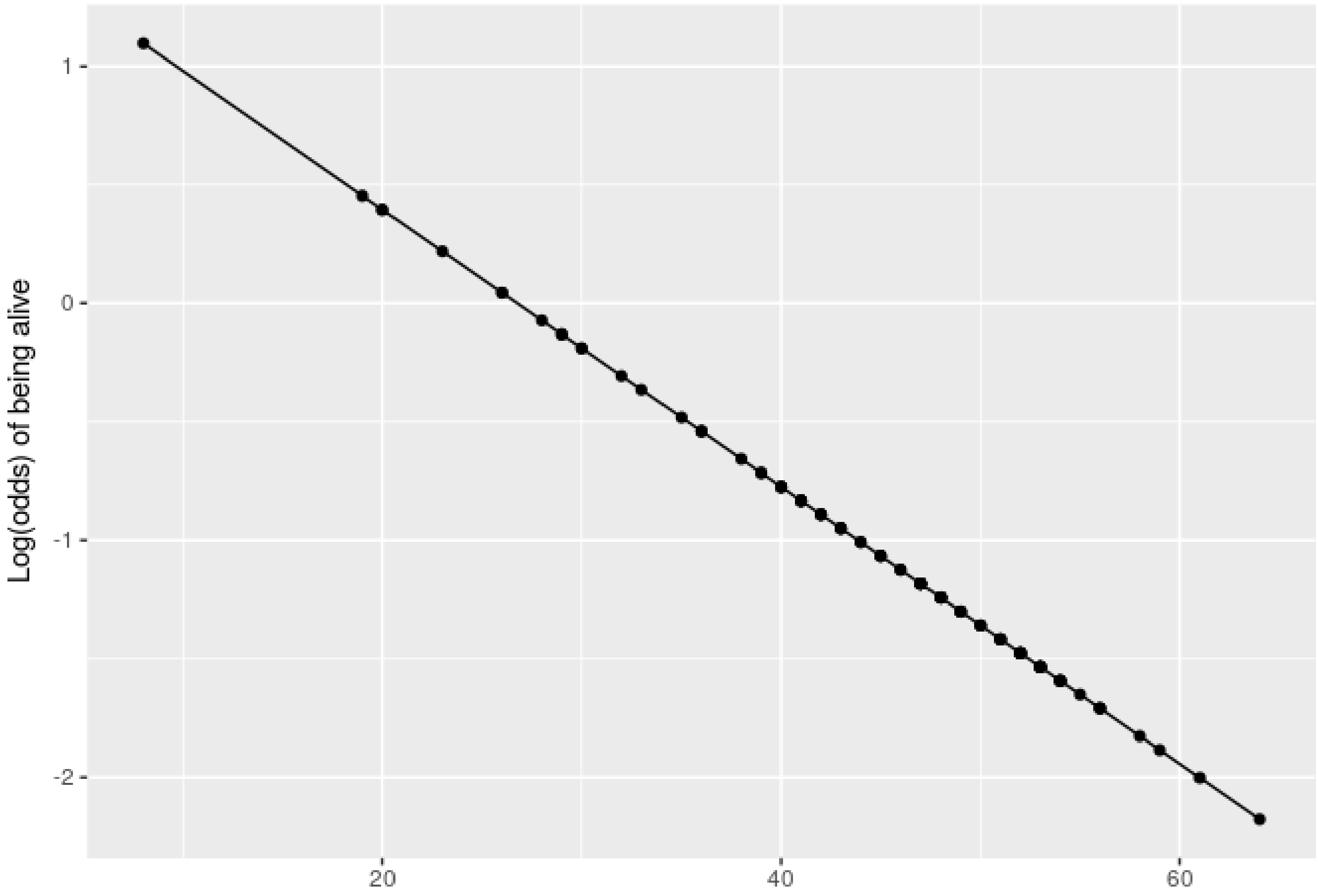
Log-odds scale

$$logit(\hat{y}) = \log\left[\frac{\hat{y}}{1-\hat{y}}\right] = \hat{\beta}_0 + \hat{\beta}_1 \cdot x$$

```
heartTr_plus <- heartTr_plus %>%
  mutate(log_odds_hat = log(odds_hat))
```

Log-odds plot

```
ggplot(heartTr_plus, aes(x = age, y = log_odds_hat)) +
  geom_point() + geom_line() +
  scale_y_continuous("Log(odds) of being alive")
```



Comparison

- Probability scale
    - scale: intuitive, easy to interpret
    - function: non-linear, hard to interpret
- Odds scale
    - scale: harder to interpret
    - function: exponential, harder to interpret
- Log-odds scale
    - scale: impossible to interpret
    - function: linear, easy to interpret

Odds ratios

$$OR = \frac{odds(\hat{y}|x+1)}{odds(\hat{y}|x)} = \frac{\exp\left(\hat{\beta}_0 + \hat{\beta}_1 \cdot (x+1)\right)}{\exp\left(\hat{\beta}_0 + \hat{\beta}_1 \cdot x\right)} = \exp \beta_1$$

```
exp(coef(mod))
```

```
(Intercept)         age
  4.7797050   0.9432099
```

Let's practice!

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Using a logistic model

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Learning from a model

```
mod <- glm(is_alive ~ age + transplant,
                    data = heartTr, family = binomial)


exp(coef(mod))
```

```
##         (Intercept)                 age transplanttreatment
##           2.6461676           0.9265153           6.1914009
```

Using augment()

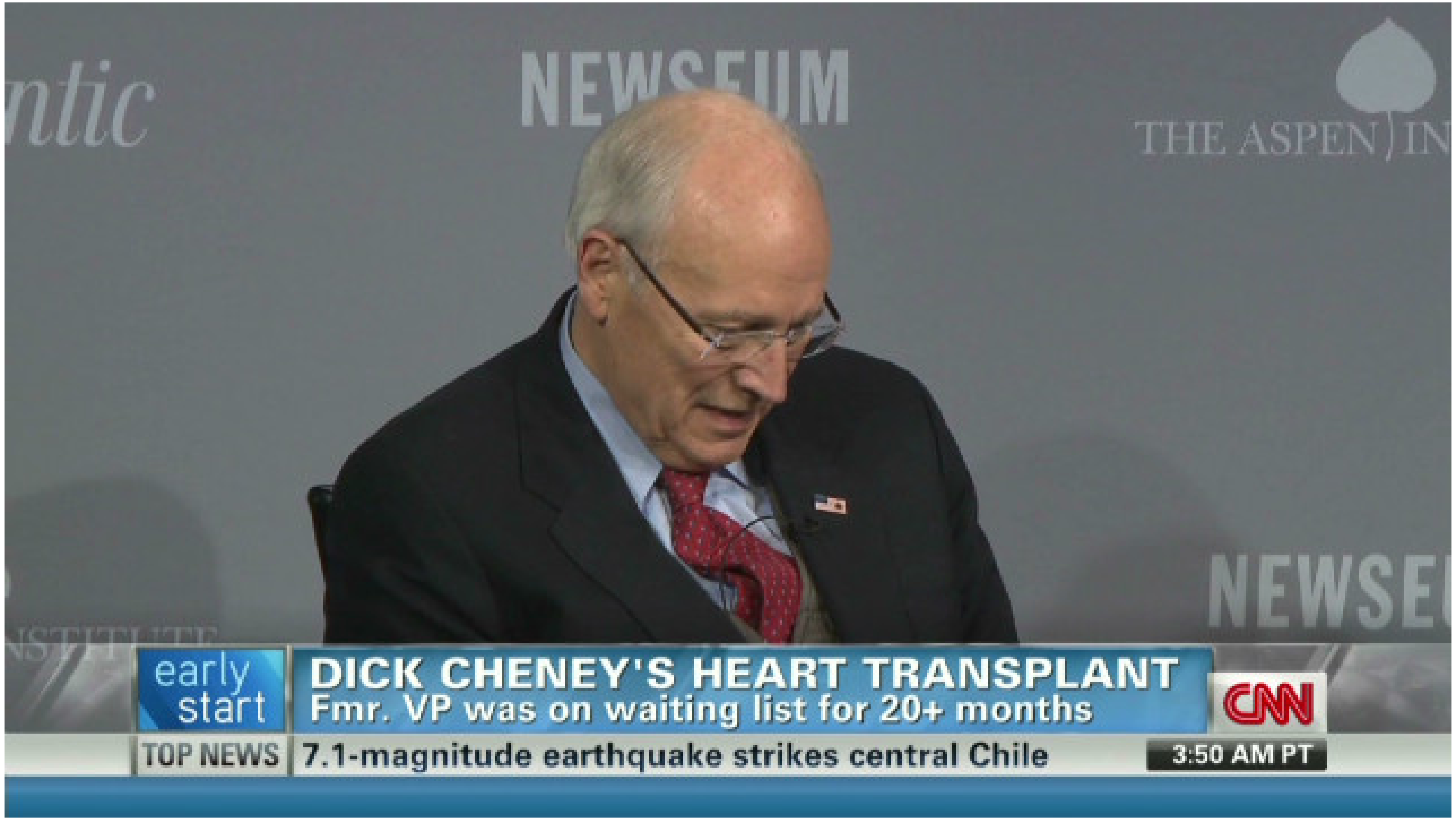
```
# log-odds scale
augment(mod)
```

```
##      is_alive age transplant    .fitted   .se.fit     .resid
## 1          0  53    control -3.0720949 0.7196746 -0.3009421 0.021
## 2          0  43    control -2.3088482 0.5992811 -0.4352986 0.029
## 3          0  52    control -2.9957702 0.7044109 -0.3123727 0.022
## 4          0  52    control -2.9957702 0.7044109 -0.3123727 0.022
## 5          0  54    control -3.1484196 0.7355066 -0.2899116 0.021
## 6          0  36    control -1.7745756 0.5704650 -0.5596850 0.040
## 7          0  47    control -2.6141469 0.6379934 -0.3759601 0.025
## 8          0  41  treatment -0.3330375 0.2810663 -1.0396433 0.019
## 9          0  47    control -2.6141469 0.6379934 -0.3759601 0.025
## 10         0  51    control -2.9194456 0.6897533 -0.3242157 0.023
```

Making probabilistic predictions

```r
# probability scale
augment(mod, type.predict = "response")
```

```
##      is_alive age transplant    .fitted    .se.fit     .resid        .hat
## 1           0  53    control 0.04427310 0.03045159 -0.3009421 0.02191525
## 2           0  43    control 0.09039280 0.04927406 -0.4352986 0.02952903
## 3           0  52    control 0.04761733 0.03194498 -0.3123727 0.02250241
## 4           0  52    control 0.04761733 0.03194498 -0.3123727 0.02250241
## 5           0  54    control 0.04115360 0.02902308 -0.2899116 0.02134668
## 6           0  36    control 0.14497423 0.07071297 -0.5596850 0.04033929
## 7           0  47    control 0.06823348 0.04056214 -0.3759601 0.02587839
## 8           0  41  treatment 0.41750173 0.06835365 -1.0396433 0.01921191
## 9           0  47    control 0.06823348 0.04056214 -0.3759601 0.02587839
## 10          0  51    control 0.05120063 0.03350761 -0.3242157 0.02311200
```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NEWSEUM
THE ASPEN IN
NEWSE
NSTITUTE
early start
DICK CHENEY'S HEART TRANSPLANT
Fmr. VP was on waiting list for 20+ months
CNN
TOP NEWS
7.1-magnitude earthquake strikes central Chile
3:50 AM PT

Out-of-sample predictions

```r
cheney <- data.frame(age = 71, transplant = "treatment")

augment(mod, newdata = cheney, type.predict = "response")
```

```
##   age transplant    .fitted    .se.fit
## 1  71  treatment 0.06768681 0.04572512
```

Making binary predictions

```r
mod_plus <- augment(mod, type.predict = "response") %>%
  mutate(alive_hat = round(.fitted))

mod_plus %>%
  select(is_alive, age, transplant, .fitted, alive_hat)
```

```
##     is_alive age transplant    .fitted alive_hat
## 1          0  53    control 0.04427310         0
## 2          0  43    control 0.09039280         0
## 3          0  52    control 0.04761733         0
## 4          0  52    control 0.04761733         0
## 5          0  54    control 0.04115360         0
## 6          0  36    control 0.14497423         0
## 7          0  47    control 0.06823348         0
## 8          0  41  treatment 0.41750173         0
```

Confusion matrix

```
mod_plus %>%
  select(is_alive, alive_hat) %>%
  table()
```

```
##         alive_hat
## is_alive  0  1
##        0 71  4
##        1 20  8
```

Let's practice!

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