# Logistic regression

Predict binary outcomes (success/failure) from numerical or categorical predictors.

# Linear vs. logistic regression

Linear regression:

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \cdots + \beta_n x_n + \varepsilon$$

# Linear vs. logistic regression

Linear regression:

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \cdots + \beta_n x_n + \varepsilon$$

Logistic regression:

$$\Pr(success) = \frac{e^t}{1 + e^t}$$

$$t = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \cdots + \beta_n x_n + \varepsilon$$

# Linear vs. logistic regression

Linear regression:

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \cdots + \beta_n x_n + \varepsilon$$

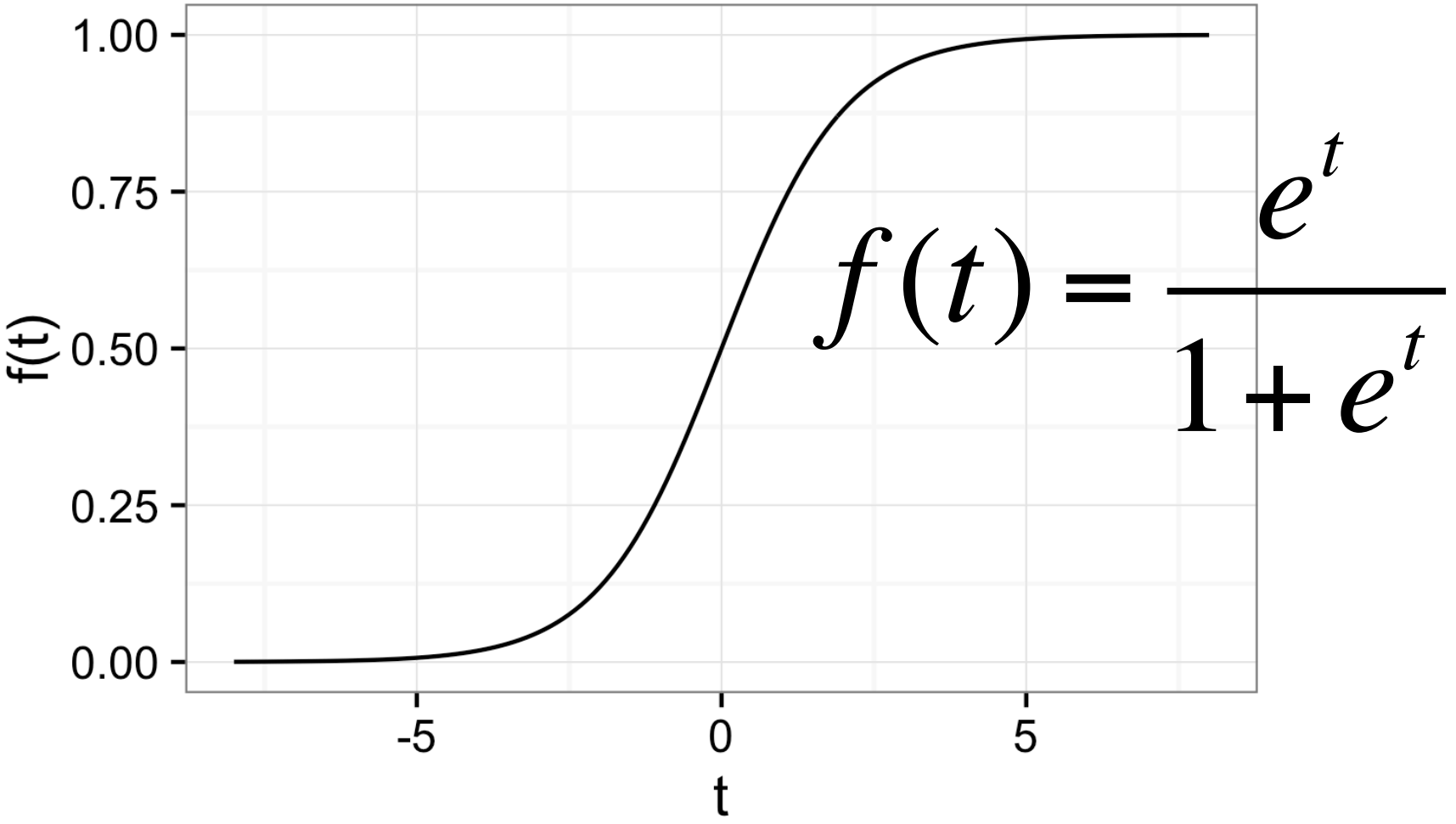
Logistic regression:

$$\Pr(success) = \frac{e^t}{1 + e^t}$$

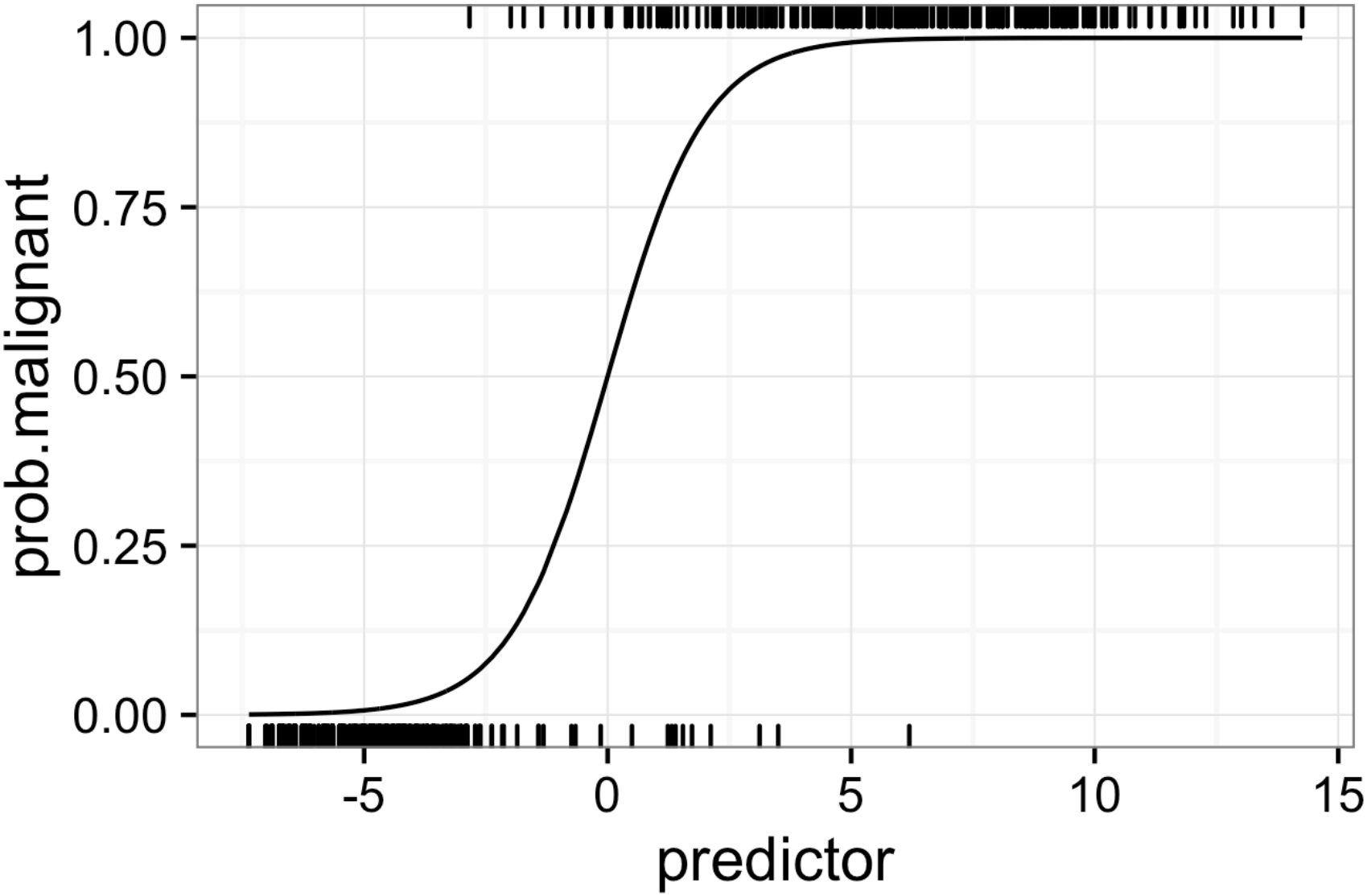
$$t = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \cdots + \beta_n x_n + \varepsilon$$

(generalized linear model, GLM)

# The logistic equation



# Example: Pr(malignant) in biopsy data set



# Let’s do this step by step…

# Recall the biopsy data set

```
> biopsy <- read.csv("http://wilkelab.org/classes/SDS348/data_sets/biopsy.csv")
> head(biopsy)
  clump_thickness uniform_cell_size uniform_cell_shape marg_adhesion
1               5                 1                  1             1
2               5                 4                  4             5
3               3                 1                  1             1
4               6                 8                  8             1
5               4                 1                  1             3
6               8                10                 10             8
  epithelial_cell_size bare_nuclei bland_chromatin normal_nucleoli mitoses
1                    2           1               3               1       1
2                    7          10               3               2       1
3                    2           2               3               1       1
4                    3           4               3               7       1
5                    2           1               3               1       1
6                    7          10               9               7       1
    outcome
1    benign
2    benign
3    benign
4    benign
5    benign
6 malignant
```

# We do logistic regression with the `glm( )` function

```
> glm.out <- glm(outcome ~ clump_thickness +
                           uniform_cell_size +
                           uniform_cell_shape +
                           marg_adhesion +
                           epithelial_cell_size +
                           bare_nuclei +
                           bland_chromatin +
                           normal_nucleoli +
                           mitoses,
                 data=biopsy,
                 family=binomial)
```

```
> summary(glm.out)

Call:
glm(formula = outcome ~ clump_thickness + uniform_cell_size +
    uniform_cell_shape + marg_adhesion + epithelial_cell_size +
    bare_nuclei + bland_chromatin + normal_nucleoli + mitoses,
    family = binomial, data = biopsy)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.4841  -0.1153  -0.0619   0.0222   2.4698

Coefficients:
                     Estimate Std. Error z value Pr(>|z|)
(Intercept)         -10.10394    1.17488  -8.600  < 2e-16 ***
clump_thickness       0.53501    0.14202   3.767 0.000165 ***
uniform_cell_size    -0.00628    0.20908  -0.030 0.976039
uniform_cell_shape    0.32271    0.23060   1.399 0.161688
marg_adhesion         0.33064    0.12345   2.678 0.007400 **
epithelial_cell_size  0.09663    0.15659   0.617 0.537159
bare_nuclei           0.38303    0.09384   4.082 4.47e-05 ***
bland_chromatin       0.44719    0.17138   2.609 0.009073 **
normal_nucleoli       0.21303    0.11287   1.887 0.059115 .
mitoses               0.53484    0.32877   1.627 0.103788
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
> summary(glm.out)

Call:
glm(formula = outcome ~ clump_thickness + uniform_cell_size +
    uniform_cell_shape + marg_adhesion + epithelial_cell_size +
    bare_nuclei + bland_chromatin + normal_nucleoli + mitoses,
    family = binomial, data = biopsy)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.4841  -0.1153  -0.0619   0.0222   2.4698

Coefficients:
                     Estimate Std. Error z value Pr(>|z|)
(Intercept)         -10.10394    1.17488  -8.600  < 2e-16 ***
clump_thickness       0.53501    0.14202   3.767 0.000165 ***
uniform_cell_size     0.00628    0.20908   0.030 0.976039
uniform_cell_shape    0.32271    0.23060   1.399 0.161688
marg_adhesion         0.33064    0.12345   2.678 0.007400 **
epithelial_cell_size  0.09663    0.15659   0.617 0.537159
bare_nuclei           0.38303    0.09384   4.082 4.47e-05 ***
bland_chromatin       0.44719    0.17138   2.609 0.009073 **
normal_nucleoli       0.21303    0.11287   1.887 0.059115 .
mitoses               0.53484    0.32877   1.627 0.103788
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
> glm.out <- glm(outcome ~ clump_thickness +
                           uniform_cell_shape +
                           marg_adhesion +
                           epithelial_cell_size +
                           bare_nuclei +
                           bland_chromatin +
                           normal_nucleoli +
                           mitoses,
                 data=biopsy,
                 family=binomial)
```

```
> summary(glm.out)

Call:
glm(formula = outcome ~ clump_thickness + uniform_cell_shape +
    marg_adhesion + epithelial_cell_size + bare_nuclei +
bland_chromatin +
    normal_nucleoli + mitoses, family = binomial, data = biopsy)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.4823  -0.1154  -0.0620   0.0222   2.4694

Coefficients:
                     Estimate Std. Error z value Pr(>|z|)
(Intercept)         -10.09765    1.15546  -8.739  < 2e-16 ***
clump_thickness       0.53456    0.14125   3.784 0.000154 ***
uniform_cell_shape    0.31816    0.17424   1.826 0.067847 .
marg_adhesion         0.32993    0.12115   2.723 0.006465 **
epithelial_cell_size  0.09612    0.15564   0.618 0.536876
bare_nuclei           0.38308    0.09384   4.082 4.46e-05 ***
bland_chromatin       0.44648    0.16986   2.628 0.008578 **
normal_nucleoli       0.21255    0.11174   1.902 0.057149 .
mitoses               0.53406    0.32761   1.630 0.103064
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
> summary(glm.out)

Call:
glm(formula = outcome ~ clump_thickness + uniform_cell_shape +
    marg_adhesion + epithelial_cell_size + bare_nuclei +
bland_chromatin +
    normal_nucleoli + mitoses, family = binomial, data = biopsy)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.4823  -0.1154  -0.0620   0.0222   2.4694

Coefficients:
                     Estimate Std. Error z value Pr(>|z|)
(Intercept)         -10.09765    1.15546  -8.739  < 2e-16 ***
clump_thickness       0.53456    0.14125   3.784 0.000154 ***
uniform_cell_shape    0.31816    0.17424   1.826 0.067847 .
marg_adhesion         0.32993    0.12115   2.723 0.006465 **
epithelial_cell_size  0.09612    0.15564   0.618 0.536876
bare_nuclei           0.38308    0.09384   4.082 4.46e-05 ***
bland_chromatin       0.44648    0.16986   2.628 0.008578 **
normal_nucleoli       0.21255    0.11174   1.902 0.057149 .
mitoses               0.53406    0.32761   1.630 0.103064
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
> glm.out <- glm(outcome ~ clump_thickness +
                           uniform_cell_shape +
                           marg_adhesion +
                           bare_nuclei +
                           bland_chromatin +
                           normal_nucleoli +
                           mitoses,
                 data=biopsy,
                 family=binomial)
```

```
> summary(glm.out)

Call:
glm(formula = outcome ~ clump_thickness + uniform_cell_shape +
    marg_adhesion + bare_nuclei + bland_chromatin +
normal_nucleoli +
    mitoses, family = binomial, data = biopsy)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.5235  -0.1149  -0.0627   0.0219   2.4115

Coefficients:
                  Estimate Std. Error z value Pr(>|z|)
(Intercept)       -9.98278    1.12610  -8.865  < 2e-16 ***
clump_thickness    0.53400    0.14079   3.793 0.000149 ***
uniform_cell_shape 0.34529    0.17164   2.012 0.044255 *
marg_adhesion      0.34249    0.11922   2.873 0.004068 **
bare_nuclei        0.38830    0.09356   4.150 3.32e-05 ***
bland_chromatin    0.46194    0.16820   2.746 0.006025 **
normal_nucleoli    0.22606    0.11097   2.037 0.041644 *
mitoses            0.53119    0.32446   1.637 0.101598
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
> summary(glm.out)

Call:
glm(formula = outcome ~ clump_thickness + uniform_cell_shape +
    marg_adhesion + bare_nuclei + bland_chromatin +
normal_nucleoli +
    mitoses, family = binomial, data = biopsy)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.5235  -0.1149  -0.0627   0.0219   2.4115

Coefficients:
                  Estimate Std. Error z value Pr(>|z|)
(Intercept)       -9.98278    1.12610  -8.865  < 2e-16 ***
clump_thickness    0.53400    0.14079   3.793 0.000149 ***
uniform_cell_shape 0.34529    0.17164   2.012 0.044255 *
marg_adhesion      0.34249    0.11922   2.873 0.004068 **
bare_nuclei        0.38830    0.09356   4.150 3.32e-05 ***
bland_chromatin    0.46194    0.16820   2.746 0.006025 **
normal_nucleoli    0.22606    0.11097   2.037 0.041644 *
mitoses            0.53119    0.32446   1.637 0.101598
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
> glm.out <- glm(outcome ~ clump_thickness +
                           uniform_cell_shape +
                           marg_adhesion +
                           bare_nuclei +
                           bland_chromatin +
                           normal_nucleoli,
                 data=biopsy,
                 family=binomial)
```

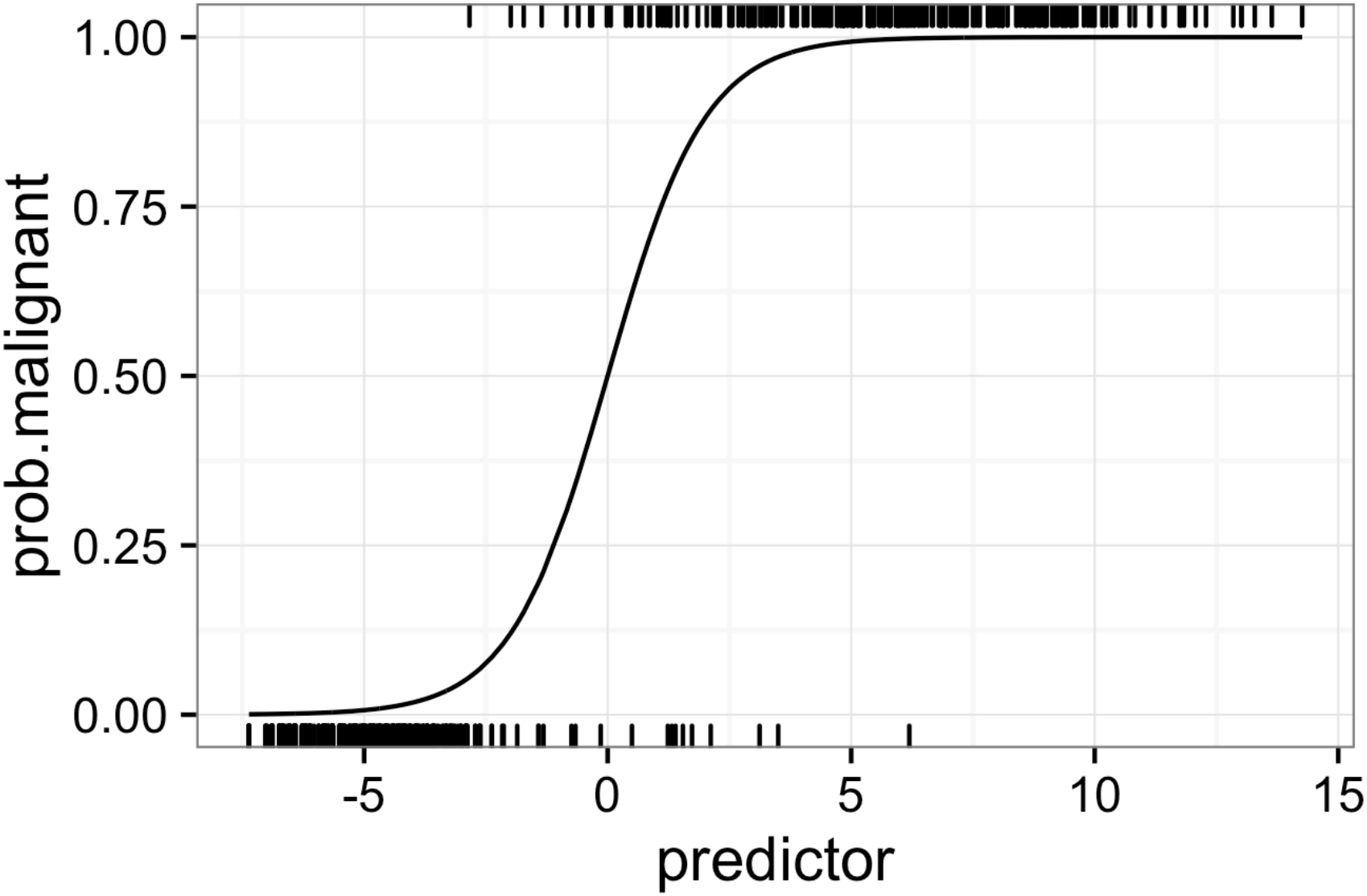
```
> summary(glm.out)

Call:
glm(formula = outcome ~ clump_thickness + uniform_cell_shape +
    marg_adhesion + bare_nuclei + bland_chromatin +
normal_nucleoli,
    family = binomial, data = biopsy)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.5201  -0.1186  -0.0570   0.0250   2.4055

Coefficients:
                  Estimate Std. Error z value Pr(>|z|)
(Intercept)       -9.76708    1.08506  -9.001  < 2e-16 ***
clump_thickness    0.62253    0.13712   4.540 5.62e-06 ***
uniform_cell_shape 0.34951    0.16503   2.118  0.03419 *
marg_adhesion      0.33753    0.11561   2.920  0.00350 **
bare_nuclei        0.37855    0.09381   4.035 5.45e-05 ***
bland_chromatin    0.47134    0.16612   2.837  0.00455 **
normal_nucleoli    0.24317    0.10855   2.240  0.02509 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

# The fitted logistic model



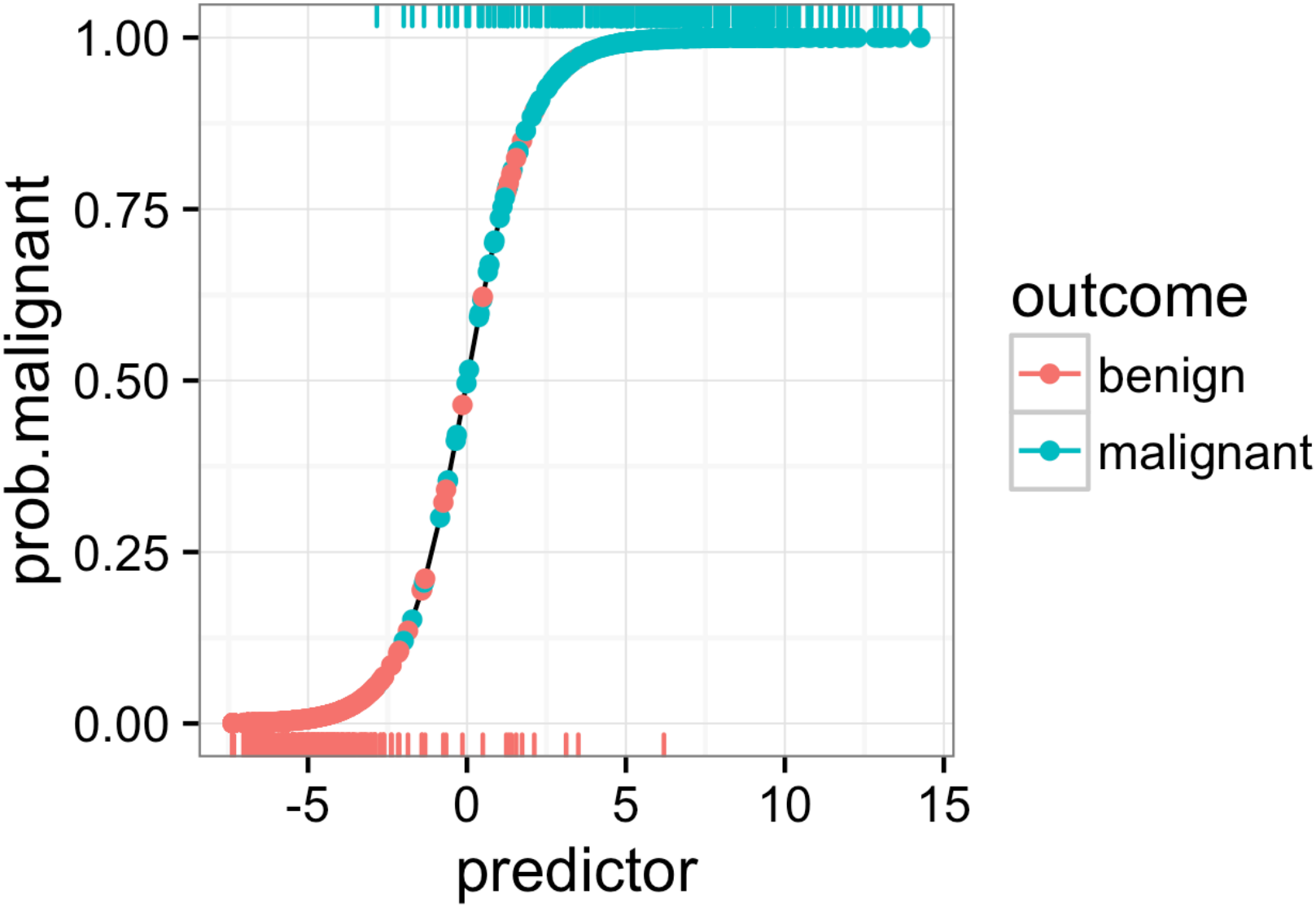
# We can extract fitted probabilities from `glm.out$fitted.values`

```
> glm.out$fitted.values
           1            2            3            4            5            6
0.0192341317 0.8925583864 0.0081774737 0.8496854505 0.0202506282 0.9999854554
           7            8            9           10           11           12
0.0467606911 0.0042790664 0.0011789931 0.0065253423 0.0016231293 0.0018875638
          13           14           15           16           17           18
0.3544332567 0.0034543023 0.9993353305 0.7371582761 0.0065253423 0.0104135504
          19           20           21           22           23           24
0.9989353409 0.0352597948 0.9969203982 0.9994994519 0.0035120154 0.0016231293
          25           26           27           28           29           30
0.7802514369 0.0035120154 0.0120927435 0.0018875638 0.0012725934 0.0035120154
          31           32           33           34           35           36
0.0030206952 0.9977220579 0.0042283384 0.0049740412 0.0018875638 0.9998755391
          37           38           39           40           41           42
0.1940709471 0.9954253327 0.6691128086 0.9536389392 0.9974078013 0.3002866244
          43           44           45           46           47           48
0.9996235802 0.0010137236 0.9583091930 0.0010137236 0.0202506282 0.9836985106
          49           50           51           52           53           54
0.7842860362 0.4122043566 0.9956800184 0.9922376046 0.9988895968 0.9870508267
          55           56           57           58           59           60
0.9927513406 0.6585108620 0.7534314353 0.8341431018 0.9032183182 0.0014795146
          61           62           63           64           65           66
0.9921570845 0.5158282353 0.0010137236 0.7040691331 0.0104135504 0.9498144607
```

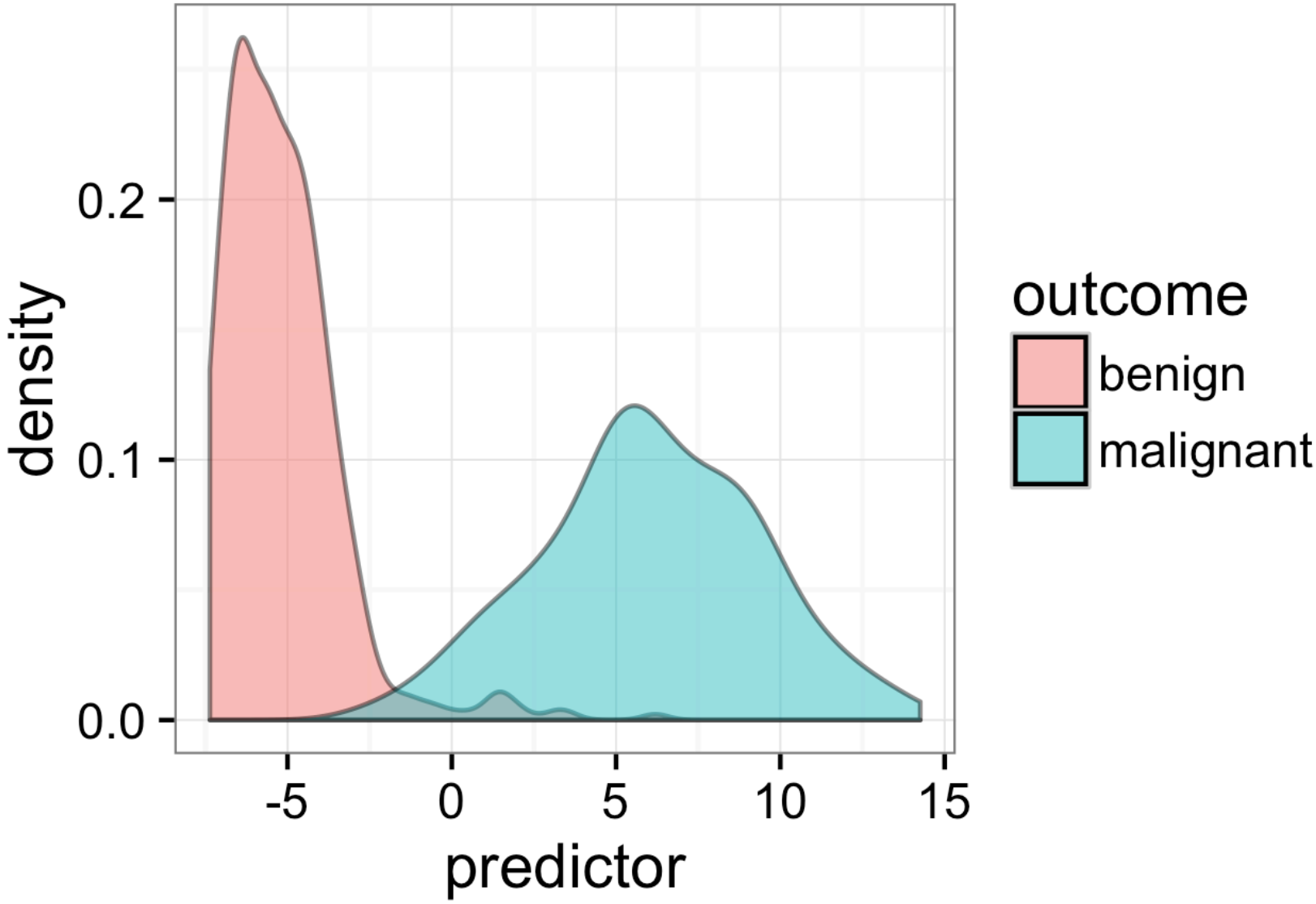
# We can extract linear predictors from `glm.out$linear.predictors`

```
> glm.out$linear.predictors
          1           2           3           4           5           6
-3.93164737  2.11714436 -4.79816093  1.73213613 -3.87911098 11.13827708
          7           8           9          10          11          12
-3.01482307 -5.44973218 -6.74191480 -5.02551514 -6.42177489 -6.27057890
         13          14          15          16          17          18
-0.59960855 -5.66467448  7.31555568  1.03125059 -5.02551514 -4.55417925
         19          20          21          22          23          24
 6.84403543 -3.30911549  5.77987063  7.59930618 -5.64804702 -6.42177489
         25          26          27          28          29          30
 1.26713222 -5.64804702 -4.40298326 -6.27057890 -6.66542501 -5.64804702
         31          32          33          34          35          36
-5.79924301  6.08220228 -5.46170888 -5.29853619 -6.27057890  8.99139484
         37          38          39          40          41          42
-1.42377192  5.38263613  0.70417516  3.02382523  5.95265328 -0.84593335
         43          44          45          46          47          48
 7.88442916 -6.89311078  3.13488983 -6.89311078 -3.87911098  4.10006298
         49          50          51          52          53          54
 1.29082051 -0.35486010  5.44017479  4.85067163  6.80192104  4.33368959
         55          56          57          58          59          60
 4.91966368  0.65666514  1.11699791  1.61527962  2.23350656 -6.51456058
         61          62          63          64          65          66
 4.84027081  0.06333410 -6.89311078  0.86675068 -4.55417925  2.94053974
```

# The linear predictor clearly separates benign and malignant outcomes



# The linear predictor clearly separates benign and malignant outcomes



# Predicting outcome for new data with the `predict()` function

```
> patient1 <- data.frame(clump_thickness = 1,
                         uniform_cell_size = 1,
                         uniform_cell_shape = 1,
                         marg_adhesion = 1,
                         epithelial_cell_size = 4,
                         bare_nuclei = 3,
                         bland_chromatin = 1,
                         normal_nucleoli = 1,
                         mitoses = 1)
```

# Predicting outcome for new data with the `predict()` function

```
> patient1 <- data.frame(clump_thickness = 1,
                         uniform_cell_size = 1,
                         uniform_cell_shape = 1,
                         marg_adhesion = 1,
                         epithelial_cell_size = 4,
                         bare_nuclei = 3,
                         bland_chromatin = 1,
                         normal_nucleoli = 1,
                         mitoses = 1)

> predict(glm.out, patient1) # linear predictor
        1
-6.607346
```

# Predicting outcome for new data with the `predict()` function

```
> patient1 <- data.frame(clump_thickness = 1,
                         uniform_cell_size = 1,
                         uniform_cell_shape = 1,
                         marg_adhesion = 1,
                         epithelial_cell_size = 4,
                         bare_nuclei = 3,
                         bland_chromatin = 1,
                         normal_nucleoli = 1,
                         mitoses = 1)

> predict(glm.out, patient1) # linear predictor
        1
-6.607346

> predict(glm.out, patient1, type="response") # probability
         1
0.00134859
```

# Predicting outcome for new data with the `predict()` function

```
> patient2 <- data.frame(clump_thickness = 4,
                         uniform_cell_size = 5,
                         uniform_cell_shape = 5,
                         marg_adhesion = 10,
                         epithelial_cell_size = 4,
                         bare_nuclei = 10,
                         bland_chromatin = 7,
                         normal_nucleoli = 5,
                         mitoses = 8)
```

# Predicting outcome for new data with the `predict()` function

```
> patient2 <- data.frame(clump_thickness = 4,
                         uniform_cell_size = 5,
                         uniform_cell_shape = 5,
                         marg_adhesion = 10,
                         epithelial_cell_size = 4,
                         bare_nuclei = 10,
                         bland_chromatin = 7,
                         normal_nucleoli = 5,
                         mitoses = 8)

> predict(glm.out, patient2) # linear predictor
       1
6.14665
```

# Predicting outcome for new data with the `predict()` function

```
> patient2 <- data.frame(clump_thickness = 4,
                         uniform_cell_size = 5,
                         uniform_cell_shape = 5,
                         marg_adhesion = 10,
                         epithelial_cell_size = 4,
                         bare_nuclei = 10,
                         bland_chromatin = 7,
                         normal_nucleoli = 5,
                         mitoses = 8)

> predict(glm.out, patient2) # linear predictor
       1
6.14665

> predict(glm.out, patient2, type="response") # probability
        1
0.9978639
```