

Expected number of effective parameters (std dev) :
 2.00 (0.00)
 Number of equivalent replicates: 43.50
 Marginal log-Likelihood: -37.99

These results show that the fitted model is equal to

$$\pi_i = \frac{\exp(2.659 - 0.016 \times \text{DeltaWeight}_i)}{1 + \exp(2.659 - 0.016 \times \text{DeltaWeight}_i)} \quad (10.4)$$

The larger the weight difference, the smaller the probability of survival. We visualised the model in Figure 10.4. To survive an attack you better not be a skinny person and encounter a large crocodile!

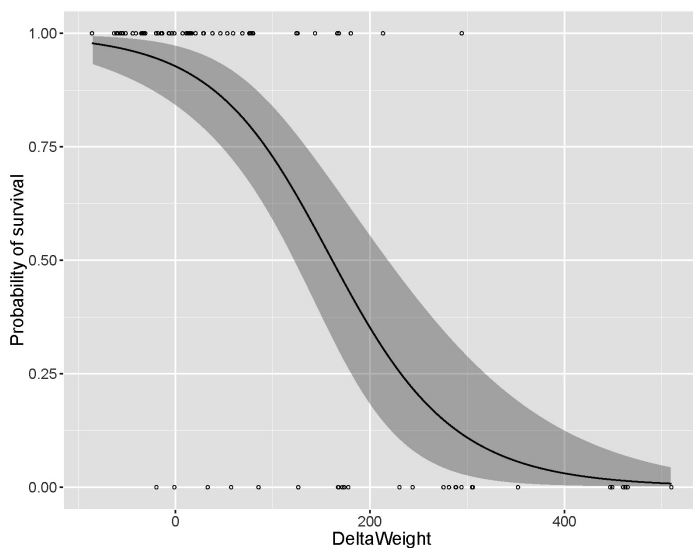


Figure 10.4. Fitted values of the Bernoulli model applied on the crocodile attack data.

The code to create Figure 10.4 is slightly different from the code presented in the previous section, and we therefore present and discuss it here. First we make a data frame `MyData` that contains 100 values for delta weight.

```
> MyData <- data.frame(
  DeltaWeight = seq(
    from = min(Crocs$DeltaWeight),
    to   = max(Crocs$DeltaWeight),
    length = 100))
```

We will generate the posterior mean values and 95% credible intervals that correspond to these 100 covariate values; these are the ones that are