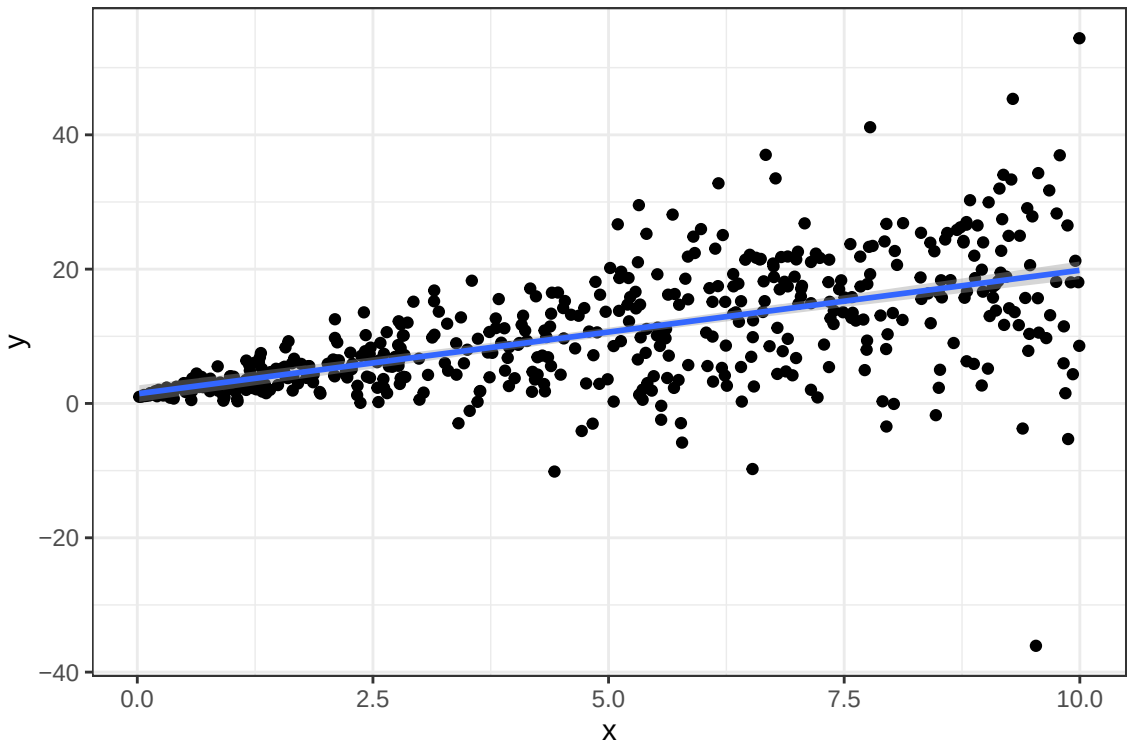
Extending GLMs

Heteroscedastic Models *Constant variance is a standard assumption in linear models. However consider data that violates that assumption.*

```
n <- 500
x <- runif(n,0,10)
beta0 <- 1
beta1 <- 2
y <- rnorm(n, mean = beta0 + x * beta1, sd = x *sqrt(2))

tibble(y = y, x = x) %>% ggplot(aes(y = y, x = x)) +
  geom_point() + theme_bw() +
  geom_smooth(formula = 'y~x', method ='lm')
```



Stan code can be written to estimate the variance as a function of x.

```
data {
  int<lower=0> N;
  vector[N] y;
  vector[N] x;
}

parameters {
  real beta0;
  real beta1;
  real<lower=0> sigma;
}

model {
  y ~ normal(beta0 + beta1 * x, sigma * x);
}
```

```
reg_ncv <- stan("heteroskedastic_regression.stan", data=list(N = n, y=y, x = x), refresh = 0)
```

```
print(reg_ncv)
```

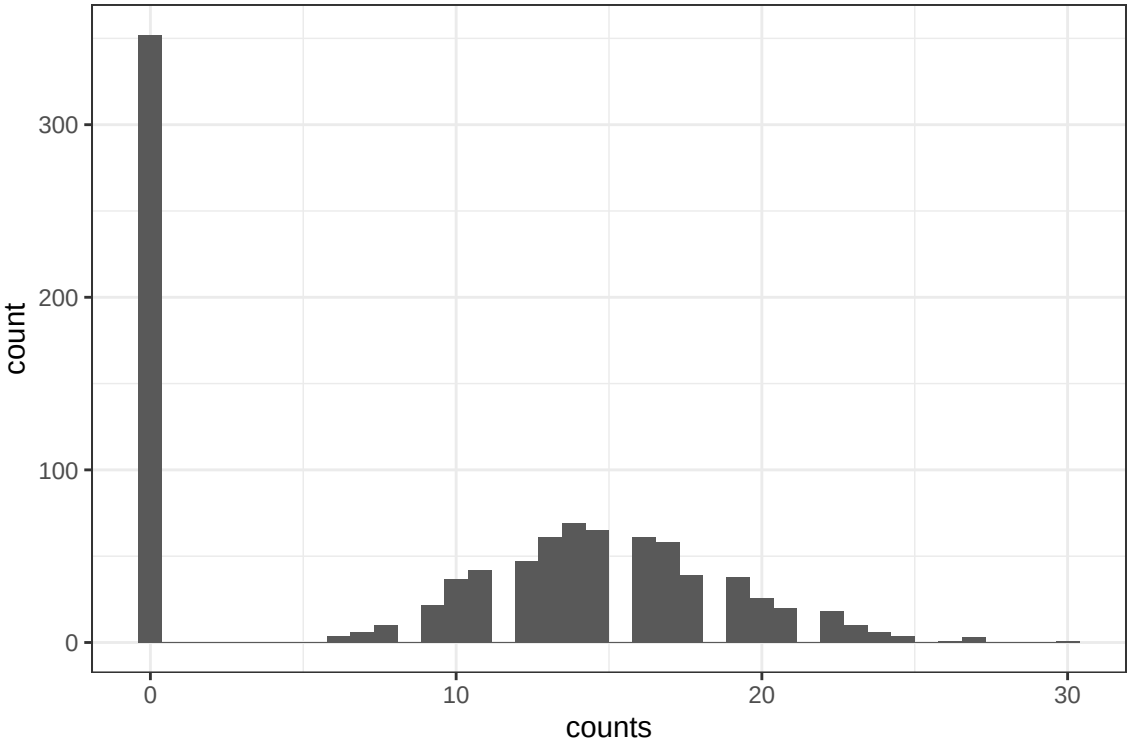
```
## Inference for Stan model: heteroskedastic_regression.
## 4 chains, each with iter=2000; warmup=1000; thin=1;
## post-warmup draws per chain=1000, total post-warmup draws=4000.
##
##           mean se_mean   sd     2.5%      25%      50%      75%    97.5% n_eff
## beta0     0.98    0.00 0.02     0.94     0.97     0.98     1.00     1.03  3284
## beta1     2.01    0.00 0.06     1.89     1.97     2.01     2.05     2.14  3166
## sigma     1.38    0.00 0.04     1.30     1.35     1.38     1.40     1.46  3475
## lp__  -1023.69    0.03 1.18 -1026.92 -1024.22 -1023.38 -1022.85 -1022.34  2220
##       Rhat
## beta0    1
## beta1    1
## sigma    1
## lp__     1
##
## Samples were drawn using NUTS(diag_e) at Mon Feb  1 13:29:26 2021.
## For each parameter, n_eff is a crude measure of effective sample size,
## and Rhat is the potential scale reduction factor on split chains (at
## convergence, Rhat=1).
```

Mixture Models

Sometimes a single probability distribution isn't sufficient to model an outcome of interest. *Recall the question about how many times you'd had skis on this winter. Sketch what you believe a sample from the student body would look like.*

```
zero_prob <- .33
n <- 1000
indicator <- rbinom(n,1,zero_prob)
counts <- tibble(counts = rpois(n, lambda = 15) * (1 - indicator))

counts %>%
  ggplot(aes(x = counts)) +
  geom_histogram(bins = 40) +
  theme_bw()
```



Formally this can be represented as a mixture of two distributions:

1. A Bernoulli distribution

2. A Poisson distribution.

If, $y \sim Poisson(\mu)$, then the pdf of y is

$$Pr[y = k] = \frac{\mu^k \exp(-\mu)}{k!}$$

$$y_i = \begin{cases} 0 \text{ (comes from either Bernoulli or Neg Binom) } = \exp(-\mu) + p \\ k(s.t.\ k > 0)(\text{comes from the Neg Binom}) = (1-p) \times \frac{\mu^k \exp(-\mu)}{k!} \end{cases}$$

This model could be coded in stan or consider using the `brms` package (bayesian regresion models in stan)

```
zip <- brm(counts ~ 1, data = counts, family = zero_inflated_poisson, refresh = 0)
# zip <- brm(counts ~ 1, data = counts, family = zero_inflated_poisson, refresh = 0, save_model = 'zip'
```

```
print(zip)
```

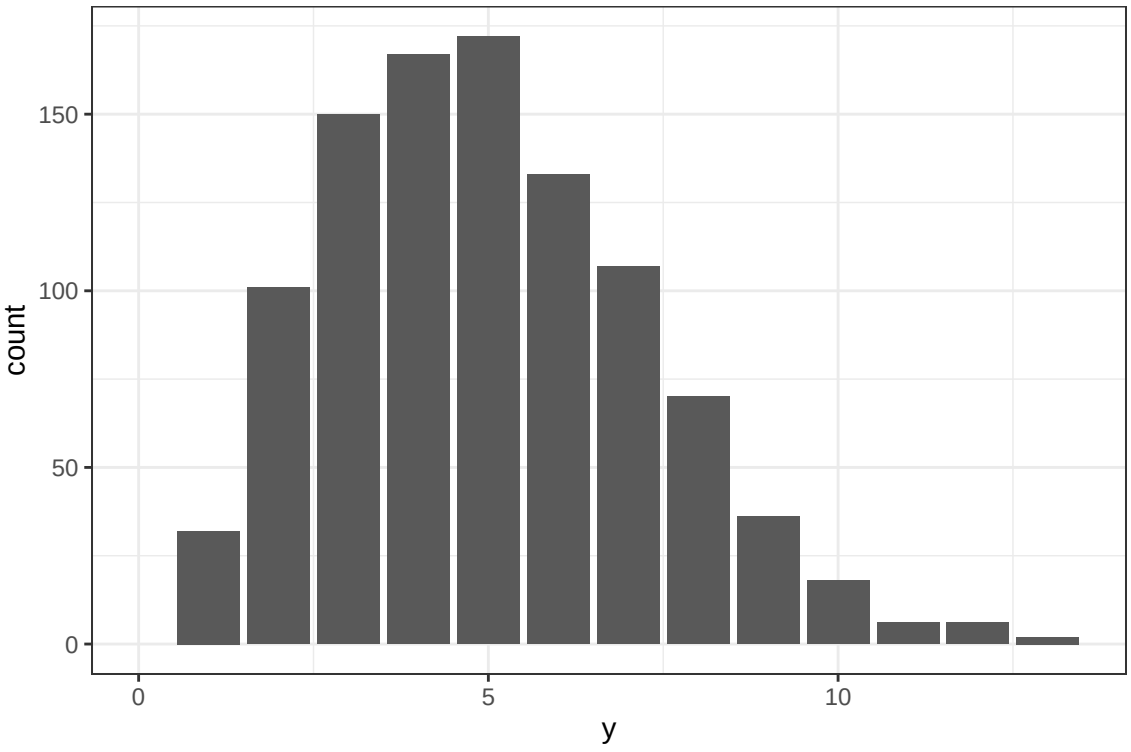
```
##  Family: zero_inflated_poisson
##   Links: mu = log; zi = identity
## Formula: counts ~ 1
##    Data: counts (Number of observations: 1000)
## Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
##          total post-warmup samples = 4000
##
## Population-Level Effects:
##           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept     2.72      0.01     2.70     2.74 1.00     3706     2254
##
## Family Specific Parameters:
##    Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## zi     0.35      0.02     0.32     0.38 1.00     3430     2279
##
## Samples were drawn using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

This model that we have specified is formally a zero-inflated Poisson distribution.

Now imagine that we are taking surveys as skiers enter the parking lot at Bridger Bowl. The minimum number of trips to Bridger for those skiers would be 1.

```
trunc_pois <- tibble(y = rtpois(n, 5, a = 0, b = Inf))

trunc_pois %>% ggplot(aes(x = y)) +
  geom_bar() + theme_bw() + xlim(0, NA)
```




```
truncated_pois <- brm(y ~ 1, data = trunc_pois, family = hurdle_poisson, refresh = 0)
```

```
## Compiling Stan program...
## Start sampling
```

```
print(truncated_pois)
```

```
##  Family: hurdle_poisson
##   Links: mu = log; hu = identity
## Formula: y ~ 1
##    Data: trunc_pois (Number of observations: 1000)
## Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
##          total post-warmup samples = 4000
##
## Population-Level Effects:
##           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept     1.60      0.02     1.57     1.63 1.00     2466     2073
##
## Family Specific Parameters:
##    Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## hu     0.00      0.00     0.00     0.00 1.00     1942     1281
##
## Samples were drawn using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

Truncated distributions and zero-inflated responses are often combined with hurdle models. The hurdle model assumes that all of the zero response comes from the "zero" process, rather than a mixture of the two.

```
hurdle_pois <- trunc_pois %>% bind_rows(tibble(y = rep(0, n)))
hurdle_poisson <- brm(y ~ 1, data = hurdle_pois, family = hurdle_poisson, refresh = 0)
```

```
## Compiling Stan program...
```

```
## Start sampling
```

```
print(hurdle_poisson)
```

```
##  Family: hurdle_poisson
##   Links: mu = log; hu = identity
## Formula: y ~ 1
##    Data: hurdle_pois (Number of observations: 2000)
## Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
##          total post-warmup samples = 4000
##
## Population-Level Effects:
##           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept     1.60      0.01     1.57     1.63 1.00     3966     2709
##
## Family Specific Parameters:
##    Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## hu     0.50      0.01     0.48     0.52 1.00     4152     2621
##
## Samples were drawn using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

Discrete / Continuous *Furthermore we can also have mixtures of continuous and discrete data. One that is seen fairly often would be concentrations and 0's.*

```
zero_prob <- .33
n <- 1000
indicator <- rbinom(n,1,zero_prob)
counts <- tibble(counts = rlnorm(n, meanlog = log(5)) * (1 - indicator))

head(counts)
```

```
## # A tibble: 6 x 1
##   counts
##    <dbl>
## 1  17.9
## 2   0
## 3   3.00
## 4   0
## 5   1.15
## 6  31.2
```

```
counts %>% ggplot(aes(x = counts)) + geom_histogram(bins = 40)
```