

# Precept 6: Models for Duration and Count Data

## Soc 504: Advanced Social Statistics

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# Outline

- 1 Duration
- 2 Poisson process
- 3 Overdispersion
- 4 Zero-inflation

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Time has to be positive

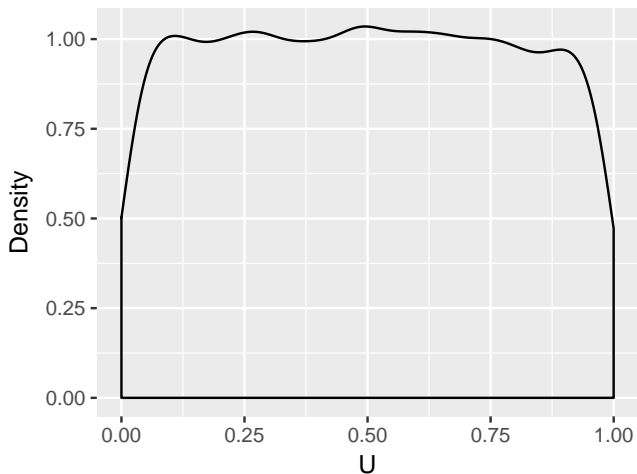
Suppose you want to model the time until an event occurs.

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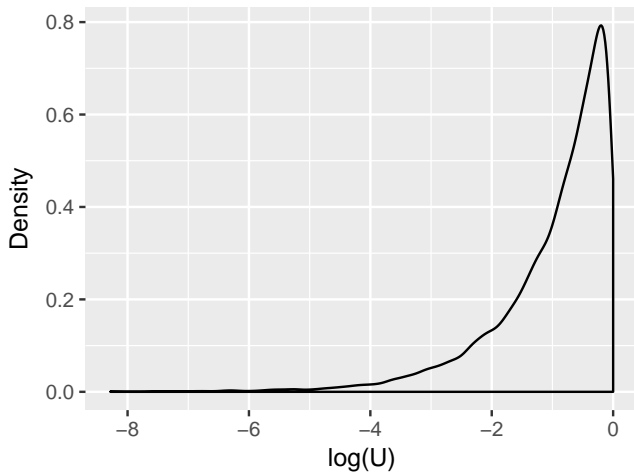
Could we construct the simplest possible distribution defined on positive values only?

Let's start with a uniform random variable.

$$U \sim \text{Uniform}(0, 1)$$



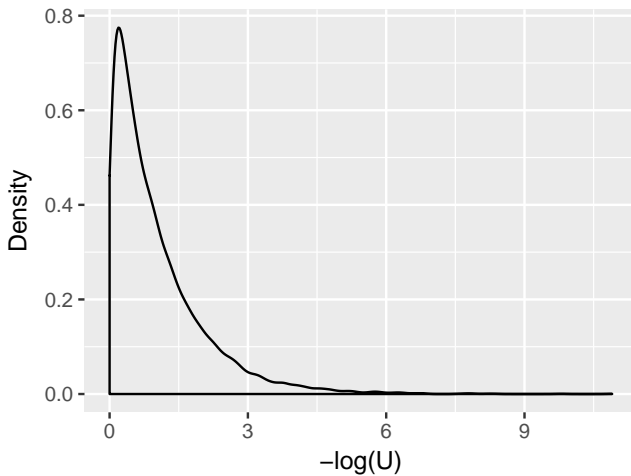
We could transform this to be defined on all negative values.





Then we could make this positive.

$$X \sim -\log(U)$$



This is the **unit exponential distribution!**

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Is this starting to look like the Exponential CDF,  $1 - e^{-\lambda x}$ ?

We can stretch it out by a **scale parameter**  $\frac{1}{\lambda}$

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We have the Exponential CDF!

$$F_X(x) = 1 - e^{-\lambda x}$$

# Exponential distribution

$$T \sim \text{Exponential}(\lambda)$$

PDF

$$f(t) = \lambda e^{-\lambda t}$$

CDF

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Survival function

$$S(t) = P(T > t) = 1 - P(T < t) =$$

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Hazard function: Risk of event at  $t$  given survival up to  $t$

$$h(t) = \frac{f(t)}{S(t)} = \frac{\lambda e^{-\lambda t}}{e^{-\lambda t}} = \lambda$$

Not a function of  $t$ ! The hazard is **constant**.

# Modeling with covariates

Suppose we want to allow the hazard to vary by some set of predictors.

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Then, we can assume a **proportional hazards** model.



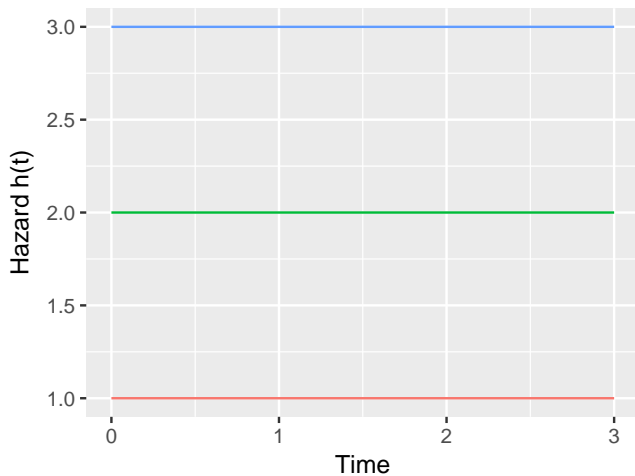
# Modeling with covariates

Suppose we want to allow the hazard to vary by some set of predictors.

Then, we can assume a **proportional hazards** model.

$$h(t | x) = \underbrace{h_0(t)}_{\text{Baseline hazard}} \underbrace{e^{x\beta}}_{\text{Hazard ratio}}$$

# Exponential hazards



# Fitting an Exponential model in Zelig

Zelig is an R package designed to make everything we do in class easier.

Note the Zelig [workflow overview](#).

We will use the [Zelig-Exponential](#).

# Zelig example: Lung cancer survival

We will walk through the example using data on lung cancer survival

```
> library(survival)
> data(lung)
> head(lung)
```

	inst	time	status	age	sex	ph.ecog	ph.karno	pat.karno	meal.cal	wt.loss
1	3	306	2	74	1	1	90	100	1175	NA
2	3	455	2	68	1	0	90	90	1225	15
3	3	1010	1	56	1	0	90	90	NA	15
4	5	210	2	57	1	1	90	60	1150	11
5	1	883	2	60	1	0	100	90	NA	0
6	12	1022	1	74	1	1	50	80	513	0

```
lung <- mutate(lung, event = as.numeric(status == 2))
```

# Variable definitions: Lung cancer survival

?lung

inst: Institution code

time: Survival time in days

status: censoring status 1=censored, 2=dead

age: Age in years

sex: Male=1 Female=2

ph.ecog: ECOG performance score (0=good 5=dead)

ph.karno: Karnofsky performance score (bad=0-good=100) rated by physician

pat.karno: Karnofsky performance score as rated by patient

meal.cal: Calories consumed at meals

wt.loss: Weight loss in last six months

# Zelig step 1: Fit a model

```
fit <- zelig(Surv(time, event) ~ age + sex,  
            model = "exp",  
            data = lung)
```

# Zelig step 1: Fit a model

```
> summary(fit)
```

Model:

Call:

```
z5$zelig(formula = Surv(time, event) ~ age + sex, data = lung)
```

	Value	Std. Error	z	p
(Intercept)	6.3597	0.63547	10.01	1.41e-23
age	-0.0156	0.00911	-1.72	8.63e-02
sex	0.4809	0.16709	2.88	4.00e-03

Scale fixed at 1

Exponential distribution

Loglik(model)= -1156.1    Loglik(intercept only)= -1162.3

Chisq= 12.48 on 2 degrees of freedom, p= 0.002

Number of Newton-Raphson Iterations: 4

n= 228

Next step: Use 'setx' method

## Zelig step 2: Use setx to set covariates of interest

```
men <- setx(fit, age = 50, sex = 1)
women <- setx(fit, age = 50, sex = 2)
```



## Zelig step 2: Use `setx` to set covariates of interest

```
> men
setx:
  (Intercept) age sex
1           1  50  1
```

Next step: Use 'sim' method

```
> women
setx:
  (Intercept) age sex
1           1  50  2
```

Next step: Use 'sim' method

## Zelig step 3: Use sim to simulate quantities of interest

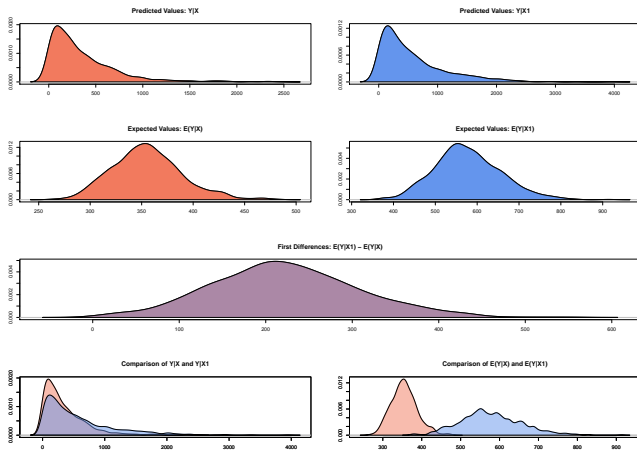
```
> sims <- sim(obj = fit, x = men, x1 = women)
> summary(sims)

sim x :
-----
ev
  mean      sd      50%      2.5%      97.5%
1 355.086 33.63733 353.5258 296.6169 428.758
pv
  mean      sd      50%      2.5%      97.5%
[1,] 351.414 361.6174 242.511 7.082744 1357.005

sim x1 :
-----
ev
  mean      sd      50%      2.5%      97.5%
1 577.5684 78.5113 571.178 438.4341 743.9957
pv
  mean      sd      50%      2.5%      97.5%
[1,] 562.8317 550.6102 382.9658 11.5627 2016.61
fd
  mean      sd      50%      2.5%      97.5%
1 222.4824 85.0493 217.0278 61.08082 396.5632
```

# Zelig step 4: Use graph to plot simulation results

```
pdf("ZeligFigures.pdf",  
    height = 5, width = 7)  
plot(sims)  
dev.off()
```



# Summarizing Zelig

Estimate your model:

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#install.packages("Zelig")
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men <- setx(fit, sex = 1, fn = mean)
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sims <- sim(obj = fit, x = men, x1 = women)
```

Plot:

```
plot(sims)
```

# Fitting an Exponential with survreg

```
> library(survival)
> fit <- survreg(Surv(time, event) ~ age + sex,
+               dist = "exponential",
+               data = lung)
> summary(fit)
```

Call:

```
survreg(formula = Surv(time, event) ~ age + sex, data = lung,
        dist = "exponential")
```

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Number of Newton-Raphson Iterations: 4

n= 228

# Interpreting hazard ratios

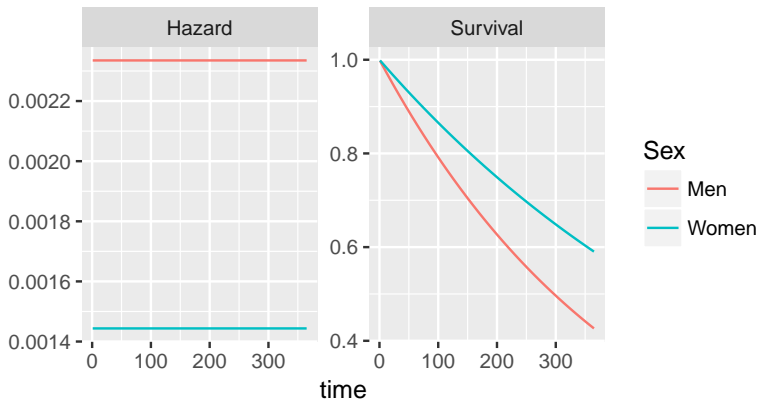
$$h(t | x) = h_0(t)e^{-x\beta}$$

```
> exp(-coef(fit))
```

(Intercept)	age	sex
0.002	1.016	0.618

# Plotting survival curves

Exponential survival fits  
for 50-year-old men and women



# Plotting survival curves

How we made the previous slide:

```
data.frame(t = seq(.5,20,.5)) %>%  
  mutate(Men.Hazard = lambda[1],  
         Women.Hazard = lambda[2],  
         Men.Survival = exp(-lambda[1]*t),  
         Women.Survival = exp(-lambda[2]*t)) %>%  
  melt(id = "t") %>%  
  separate(variable, into = c("Sex","QOI")) %>%  
  ggplot(aes(x = t, y = value, color = Sex)) +  
  geom_line() +  
  facet_wrap(~QOI, scales = "free") + ylab("") + xlab("time") +  
  ggtitle("Exponential survival fits, for 50-year-old men and women") +  
  ggsave("ExpoFit.pdf",  
        height = 3, width = 5)
```

# Scales and rates

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In general, you have to be careful with the parameterization of survival distributions.

# Weibull distribution

$$T \sim \text{Weibull}(\alpha, \lambda)$$

PDF <sup>2</sup>

$$f(t) = t^{\alpha-1} \alpha \lambda^\alpha e^{-(\lambda t)^\alpha}$$

CDF

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$$h(t) = \frac{f(t)}{S(t)} =$$

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<sup>2</sup>I have used the rate parameterization for  $\lambda$ ; in lecture slides Brandon uses the scale parameterization.

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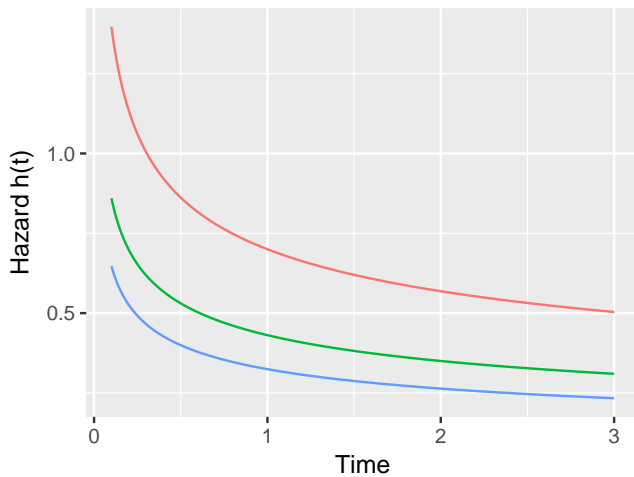
The hazard **decreases** with  $t$  when  $\alpha < 1$

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In that case, it's the exponential!

$$h(t \mid \alpha = 1) = t^{\alpha-1} \alpha \lambda^\alpha = t^{1-1} 1 \lambda^1 = \lambda$$

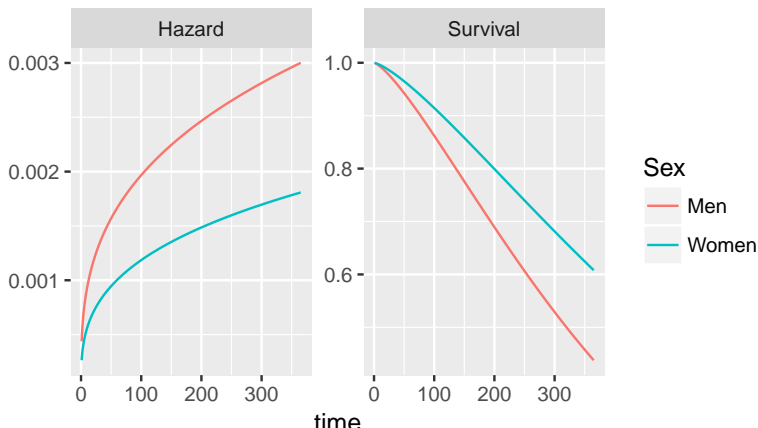
# Weibull hazards



# Fitting a Weibull model

```
## Fitting a Weibull model  
fit <- survreg(Surv(time, event) ~ age + sex,  
              dist = "weibull",  
              data = lung)
```

## Weibull survival fits, for 50-year-old men and women



# Lognormal distribution

$$T \sim \text{LogNormal}(\mu, \sigma^2) \sim e^Z \quad (\text{where } Z \sim N(\mu, \sigma^2))$$

$$f(t) = \frac{1}{Y_i \sigma \sqrt{2\pi}} \exp\left(-\frac{(\ln(Y_i) - \mu)^2}{2\sigma^2}\right)$$

CDF

$$F(t) = \int_0^t f(x) dx = \text{ugly formula}$$

Survival function

$$S(t) = P(T > t) =$$

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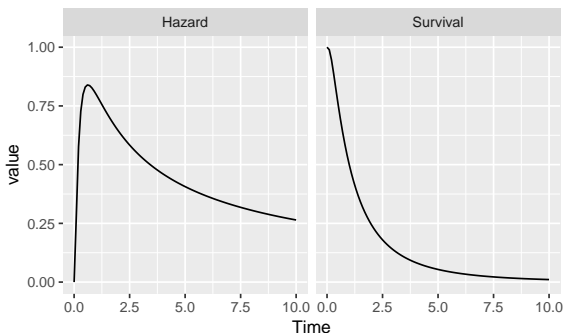
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# Fitting a Lognormal

```
fit <- survreg(Surv(time, event) ~ age + sex,  
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```

NOTE: This figure doesn't correspond to the model above - just an example of a LogNormal



# Gompertz distribution

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The log of the hazard function is linear in time!

This is why people like the Gompertz.

# Gompertz distribution

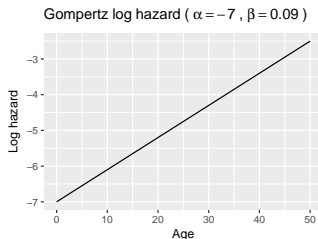
Gompertz hazard with  $\alpha = -7, \beta = .09$

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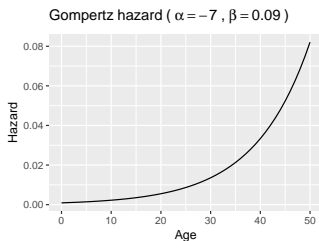
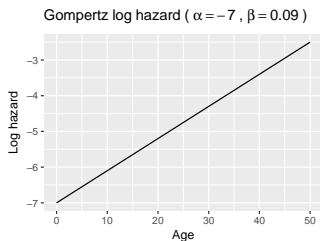
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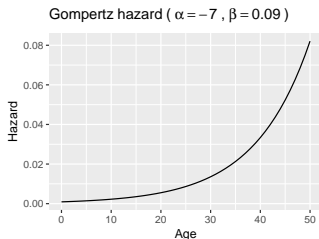
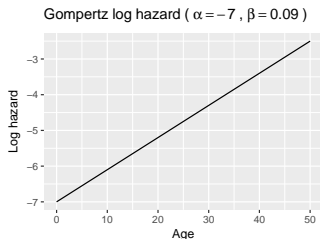
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Note: Example motivated by U.S. mortality; see German Rodriguez's [example here](#).

As I said at the beginning, **all** of the survival models above have the form:

$$\underbrace{h_i(t)}_{\text{Hazard function}} = \underbrace{h_0(t)}_{\text{Baseline hazard}} \underbrace{e^{X_i\beta}}_{\text{Hazard ratio}}$$

$$S(t) = e^{-\int_0^t h(u)du}$$

Different models allow different kinds of flexibility in the **baseline hazard**  $h_0(t)$ .

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Different models allow different kinds of flexibility in the **baseline hazard**  $h_0(t)$ .

Can we model hazard ratios without any assumptions about  $h_0(t)$ ?

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Then we can fit a Cox proportional hazards model!



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You can fit one with `coxph()`

# Outline

- 1 Duration
- 2 Poisson process**
- 3 Overdispersion
- 4 Zero-inflation

Most probability distributions are related!

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In fact, people have put together charts of them all.

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Here's one by Larry Lemis (William and Mary)

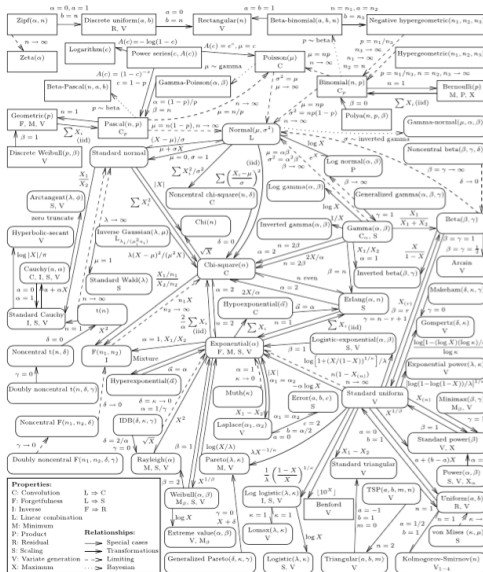


Figure 1. Univariate distribution relationships.

[link]



We won't go into all of those.

We will explore some of these relationships in the **Poisson process**.

I'd like to take you to the wilderness of the Sierra Nevada mountains, to one of my favorite places: Rae Lakes.



PC: <http://wilderness.org/30-prettiest-lakes-wildlands>

Imagine laying out on your pad on the granite, looking up at the sky.

We will count shooting stars and record the times we see them.<sup>3</sup>

---

<sup>3</sup>Thanks to William Chen for the shooting stars example. See more at <http://www.wzchen.com/probability-cheatsheet/>

# Exponential distribution: Memoryless property

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So, the probability of surviving an additional  $t$  years is independent of whether you have already survived  $s$  years!

# Exponential ratio

Suppose

$$X_1, X_2 \stackrel{\text{iid}}{\sim} \text{Exponential}(1)$$

What is the distribution of:

$$\frac{X_1}{X_1 + X_2} \sim$$

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What if  $X_1$  and  $X_2$  are distributed  $\text{Exponential}(2)$ ? The result still holds!

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Then we say

$$G_k \sim \text{Gamma}(k, \lambda)$$

The **Gamma distribution** characterizes the wait time until the  $k$ th bus arrives.

# Gamma distribution

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$$f(t) = \frac{1}{\Gamma(k)} \frac{(\lambda t)^k e^{-\lambda t}}{t}$$

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$$G_k \sim \text{Gamma}(k, \lambda) \sim X_1 + \dots + X_k$$

$$E(T) = E(X_1 + \dots + X_k) = E(X_1) + \dots + E(X_k) = \frac{k}{\lambda}$$

$$V(T) = V(X_1 + \dots + X_k) = V(X_1) + \dots + V(X_k) = \frac{k}{\lambda^2}$$

$$f(t) = \frac{1}{\Gamma(k)} \frac{(\lambda t)^k e^{-\lambda t}}{t}$$

CDF is hard to write.

# Poisson: Events in an interval

Suppose

$$X_1, X_2, \dots \stackrel{\text{iid}}{\sim} \text{Exponential}(\lambda)$$

Then the number of events occurring in a window of length 1 follows a Poisson distribution with rate  $\lambda$ .

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No! By the memoryless property of the Exponential, the wait times for events in these two periods are **independent** given the rate parameter  $\lambda$ .

# Poisson: Intervals of non-unit length

What would you expect for the distribution of events occurring in a window of length 2?

## Poisson: Intervals of non-unit length

What would you expect for the distribution of events occurring in a window of length 2?

$$E(N_T | T = 2) = 2\lambda, \quad V(N_T | T = 2) = 2\lambda$$

In general it will be the case that the number of events in a time period of length  $t$  follows a Poisson distribution with rate  $\lambda t$ .

$$N_t \sim \text{Poisson}(\lambda t)$$

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The ratio of Gammas is a **Beta distribution!**



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Gamma(5,  $\lambda$ )

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Suppose someone says to you, “I ran 100 hypothesis tests. What’s the probability that the 7th-smallest  $p$ -value is less than 0.05 if nothing is really happening?”



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You say...let me take you to the wilderness. We will count shooting stars.

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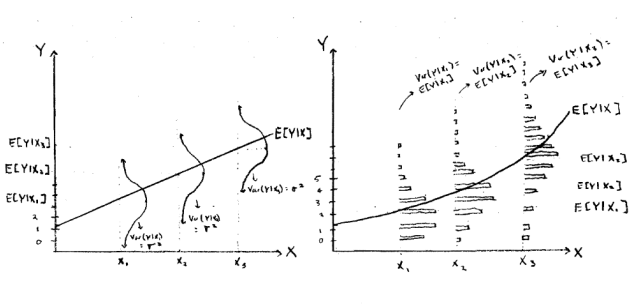
So, it's not that strange to see 7  $p$ -values less than 0.05. And we learned this all from shooting stars!

# Outline

- 1 Duration
- 2 Poisson process
- 3 Overdispersion**
- 4 Zero-inflation

In the Poisson distribution,

$$E(Y) = V(Y) = \lambda$$



This is fairly restrictive. Can we allow the variance to differ from the mean?

# Negative Binomial: Three constructions

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$$P(Y = y) = P(Y \text{ failures})P(\text{Final success}) = (1 - p)^y p$$

## Negative Binomial distribution: Tails until the $k$ th heads

$$Y_i \sim \text{NegBin}(p_i, k)$$

$$P(Y_i = y_i) = \binom{k + y_i - 1}{k} (1 - p_i)^y p_i^k$$

Note: This is a model for counts involving two parameters, so has flexibility beyond the Poisson.

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# Negative Binomial: A Gamma-Poisson mixture<sup>4</sup>

$$Y_i | \varsigma_i \sim \text{Poisson}(\varsigma_i \lambda_i)$$
$$\varsigma_i \sim \frac{1}{\theta} \text{Gamma}(\theta, 1)$$

---

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Note that  $\text{Gamma}(\theta, 1)$  has mean  $\theta$ . This means that  $\frac{1}{\theta} \text{Gamma}(\theta)$  has mean 1, and so  $\text{Poisson}(\varsigma_i \lambda_i)$  has mean  $\lambda_i$ .

---

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Using a similar approach to that described in UPM pgs. 51-52 we can derive the marginal distribution of  $Y$  as

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Notes:

1.  $E[Y_i] = \lambda_i$  and  $\text{Var}(Y_i) = \lambda_i + \frac{\lambda_i^2}{\theta}$ . What values of  $\theta$  would be evidence *against* overdispersion?

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2. we still have the same old systematic component:  $\lambda_i = \exp(X_i \beta)$ .

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# Negative Binomial: Poisson with an overdispersion parameter

$$E(Y_i) = \lambda_i$$

$$V(Y_i) = \theta \lambda_i$$

$$p(y_i) = \frac{\Gamma\left(Y_i + \frac{\lambda_i}{1-\theta}\right)}{Y_i! \Gamma\left(\frac{\lambda_i}{1-\theta}\right)} \left(\frac{\lambda_i}{\lambda_i + \frac{\lambda_i}{1-\theta}}\right)^{Y_i} \left(\frac{\frac{\lambda_i}{1-\theta}}{\lambda_i + \frac{\lambda_i}{1-\theta}}\right)^{\frac{\lambda_i}{1-\theta}}$$

# Harmonizing the three constructions

## Failures before $k$ th success

$$p(y) = \underbrace{\binom{k+y-1}{k}}_{\text{Part 1}} \underbrace{(1-p)^y}_{\text{Part 2}} \underbrace{p^k}_{\text{Part 3}}$$

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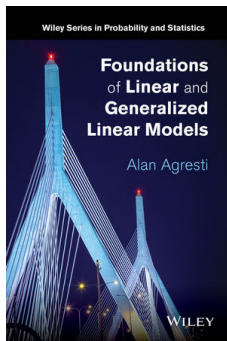
Given that you fish, there's some count distribution for the number of fish caught.

# Example

Keeping with the nautical theme, we will use an example with Horseshoe crabs.

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Keeping with the nautical theme, we will use an example with Horseshoe crabs. These data come from Alan Agresti's book on GLMs:



We will model the number of satellites around female horseshoe crabs.

You ask - what does it mean for a crab to have satellites?

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That's a bit awkward to type up.

You ask - what does it mean for a crab to have satellites?

That's a bit awkward to type up.

Let's [just see online](#).



PC: <http://myfwc.com/research/saltwater/crustaceans/horseshoe-crabs/facts/>



# Horseshoe crab data

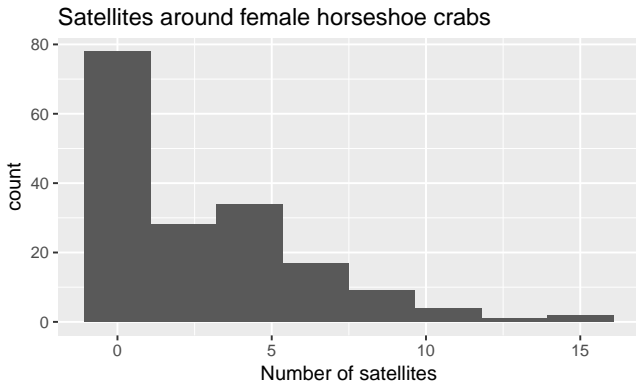
## Load the data

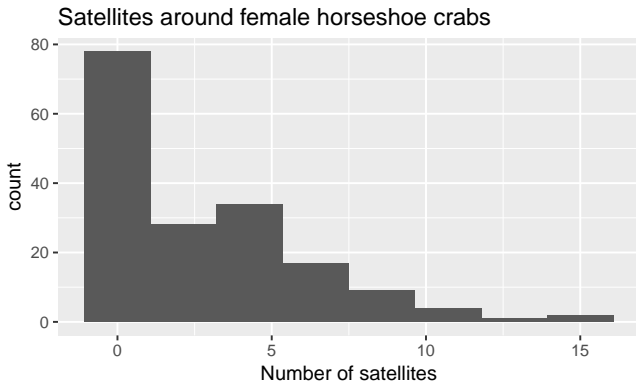
```
> d <- read.table("http://www.stat.ufl.edu/~aa/glm/data/Crabs.dat",  
+                 header = T)
```

```
> head(d)
```

	crab	y	weight	width	color	spine
1	1	8	3.05	28.3	2	3
2	2	0	1.55	22.5	3	3
3	3	9	2.30	26.0	1	1
4	4	0	2.10	24.8	3	3
5	5	4	2.60	26.0	3	3
6	6	0	2.10	23.8	2	3

*y* is the number of satellites





The number of 0s is higher than you might expect!

# Data generating process

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# Data generating process

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**Us:** The mixture model allows a **more flexible** distribution of counts. It allows us to construct a data generating process that could create disproportionately more 0s than either the Poisson or Negative Binomial would have without the mixture.

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**Student:** Is this the same as if we estimated one model for whether a crab had any satellites, and another model for the number of satellites around crabs with at least one satellite?

**Us:** These are not quite the same, since crabs with  $Z_i = 1$  may still have 0 satellites if the count portion of the mixture randomly draws a 0.

We know that crabs with satellites have  $Z_i = 1$ , but for those without satellites they may have  $Z_i = 0$ , or they may have  $Z_i = 1$  and just have 0 satellites because the count drawn was 0.

Likelihood<sup>6</sup>

$$\begin{aligned}
 L(\beta, \gamma, \theta \mid Y) &\propto f(y \mid \beta, \gamma, \theta) \\
 &= \prod_{i=1}^n f(y_i \mid \beta, \gamma, \theta) \\
 &= \prod_{i=1}^n \underbrace{\left( f(y_i \mid Z = 0, \gamma)P(Z = 0 \mid \beta) + f(y_i \mid Z = 1, \gamma, \theta)P(Z = 1 \mid \beta) \right)}_{\text{Apply the law of total probability}} \\
 &= \prod_{i=1}^n \underbrace{\left( \mathbb{I}(y_i = 0)(1 - p_i) + \frac{\Gamma(\theta + y_i)}{y_i! \Gamma(\theta)} \frac{\lambda_i^{y_i} \theta^\theta}{(\lambda_i + \theta)^{\theta + y_i}} p_i \right)}_{\text{Substitute the PDF and PMF}} \\
 &= \prod_{i=1}^n \left( \mathbb{I}(y_i = 0)(1 - \text{logit}^{-1}[X_i \beta]) \right. \\
 &\quad \left. + \frac{\Gamma(\theta + y_i)}{y_i! \Gamma(\theta)} \frac{(\exp[X_i \gamma])^{y_i} \theta^\theta}{(\exp[X_i \gamma] + \theta)^{\theta + y_i}} \text{logit}^{-1}[X_i \beta] \right) \\
 &\quad \underbrace{\hspace{10em}}_{\text{Replace parameters with inverse link of linear predictors}}
 \end{aligned}$$

<sup>6</sup> $\mathbb{I}(y_i = 0)$  is an *indicator function* coded 1 if  $y_i = 0$  and 0 otherwise. 

## Code our likelihood

$$\ell(\beta, \gamma, \theta, | Y) = \sum_{i=1}^n \log \left( \mathbb{I}(y_i = 0)(1 - \text{logit}^{-1}[X_i\beta]) + \frac{\Gamma(\theta + y_i)}{y_i! \Gamma(\theta)} \frac{(\exp[X_i\gamma])^{y_i} \theta^\theta}{(\exp[X_i\gamma] + \theta)^{\theta + y_i}} \text{logit}^{-1}[X_i\beta] \right)$$

```
zinb.loglik <- function(par, y, X) {
  k <- ncol(X)
  beta <- par[1:k]
  gamma <- par[(k + 1):(2*k)]
  theta <- exp(par[(2*k + 1)])
  p <- plogis(X %*% beta)
  lambda <- exp(X %*% gamma)
  log.lik <- sum(log(
    (y == 0)*(1 - p) +
    dnbinom(y, size = theta, mu = lambda) * p
  ))
  return(log.lik)
}
```

# Code our likelihood

Notes about how we coded that likelihood:

- We defined  $p_i$  and  $\lambda_i$ , and  $\theta$  based on parameters, then coded the log likelihood as a function of those rather than as a function of  $\beta$  and  $\gamma$  directly. This is just one of several reasonable approaches.
- We used `plogis()` for the inverse logit, but we could just as well have typed `log(p / (1-p))`.
- We used `dnbinom()` rather than writing out the negative binomial density. In general, we prefer to write the density, but we used the canned version here to avoid computational issues in this particular model.



# Optimize

```
opt.zinb <- optim(par = rep(0, 2*ncol(X) + 1),  
                y = y,  
                X = X,  
                fn = zinb.loglik,  
                method = "BFGS",  
                control = list(fnscale = -1),  
                hessian = TRUE)
```

## Report coefficients and standard errors

```
results <- data.frame(  
  Predictor = c("Intercept", "Weight", "Width"),  
  Beta = opt.zinb$par[1:3],  
  SE.Beta = sqrt(diag(-solve(opt.zinb$hessian)))[1:3],  
  Gamma = opt.zinb$par[4:6],  
  SE.Gamma = sqrt(diag(-solve(opt.zinb$hessian)))[4:6]  
)  
print(xtable(results),  
      include.rownames = F)  
theta <- exp(opt.zinb$par[7])
```

# Report coefficients and standard errors

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$$\text{logit}(p_i) = X_i \beta \quad \log(\lambda_i) = X_i \gamma$$

Predictor	$\hat{\beta}$	$\widehat{SE}(\hat{\beta})$	$\hat{\gamma}$	$\widehat{SE}(\hat{\gamma})$
Intercept	-10.45	4.04	2.66	1.44
Weight	0.71	0.81	0.53	0.28
Width	0.37	0.21	-0.10	0.08

$$\hat{\theta} = 5.24$$

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$$\hat{\theta} = 5.24$$

What do the  $\beta$  mean? The  $\gamma$ ?

# Simulate

```
sim.par <- mvrnorm(  
  10000,  
  mu = opt.zinb$par,  
  Sigma = -solve(opt.zinb$hessian)  
)
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We found before that  $\hat{\theta} = 5.24$ . Can we calculate  $\widehat{SE}(\hat{\theta})$ ?

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We found before that  $\hat{\theta} = 5.24$ . Can we calculate  $\widehat{SE}(\hat{\theta})$ ?

```
> sim.theta <- exp(sim.par[,7])  
> sd(sim.theta)  
[1] 2.067322
```

After break: expectation maximization, missing data



After break: expectation maximization, missing data

Questions?