Generalized Linear Models

In the preceding chapters we got acquainted with the linear model as an extremely flexible tool to represent dependencies between predictors and outcome variables. We saw how factors and covariates gracefully work together and how complex research designs can be captured by multiple random effects. It was all about specifying an appropriate (and often sophisticated) right-hand side of the regression formula, the predictors term. Little space has been dedicated to the outcome variables. That is now going to change, and we will start by examining the assumptions that are associated with the outcome variable.

Have you wondered about the abundance of simulated data sets up to this point? The reason for using simulated data is: the linear model, as introduced so far, makes assumptions that are *never* truly met by real data. The simulated data sets so far were meant to demonstrate some features found in real data sets, but generously wiped over some other frequent peculiarities.

Another question is probably lurking in the minds of readers with some classic statistics training: what has happened to the assumptions of ANOVA and the like and where are all the neat tests that check for normality, constant variance and such? In the next section we will review these assumptions and lead them ad absurdum. Simply put, in the real world is no such thing as Normal distribution and linearity. Checking assumptions on a model that you know upfront is inappropriate, is a futile exercise, at least when better alternatives are available, and that is the case: with *Generalized Linear Models* (GLM) we extend the regression modelling framework once again.

The GLM framework rests on two extensions that bring us a huge step closer to the data. The first one is a minor mathematical trick to establish linearity, the *link function*. The second is the informed choice about the expected *pattern of randomness*. As we will see, most of the time it is more or less obvious what statistical distribution, other than the Gaussian, matches the data.

In the following three sections I will explain the three core assumptions of linear models, recall the canonical model formulation:

$$\mu_i = \beta_0 + \beta_1 x_1 i + \ldots + \beta_k x_{ki} y_i \sim \text{Norm}(\mu_i, \sigma)$$

The first term, we call the likelihood and it represents the systematic quantitative relations we expect to find in the data. When it is a sum of products, like above, we call it linear. *Linearity* is a frequently under-regarded assumption of linear models and it is doomed to fall. The second term defines the pattern of randomness and it hosts two further assumptions: *normal distribution* and *constant error variance* of the random component.

Some classic textbooks tend to present these assumptions as preconditions for a successful ANOVA or linear regression. The very term *pre*condition suggest, that they need to be checked upfront and the classic statisticians is used to employ a zoo of null hypothesis tests on the data. If one fails, let's say the Kolmogorov-Smirnoff test on normality, researchers often turn to non-parametric tests. Many also just continue with ANOVA, but add some shameful statements to the discussion of results or bravely cite some research paper that claims ANOVAs robustness to violations.

I have met at least one seasoned researchers who divided the world of data into two categories: parametric data, that meets ANOVA assumptions, and non-parametric that does not. All models (or families) in the present chapter, he would have regarded as non-parametric. Let me get this straight:

First of all, *data is neither parametric nor non-parametric*. Instead, data is distributed in some form and a good model aligns to this form. A *model is parametric*, when the statistics it produces have a useful interpretations, like the intercept is the group mean of the reference group and the intercept random effect represents the variation betrween individuals. The parameters of a polynomial model usually don't have a direct interpretation. However, we saw that useful parameters, such as the minimum of the curve, can be derived. Therefore, polynomial models are often called *semiparametric*. [CROSSREF]. As an example for a *non-parametric* test, the Mann-Withney U statistic is composed of the number of times observations in group A are larger than in group B. The resulting sum U usually bears no relation to any real world process or question. Strictly speaking, the label non-parametric has nothing to do with ANOVA assumptions. It refers to the usefulness of parameters. A research problem, where U as the sum of wins has a useful interpretation For example, in some dueling disciplines, such as Fencing, team competitions are constructed by letting every athlete from a team duel every member of the opponent team. We could call the U-test parametric, and perhaps, the group means turn out to be meaningless.

Here, I will not present any tests on assumption, other than exploratory plots. Non-parametric tests are completely at odds with the philosophy of this book, as they don't produce parameters that can be interpreted quantitatively. Instead, I will right-away debunk all three assumptions for those type of measures design researchers are routinely dealing with. Every assumption that crumbles, rebounces from two new building blocks that add to our regression framework:

1. *link functions* re-establish linearity
2. *random distributions* cover the expected pattern of randomness and the relation of mean and variance

By these two concepts, the *GLM* framework rises from the ashes of *LM*. It hosts a variety of models that leaves little reason for crude approximations, aka the *Gaussian LM*, let alone non-parametric procedures and data transformations. There almost always is a reasonable choice that largely depends on the properties of the response variable: the *Poisson LM* is the first choice for outcome variables that are counted (with no limit), like number of errors. *Binomial (aka logistic) LM* covers the case of successful task completion, where counts have an upper boundary. These two GLM members have been around for more than half a century in statistics. The quest for a good model for reaction time and time-on-task was more difficult as there does not seem to be a generally accepted default. Luckily, with recent developments in Bayesian regression engines the choice of random distributions has become much broader. For RT and ToT, I will suggest primarily the exponentially-modified Gaussian *(ExGauss) LM* and, to some extent, *Gamma LM*. Along the path, the same chapter introduces a basic way to choose between response distributions based on model comparison. For binned rating scales, where response fall into a few ordered categories, *ordinal logistic regression* is a generally accepted approach. For (quasi)continuous rating scales will I make a novel suggestion, the *Beta LM*.

Debunking the Gaussian linear model

The Gaussian linear model makes many assumptionsl, where numbers often vary between sources. In my view, the three crucial assumptions are:

1. *Linearity* of the association between predictors and outcome variable.
2. *Normal distribution of responses*
3. *constant variance of response distribution*

Researchers routinely check these assumptions by means of visual exploration or null hypothesis tests. However, on closer examination, it turns out that the first two assumptions strictly cannot be true for any real data, and the third is highly susceptible, at least.

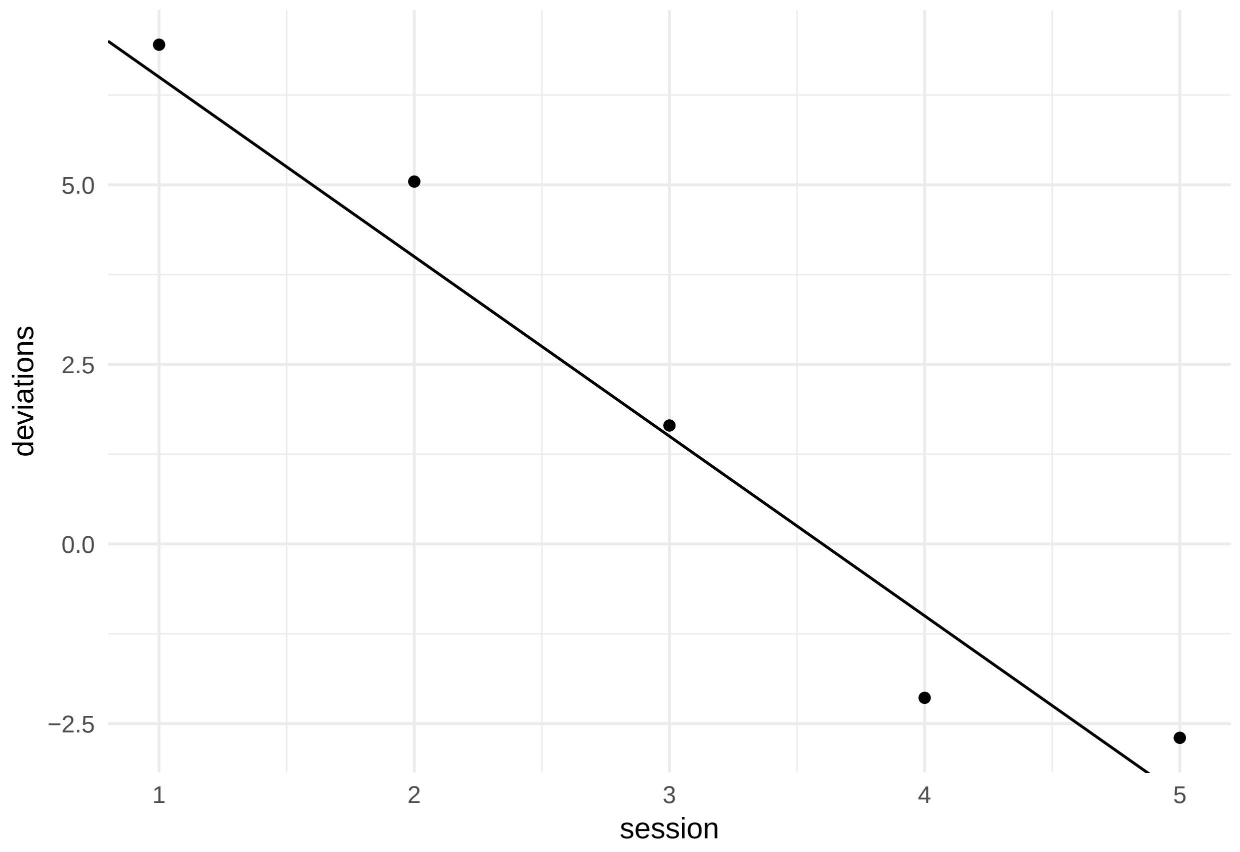
Assuming linearity

Recall the principle, "all-finite-in-the-endless": when two or more interventions improve the same process, e.g. visual recognition of letters, the sum is less than the summands. This results in a non-linearity when the boundary of performance is reached. With a small set of predictors this can gracefully be modelled as saturation interaction effects.

Consider a study that assesses the improvement of safe operation with continued practice. For simplicity, we regard just a single nurse whose number of errors were measured on a chain of 8 tasks. Errors in operation were measured as number of deviations from the shortest possible interaction sequence.

We simulate a linear model, assuming there is an improvement of one error less with every repetition of the sequence, with expected 7 deviations in the first session. We assume that path deviations has a normally distributed random component with $\sigma = 1$.

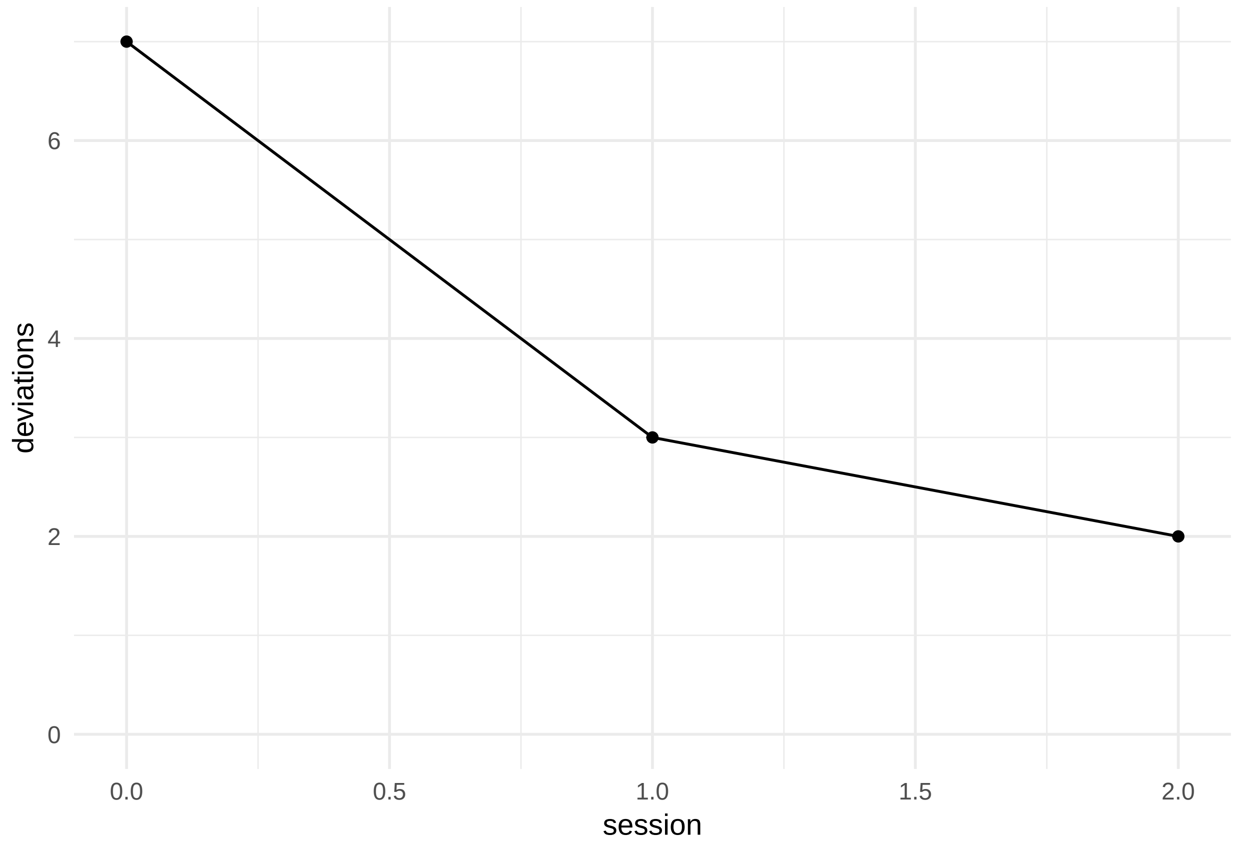
```r
data_frame(session = as.integer(1:5),
           mu = 9 - session * 2.5,
           deviations = rnorm(5, mu, sd = 1)) %>%
  ggplot(aes(x = session,
             y = deviations)) +
  geom_point() +
  geom_abline(aes(intercept = 9, slope = -2.5))
```



See what happens when the linear model is naively applied to the deviation counts. In no time, negative values are produced, which is an impossibility. Similar to saturation effects, we would expect some asymptotic behaviour, rather than a straight line, when the outcome variable approaches its natural lower boundary.

Here is some real world data from the IPump study. We take a look at a small slice of it: the total number of deviations of one participant across the three sessions.

```r
attach(IPump)

D_pumps %>%
  filter(Part == 5, Design == "Novel") %>%
  group_by(Part, session) %>%
  summarize(deviations = sum(deviations)) %>%
  ggplot(aes(x = session, y = deviations)) +
  geom_point() +
  geom_line() +
  ylim(0,7)
```



```
detach(IPump)
```

What really happens, when a performance measure approaches its natural limit, is an asymptotic leaning-on. Neither will the line break through the limit, nor will it stop there abruptly.

Such a non-linearity happens to all outcome variables that have natural lower or upper boundaries, and that includes all outcome variables in the universe, except its very own spatial extension, perhaps. All outcome variables in design research suffer from the problem of impossible predictions as a consequence of their boundedness:

- Errors and other countable incidences are bound at zero
- ToT is bounded at zero and probably also bound above when users loose their patience
- Rating scales are bound at the lower and upper extreme item
- Task completion has a lower bound of zero and upper bound is the number of tasks. Or the average task completion is in the range $[0, 1]$

Assuming Normal distribution of randomness

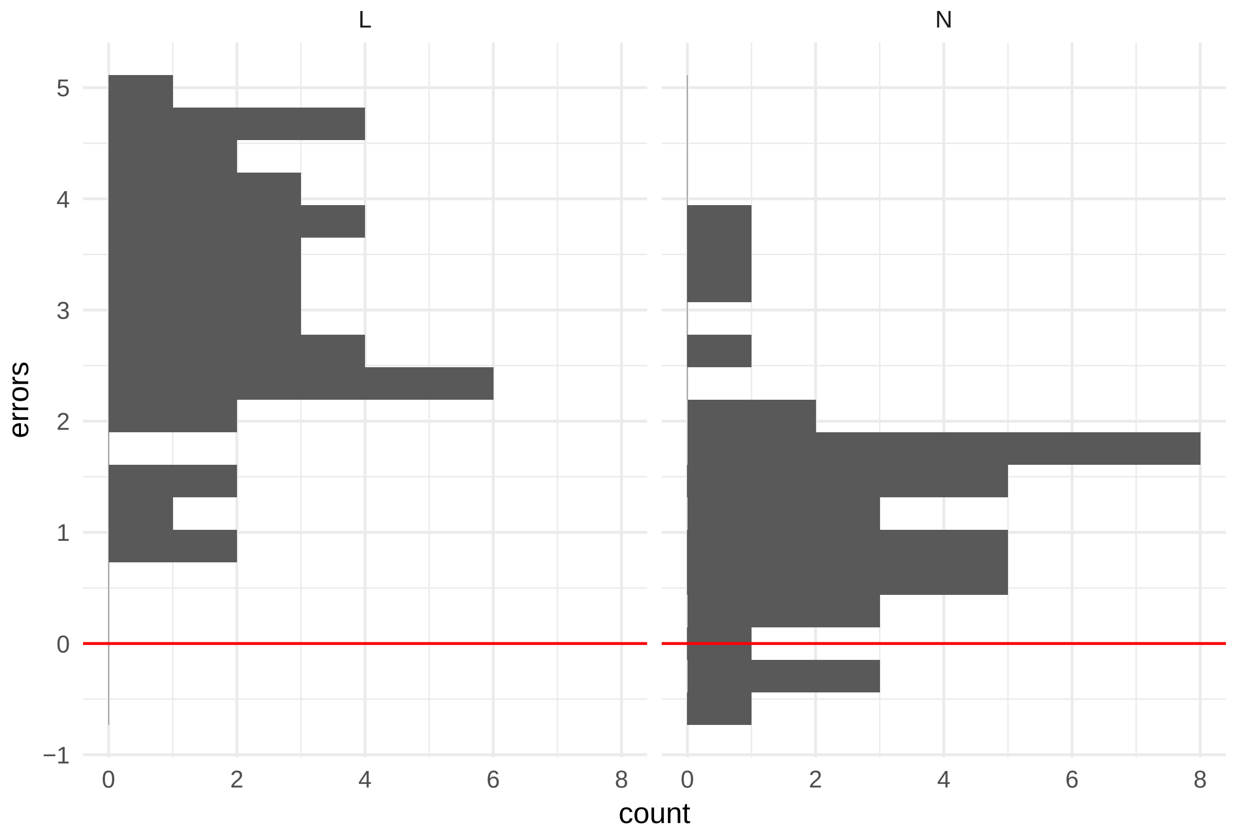
The second term of a linear model, $y_i \sim Norm(\mu_i, \sigma)$ states that the observed values are drawn from normal distributions (see @ref(resid_normality)). Two observed values y_i and y_j are only drawn from the same distribution, when they have the same expected value $\mu_i = \mu_j$. The Normal distribution has been used ubiquitously in statistics. But in fact, the normal distribution is a reasonable approximation when the measures are far off the boundaries of measures and the error is much smaller than the predicted values (@ref(normal_distributions)).

In design research studies this is frequently not the case. We begin with a simulated study comparing a novel and a legacy interface design for medical infusion pumps. The researchers let trained nurses perform a single task on both devices and count the errors. Assuming, the average number of errors per tasks is $\mu_L = 3$ for the legacy device and $\mu_N = 1.2$ for the novel device, with standard deviation of $\sigma = .8$. We can simulate a basic data set as:

```
N = 80
pumps_2 <-
  data_frame(Design = rep(c("L", "N"), N/2),
             mu = if_else(Design == "L", 3, 1.2),
             errors = rnorm(N, mu, sd = 1))
```

We illustrate the data set using histograms:

```
pumps_2 %>%
  ggplot(aes(x = errors)) +
  facet_grid(~Design) +
  geom_histogram(bins = 20) +
  geom_vline(col = "red", xintercept = 0) +
  coord_flip()
```

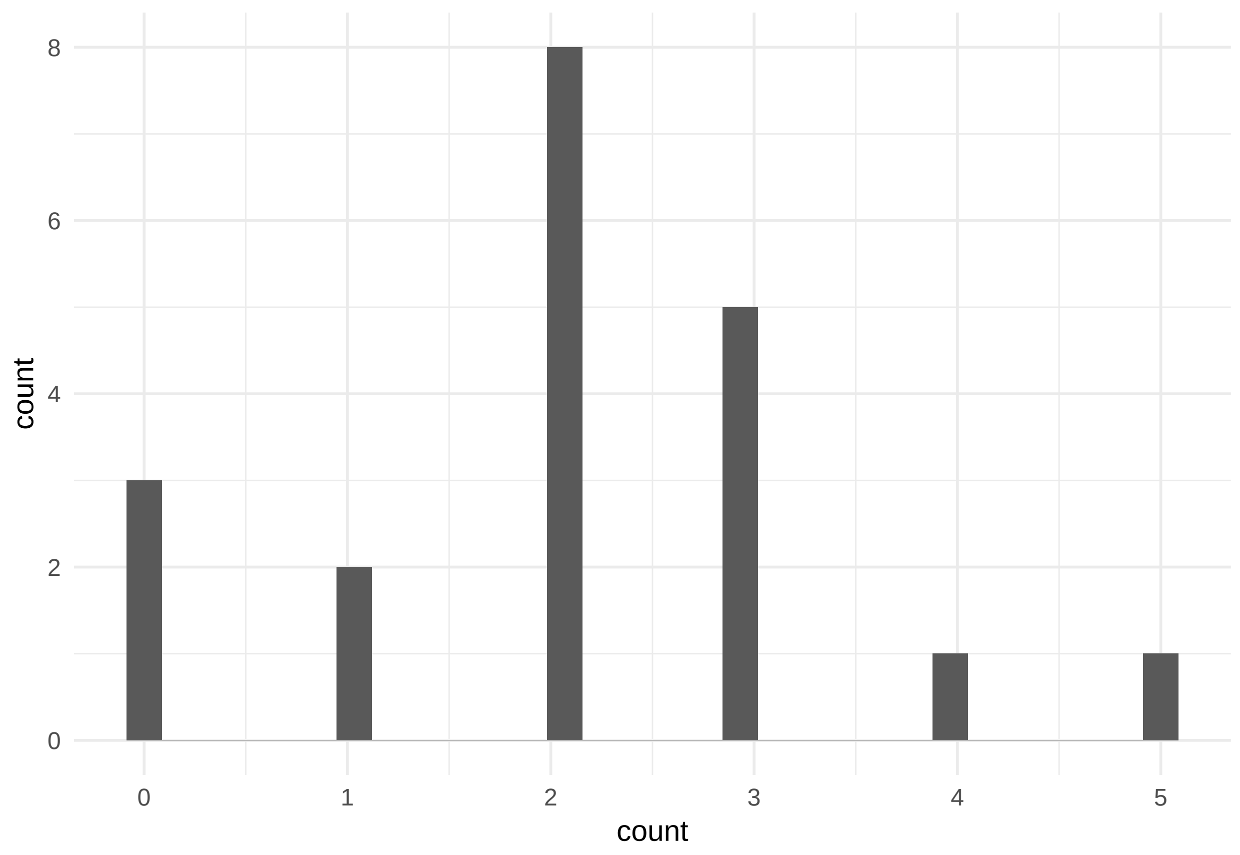


The simulated predicted values (μ_i) and errors are in a fairly realistic range. Still, we immediatly see, that simulation with Normal distributions is rather inappropriate: a substantial number of simulated observations is *negative*, which strictly makes no sense for error counts. The pragmatic and impatient reader may suggest to adjust the standard deviation (or move the averages up) to make negative values less unlikely. That would be a poor solution for the following two reasons. First, Normal distributions support the full range of real numbers. There is always a chance of negative simulations, as tiny as it may be. Repeatedly running the simulation until `pumps` contains exclusively positive numbers (and zero), obviously is poor practice. The second reason is that the simulations very purpose was to express and explore expectations from the linear model (CG). We can simply conclude that any model that assumes normally distributed errors must be wrong when the outcome is bounded below or above, which means: always.

Recall how linearity is gradually bended when a magnitude approaches its natural limit. A similar effect occurs for distributions. Distributions that respect a lower or upper limit get squeezed like chewing gum into a corner, when approaching the boundaries. Review Binomial and Poisson distribution in chapter 1 for illustrations. As a matter of fact, a lot of real data in design research is skewed that way, whereas the normal distribution eternally claims symmetry.

A common misconception is that random distributions approach the normal distribution with larger sample sizes. The only thing that happens is that increasing the number of observations renders the true distribution more fidel. Examine yourself, how the shape of Poisson distributions changes by mean count, as well as sample size. The following code simulates a Poisson distribution with a given λ and N. With every new run of the code, `rpois` generates a new random set of counts. By repeatedly running this code and watching the output, you can get a good idea of how varied the shape of the distribution can be.

```
data_frame(count = rpois(n = 20,
                         lambda = 2)) %>%
  ggplot(aes(x = count)) +
  geom_histogram()
```



Assuming constant variance of randomness

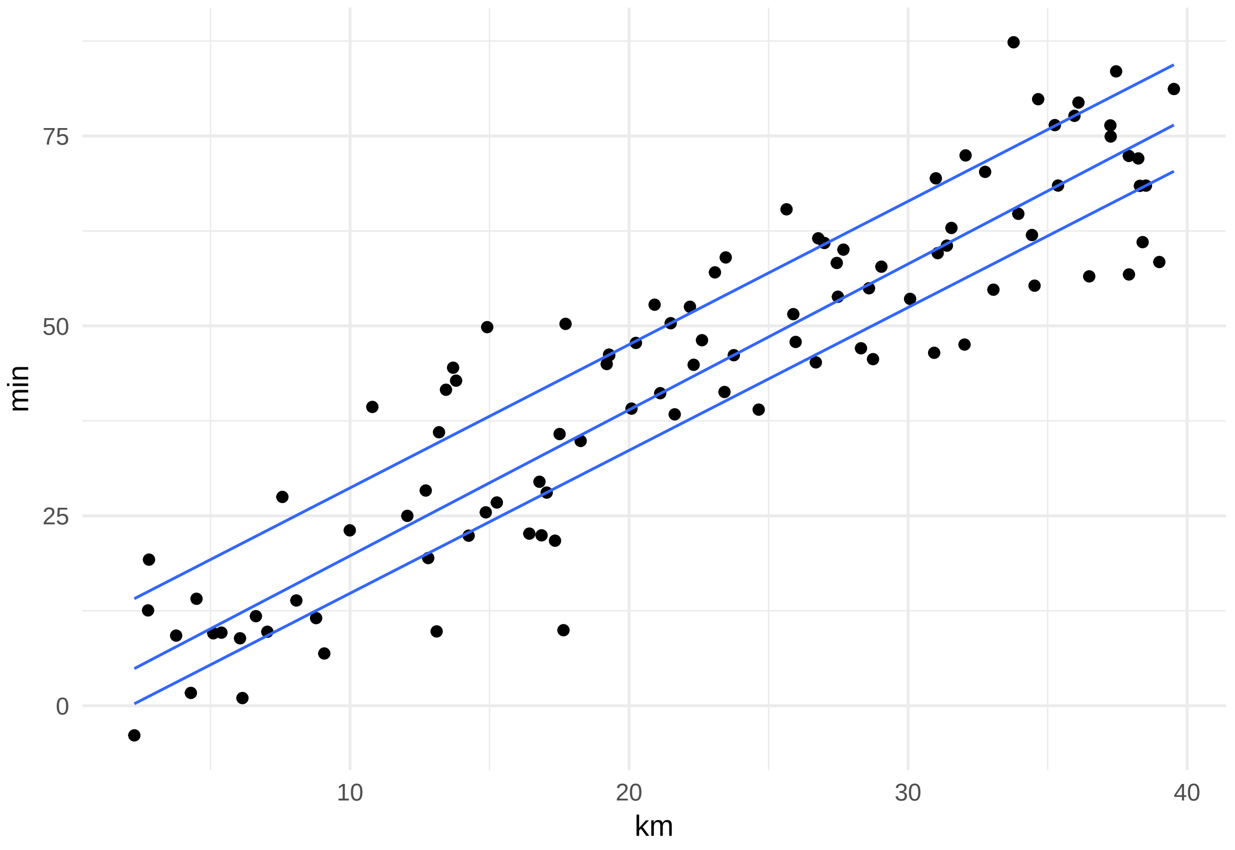
The third assumption of linear models is rooted in the random component term, as well. Recall, that there is just one parameter σ for the dispersion of randomness and that any Normal distribution's dispersion is exclusively determined by σ. That is less harmless than it may sound. In most real data, the dispersion of randomness depends on the expected value, as can be illustrated by the following example.

Imagine a simple survey where commuters are asked three questions about their daily way to work:

1. How long is the route?
2. How long does it *typically* take?
3. What are the maximum and minimum travel times you remember?

If we simulate such data from a linear model, the relationship between length of route and travel time would inevitably look like a evenly wide band.

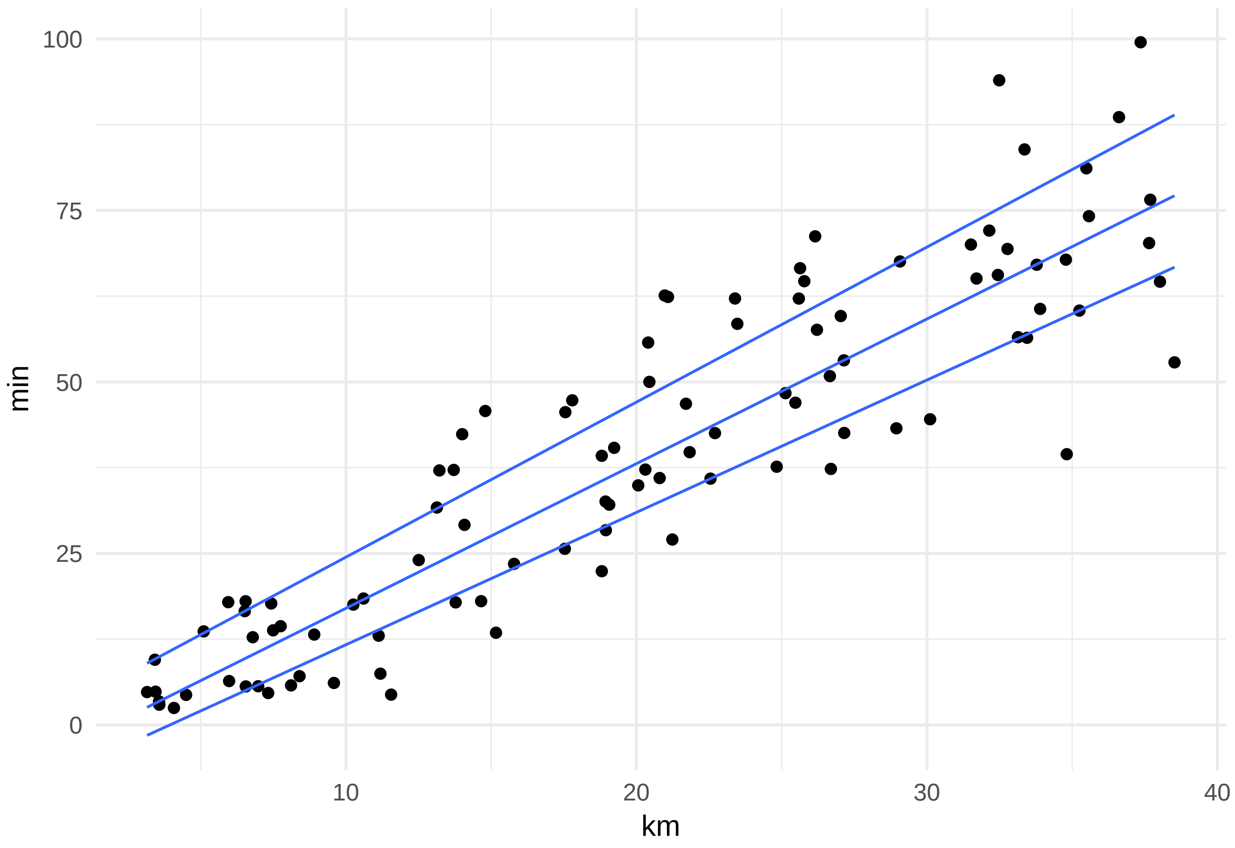
```r
N = 100
data_frame(Obs = as.factor(1:N),
           km  = runif(N, 2, 40),
           min = rnorm(N, km * 2, 10)) %>%
  ggplot(aes(x = km, y = min)) +
  geom_point() +
  geom_quantile(quantiles = c(.25, .5, .75))
```



It is very unrealistic that persons who live right around the corner experience the same range of possible travel times than people who drive dozens of kilometers. Most of the time, we intuit the dispersion of randomness to increase with the magnitude of the expected value. For example, a Gamma distribution takes two parameters, shape α and scale τ and both of them influence mean and variance of the distribution, such that the variance increases by the mean by square.

$$X \sim \text{Gamma}(\alpha, \theta) E(X) = \alpha\theta \text{Var}(X) = \alpha\theta^2 \text{Var}(X) = E(X)\theta$$

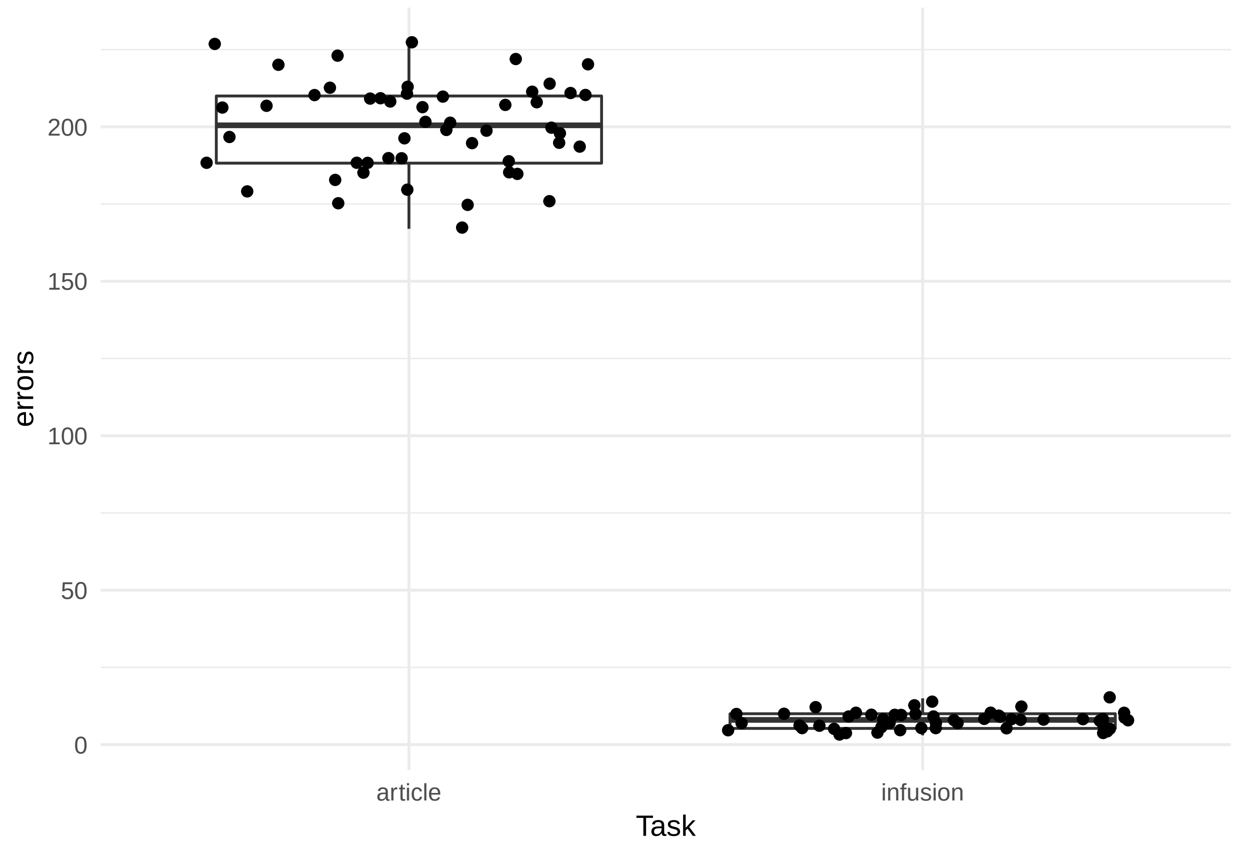
```
data_frame(Obs = as.factor(1:100),
           km  = runif(100, 2, 40),
           min = rgamma(100, shape = km * .5, scale = 4)) %>%
  ggplot(aes(x = km, y = min)) +
  geom_point() +
  geom_quantile(quantiles = c(.25, .5, .75))
```



A similar situation arises for count data. When counting user errors, we would expect a larger variance for complex tasks and interfaces, e.g. writing an article in a word processor, as compared to the rather simple situation like operating a medical infusion pump. For count data, the Poisson distribution is often a good choice and for Poisson distributed variables, mean and variance are both exactly determined by the Poisson rate parameter λ, and therefore linearly connected.

$$X \sim \text{Poisson}(\alpha, \theta) \lambda = E(X) = \text{Var}(X)$$

```
data_frame(Obs = as.factor(1:100),
           Task  = rep(c("article", "infusion"), 50),
           errors = rpois(100, lambda = if_else(Task == "article", 200, 8))) %>%
  ggplot(aes(x = Task, y = errors)) +
  geom_boxplot() +
  geom_jitter()
```

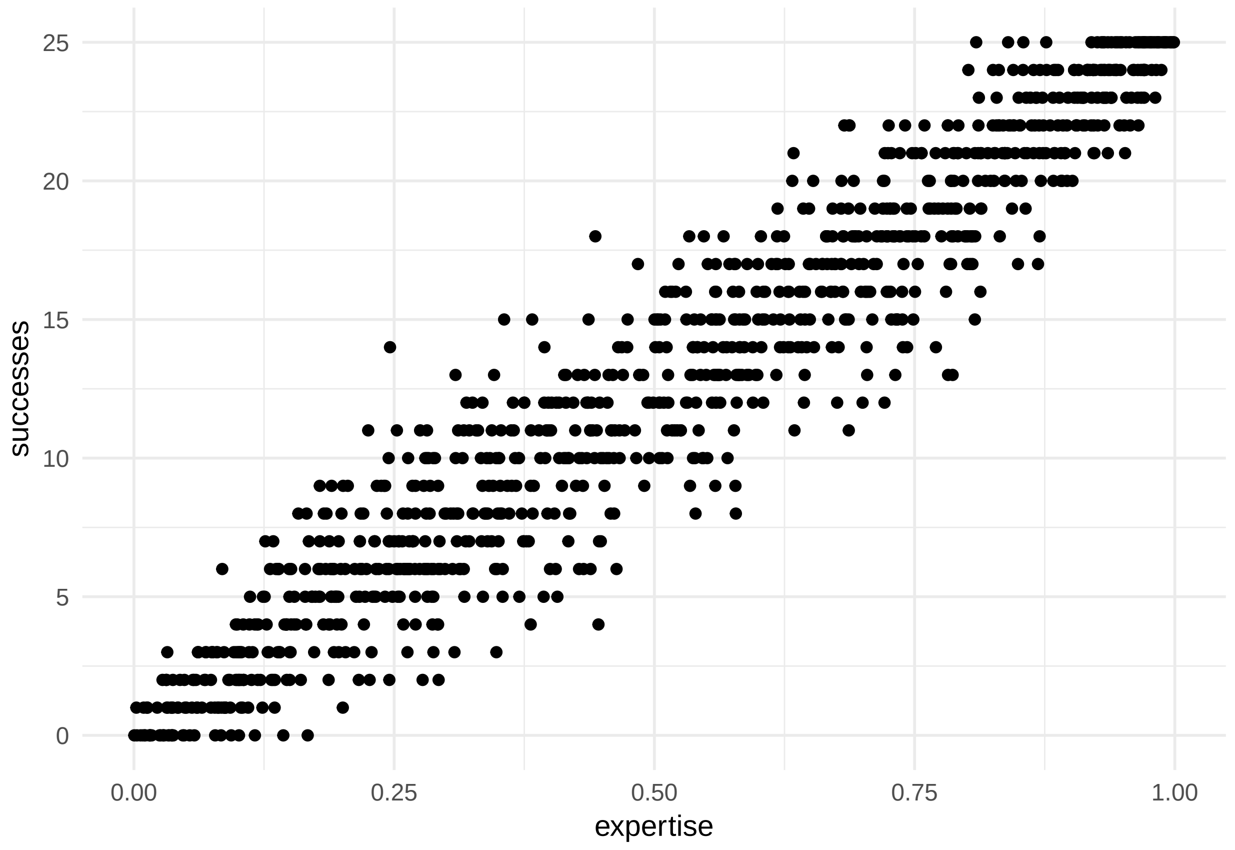


Not by coincidence, practically all distributions with a lower boundary have variance increase with the mean. Distributions that have two boundaries, like binomial or beta distributions also have a mean-variance relationship, but a different one. For binomially distributed variables, mean and variance are determined as follows:

$$X \sim \text{Binom}(p, k) E(X) = pk \text{Var}(X) = p(1-p)k \text{Var}(X) = E(X)(1-p)$$

To see this, imagine a study that examines the relationship between user expertise (for the convenience on a scale of zero to one) and success rate on ten tasks. The result is a cigar-like shape. For binomial distributions, variance gets largest, when the chance of success is centered at $p = .5$. This is very similar for other distributions with two boundaries, such as beta and logit-normal distributions.

```
data_frame(expertise  = runif(1000, 0, 1),
           successes = rbinom(1000, 25, expertise)) %>%
  ggplot(aes(x = expertise, y = successes)) +
  geom_point()
```



In conclusion, the Normal distribution assumption is flawed in two ways: real distributions are typically asymmetric and have mean and variance linked. Both phenomena are tightly linked to the presence of boundaries. Broadly, the deviation from symmetry gets worse when observations are close to the boundaries (e.g. low error rates), whereas differences in variance is more pronounced when the means are far apart from each other.

Elements of Generalized Linear Models

GLM is a *framework for modeling* that produces a *family of models*. Every member of this family uses a specific *link functions* to establish linearity and chooses a particular *random distribution*, that has an adequate shape and mean-variance relationship.

Sometimes GLM are confused as a way to relax assumptions of linear models, (or even called non-parametric). They absolutely are not! Every member of its own makes precise assumptions on the level of measurement and the shape of randomness (see Table A). One can even argue that Poisson, Binomial and exponential regression are stricter than Gaussian, as they use only one parameter, with the consequence of a tight association between variance and mean. A few members of GLM are classic: Poisson, Binomial (aks logistic) and exponential regression have routinely been used before they were united under the hood of GLM. These and a few others are called *canonical* GLM, as they possess some convenient mathematical properties, that made efficient estimation possible, back in the days of expensive computer time.

Re-linking linearity (#relinking_linearity) [TBC]

The strength of the linear term (the likelihood) is its endless versatility in specifying relations between predictor variables and outcome. Unfortunately, it represents all associations as straight lines. These lines extend from $-\infty$ to ∞ and will cross the lower or upper boundaries of every known outcome variable. All linear models predict events that cannot happen.

Generalized linear models use a simple mathematical trick to keep the linear term, but confine the expected values to the natural boundaries of the measures. In linear models, the linear term is mapped to expected values, directly, causing the before mentioned problems. In GLM, a layer is drawn between expected value μ and the linear term, *linear predictor* θ. The *link function* transforms between μ and θ. In order to transform back to the scale of measurement, the inverse of the link function, the *mean function* is used.

In arithmetics an abundance of functions exists for every possible purpose. However, link functions must fulfill two criteria,

1. they must map to the range $[-\infty; \infty]$, as that ensures linearity
2. they must be monotonically increasing

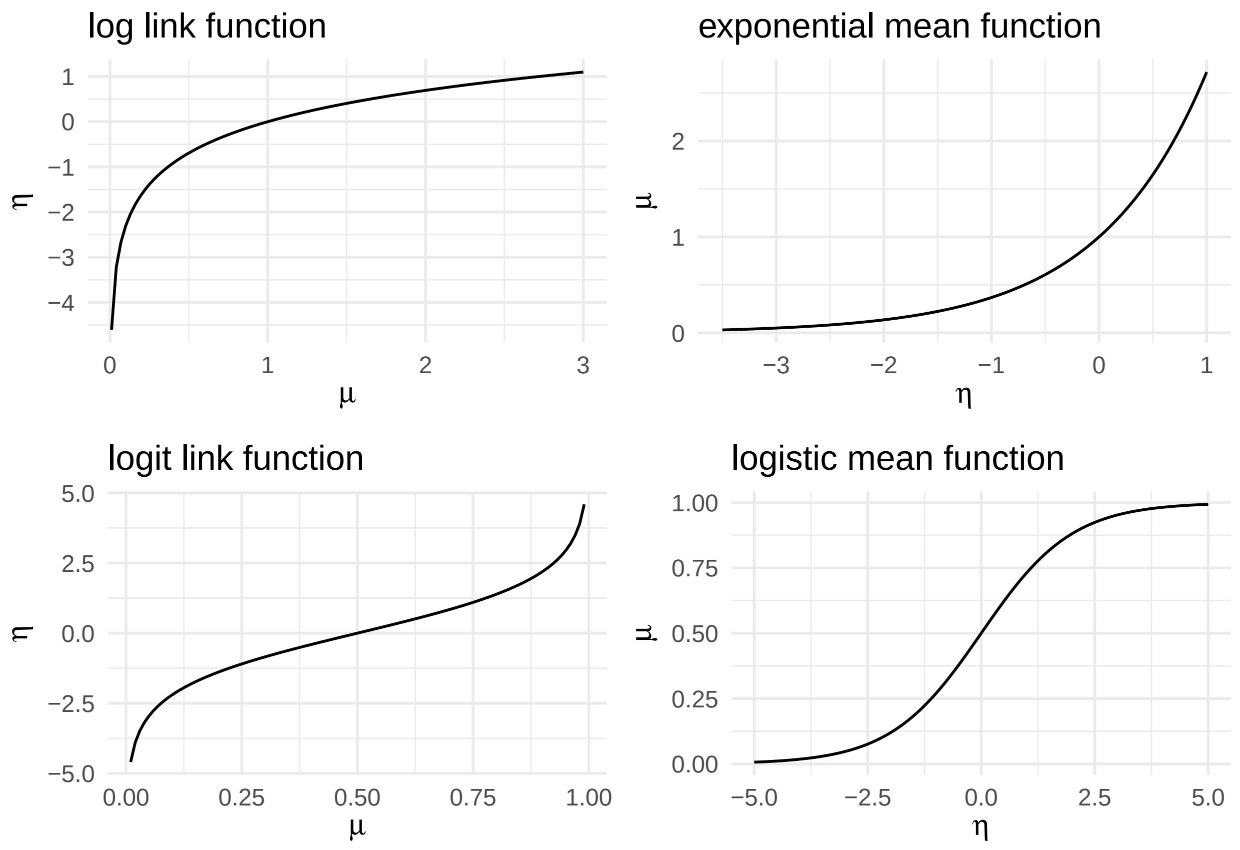
Intuitively speaking, a monotonically increasing function preserves the order in magnitude, such that the following holds for a link function.

$$\mu_a > \mu_b \rightarrow \theta_a > \theta_b$$

The primary reason for this requirement is that for a link function ϕ there must exist the inverse, that is the mean function (ϕ^{-1}). A function that is *not* monotonically increasing, such as x^2 does not have an inverse function. For example, x^2 is not a proper link function, because its inverse, $\sqrt{x}$ can take *two* values (e.g., $\sqrt{x} = [2, -2]$) and therefore is not a function, strictly.

An adequate link function for count variables would map the range of natural numbers to the *linear range* of η that is $[-\infty; \infty]$. The logarithm is such a function and its inverse is the *exponential* function, which bends the linear range back into the boundary. Figure XY shows them side-by-side. Note that the logarithm is *not asymptotic* as it may seem. This function truly approaches ininity, albeit at a decelerating pace (which is mind boggling). Other variables, like success rates or rating scales, have lower and upper boundaries. A suitable pair of functions is the *logit* link function and the *logistic* mean function.

```r
plot_glmfun <- function(f = log,
                        title = "log link function",
                        lower = .01, upper = 3,
                        dir = "link"){
  out <-
    data_frame(x = seq(lower, upper, (upper - lower)/100)) %>%
    ggplot(aes(x)) +
    stat_function(fun = f) +
    labs(title = title) +
    labs(x = expression(mu), y = expression(eta))
  if(dir == "mean") out <- out + labs(x = expression(eta),
                                      y = expression(mu))
  out
}

gridExtra::grid.arrange(
  plot_glmfun(),
  plot_glmfun(f = exp, "exponential mean function",  -3.5, 1, dir = "mean"),
  plot_glmfun(f = logit, "logit link function", 0.01, .99),
  plot_glmfun(f = inv_logit, "logistic mean function",  -5, 5, dir = "mean"))
```



Using the link function comes at a cost: the linear coefficients β_i no longer has a natural interpretation, like "moving one unit on the predictor lets the outcome change by β_i". Later will see that logarithmic and logit scales gain an intuitive interpretation when parameters are exponentiated, $\exp(\beta_i)$ (@ref(poisson-regression) and @ref(logistic-regression)

Choosing patterns of randomness (#choosing_randomness)

In chapter @ref(distributions) a number of random distributions were introduced, together with conditions of when they arise. The major criteria were related to properties of the outcome measure: how it is bounded and whether it is discrete (countable) or continuous.

In GLM, the researcher has a larger choice for modelling the random component and Table XY lists some common candidates.

boundaries	discrete	continuous
unbounded	NA	Normal
lower	Poisson	Exponential
lower and upper	Binomial	Beta

That is not to say that these five are the only possible choices. Many dozens of statistical distributions are known and these five are just making the least assumptions on the shape of randomness in their class (mathematicians call this *maximum entropy distributions*). In fact, we will soon discover that real data frequently violates principles of these distributions. For example, count measures in behavioural research typically show a variance that exceeds the mean, which speaks against the Poisson distributions. As we will see in @ref(overdispersion) and @ref(zero-inflation), Poisson distribution can still be used in such cases with some additional tweaks.

As we will see, response times in design research are particularly misbehaved, as they do not have their lower boundary at zero, but at the lowest human possible time. In contrast, most continuous distributions assume that measures near zero are possible, at least. In case of response times, we will take advantage of the fact, that modern Bayesian estimation engines support a large range of distributions, by far exceeding the available choices in asymptotic methods of frequentist statistics. The `stan_glm` regression engine has been designed with downwards compatibility in mind, which is why it only includes the classic distributions. Luckily, there is a sibling engine in the package `brms`, which is more progressive and gives many more choices.

Still, using distributions that are not Gaussian sometimes carries minor complications. Normal distributions have the convenient property that the amount of randomness is directly expressed as the parameter σ. That allowed us to compare the fit of two models A and B by comparing σ_A and σ_B (note, however that this is not a rigorous method for model selection). In random distributions with just one parameter, the random component is either determined by the location (e.g., Poisson λ or Binomial p). For distributions with more than one parameter, dispersion of randomness typically is a function of two or more parameters. For example, Gamma distributions have two parameters, but these do not pull location and dispersion neatly apart, as Normal distributions do. Instead, mean and variance Gamma distributions depend on both parameters.

Using distributions with entanglement of location and dispersion seems to be a step back, but frequently is necessary to render a realistic association between the expected value and amount of absolute randomness. Most distributions with a lower bound (e.g., Poisson, exponential and Gamma) increase variance with mean, whereas double bounded distributions (beta and binomial) typically have maximum variance when the distribution is centered.

Case: user testing infusion pumps

Medical infusion pumps are unsuspicious looking devices that are en-mass installed in surgery and intensive care. Their only purpose is controlled injection of medication in the blood stream of patients. Pumps are rather simple devices as infusion is not more than a function of volume and time. They are routinely used by trained stuff, anaesthesiologists and nurses, mostly. We should have great faith in safe operation under such conditions. The truth is, medical infusion pumps have reportedly killed dozens of people, thousands were harmed and an unknown number of nurses lost their jobs. The past generation of pumps is cursed with a chilling set of completely unnecessary design no-gos:

- tiny 3-row LCD displays
- flimpsy foil buttons without haptic marking or feedback
- modes
- information hidden in menus

For fixing these issues no additional research is needed, as the problems are pretty obvious to experienced user interface designers. What needs to be done, though, is proper validation testing of existing and novel interfaces, for example:

- is the interface safe to use?
- is it efficient to learn?
- is a novel interface better than a legacy design? And by how much?

We conducted such a study. A novel interface was developed after an exetensive study of user requirements and design guidelines. As even the newest national standards for medical devices do not spell precise quantitative user requirements (such as, a nurse must be able to complete a standard task in t seconds and no more than e errors may occur), the novel interface was compared to a device with a legacy design. The participants were nurses and they were asked to complete a set of eight standard tasks with the devices. In order to capture learnability of the devices, every nurse completed the sequence of tasks in three consecutive sessions. A number of performance measures were recorded to reflect safety and efficiency of operation:

1. *task completion*: for every task it was assessed whether the nurse had completed it successfully.
2. *deviations from optimal path*: using the device manual for every task the shortest sequence was identified that would successfully complete the task. The sequence was then broken down into individual operations that were compared to the observed sequence of operations. An algorithm called *Levenshtein distance* was used to count the number of deviations.
3. *time on task* was recorded as a measure for efficiency.
4. *mental workload* was recorded using a one-item rating scale.

As can be expected in the light of what has been said above, each one these measures violate one or more assumptions of the Gaussian linear model. In the following chapters, proper models from teh GLM family are introduced for commonly occuring measures of types:

1. *count data*, such as the number of completed tasks and path deviations
2. *temporal data*, such as time-on-task
3. *rating scales*

Count data

Normal distributions assume that the random variable under investigation is continuous. For measures, such as time, that is natural and it can be a reasonable approximation for measures with fine-grained steps, such as average scores of self-report scales with a larger number of items. Other frequently used measures are clearly, i.e. naturally, discrete, in particular everything that is counted. Examples are: number of errors, number of succesfully completed tasks or the number of users. Naturally, count measures have a lower bound and frequently this is zero. A distinction has to be made, though, for the upper bound. In some cases, there is no well defined upper bound, or it is very large, at least (e.g., number of users) and Poisson regression applies. In other cases, the upper bound is given by the research design, for example the number of tasks given to a user. When there is an upper bound, logistic regression applies.

Poisson regression

When data can be considered successes in a fixed number of trials, logistic regression is the model type of choice. When the outcome variable is a count, but there is no apparent upper limit, Poisson regression applies.

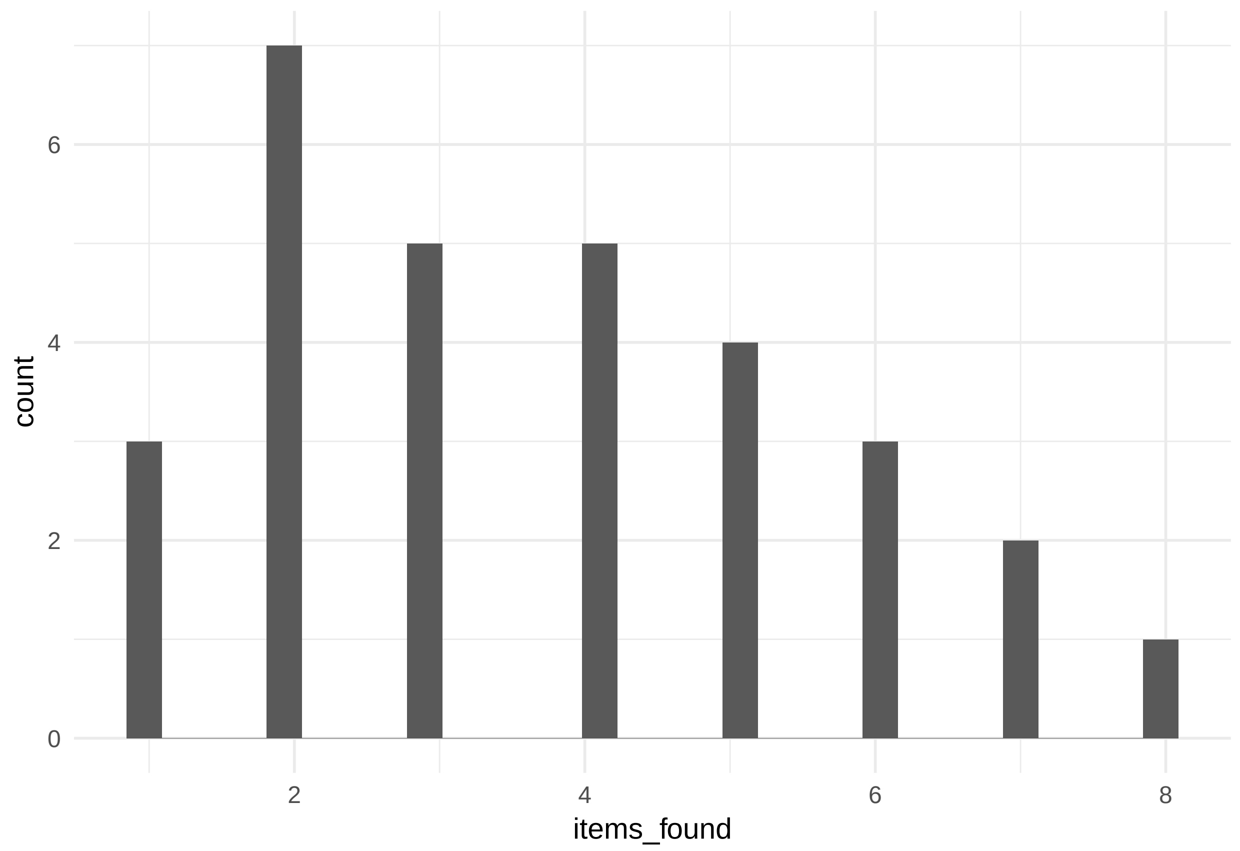
In brief, Poisson regression has the following attributes:

1. The outcome variable is bounded at zero (and that must be a possible outcome, indeed).
2. The linear predictor is on a logarithmic scale, with the exponential function being the inverse.
3. The random component follows a Poisson distribution.
4. Variance of randomness increases linearly with the mean.

The link function is the logarithm, as it transforms from the non-negative range of numbers to real numbers. For the start, we have a look at a Poisson GMM: In an advanced level of the smart smurfer game, the items are hidden from the player and therefore extremely difficult to catch. To compensate for the increased difficulty somewhat, the level carries an abundance of items. On average, the player is not supposed to find more than three items. We simulate a data set for one player repeating the level 30 times and run a Poisson regression model:

```
set.seed(6)
D_Pois <-
  data_frame(Obs = 1:30,
  items_found = rpois(30, lambda = 3.4))
```

```
D_Pois %>%
  ggplot(aes(x = items_found)) +
  geom_histogram()
```



```
M_Pois <-
  stan_glm(items_found ~ 1,
           family = poisson,
           data = D_Pois, iter = iter)
```

```
fixef(M_Pois)
```

Table 2: Estimates with 95% credibility limits

model	type	fixef	center	lower	upper
object	fixef	Intercept	1.31	1.16	1.48

```
# bayr:::knit_print.tbl_coef(M_Pois)
```

The Poisson parameter λ (lambda) has a direct interpretation as it represents the expected mean (and variance) of the distribution. Instead, the regression coefficient is on a logarithmic scale, to ensure it has no boundaries. To scale it down to the scale of measurement, the exponential function is the canonical mean function in Poisson regression:

```
fixef(M_Pois, mean.func = exp)
```

Table 3: Estimates with 95% credibility limits

model	type	fixef	center	lower	upper
object	fixef	Intercept	3.72	3.18	4.41

The exponentiated intercept coefficient can be interpreted as the expected number of items found per session. Together with the credibility limits it would allow the conclusion that the items are slightly easier to find than three per session.

Speaking multiplicative

To demonstrate the interpretation of coefficients other than the intercept (or absolute group means), we turn to the more complex case of the infusion pump study. In this study, the deviations from normative path were counted to serve as a measure for safety of operation. In the following regression analysis, we examine the reduction of deviations by training sessions as well as the differences between the two devices. As we are interested in the improvement from first to second session and second to third, successive difference contrasts apply.

```
attach(IPump)
```

```
M_dev <-
  stan_glmer(deviations ~ Design + session + session:Design +
               (1 + Design + session|Part) +
               (1 + Design|Task) +
               (1|Obs), ## observation-level ramdom effect
             family = poisson,
             data = D_pumps, iter = iter)

M_dev
```

```
fixef(M_dev)
```

Table 4: Estimates with 95% credibility limits

fixef	center	lower	upper
Intercept	0.838	0.311	1.362
DesignNovel	-1.511	-2.247	-0.780
session	-0.233	-0.350	-0.139
DesignNovel:session	-0.081	-0.242	0.113

Again, the coefficients are on a logarithmic scale and cannot be interpreted right away. By using the exponential mean function, we obtain the following table:

```
fixef(M_dev, mean.func = exp)
```

Table 5: Estimates with 95% credibility limits

fixef	center	lower	upper
Intercept	2.312	1.365	3.904
DesignNovel	0.221	0.106	0.459
session	0.792	0.705	0.870
DesignNovel:session	0.922	0.785	1.120

The intercept now has the interpretation as the expected number of deviations with the legacy design in the first session. However, it is incorrect to speak of the effects in terms of differences. i.e. summative. Fortunately, the following arithmetic law tells that what is summative on the level of the linear predictor, becomes *multiplicative* on the original scale:

$$\exp(\beta_0 + x_1\beta_1 + x_2\beta_2) = \exp(\beta_0)\exp(x_1\beta_1)\exp(x_2\beta_2)$$

Hence, the exponentiated coefficients have a *multiplicative interpretation*, like the following:

1. In the first session, the novel design produces 2.312 *times* the deviations than with the legacy design.
2. For the legacy design, every new training session reduces the number of deviations *by factor* 0.792

3. The reduction rate per training session of the novel design is *92.229% as compared to the legacy design.

With counts we usually expect the variance of randomness to rise with the mean. The Poisson distribution is very strict in the sense that the variance equals the mean

$$y_i \sim \text{Pois}(\lambda) \rightarrow \text{Var}(x_i) = \text{Mean}(x_i) = \lambda$$

.

Real count data frequently has variance that raises proportionally with the mean, but is inflated. This is called *overdispersion* and is accounted for by an observation-level random effect, which will be explained in a separate section @ref(overdispersion).

Hence, the novel design reduces the initial number of deviations by factor

```
detach(IPump)
```

Monotony and quantiles

The transformation of coefficients to the original scale has been applied to the point and range estimates as produced by the `fixef` command, that is *after* summarizing the posterior distribution. One may wonder if this is valid. Would we get the same estimates when applying the mean function to all draws of the MCMC chain and then summarize? The general answer is that applying the mean function after summarizing is allowed if the summary function is invariant under the exponential function.

For all GLM, the link and mean functions are monotonically increasing, with the consequence that the order of observations is preserved. Formally, for any two MCMC iterations i and j for a parameter β_i:

$$\beta_{1i} < \beta_{1j} \rightarrow \exp(\beta_{1i}) < \exp(\beta_{1j})$$

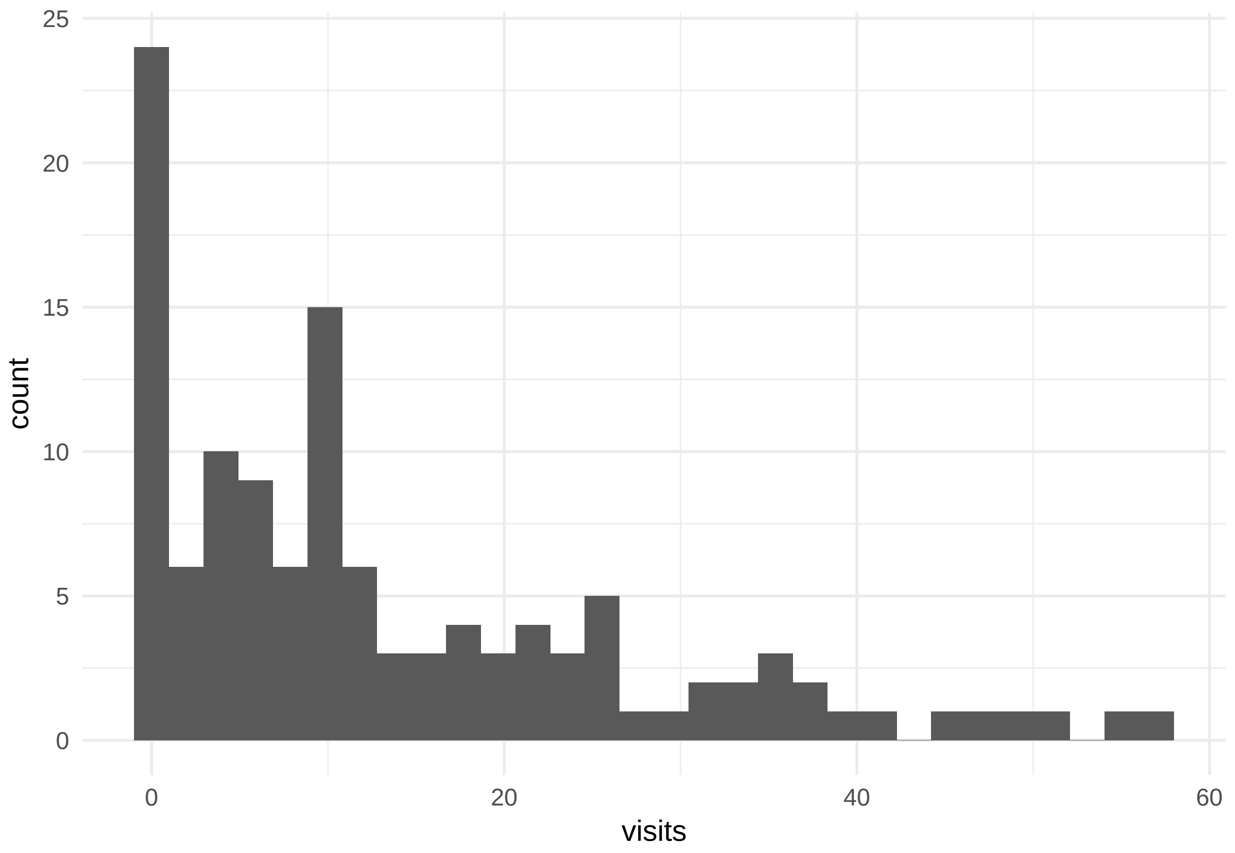
Recall that throughout this book, center and interval estimates have been obtained by simple quantiles, marking the points where 2.5%, 50% and 97.5% of all iterations are smaller. Order does not change with monotonous transformations, if 2.5% (50%, 97.5%) of draws are smaller on the linear scale, they will still be after applying the mean function. Quantiles are not affected by monotonous transformation and transformation after summary is therefore valid. Some researchers prefer the mode of the posterior to represent its center location. The mode is the point of highest density and does not rely on ranks, it therefore even invariant under all transformations that preserve identity.

This is different for higher order methods for obtaining point and interval estimates. Most notably the mean and the highest posterior density intervals are not invariant to mean functions. When using those, the mean function must be applied before summarizing the posterior, which is inconvenient and inconsistent.

Zero inflation

Imagine a study that examines the frequency of visits to the social media website Fakebook. While other researchers already set out to find predictive factors, like extrovert personality and the like, we are here interested in the frequency of daily use.

```
sim_zi <- function(
  beta_0  = 2.5,
  N_Part  = 120,
  p_zero  = .2, # proportion of non-users
  sd_Part = 0.8, # individual differences (lp scale)
  seed    = 23 # parameters passed on to simulate_1
){
  set.seed(seed)
  data_frame(Part = 1:N_Part,
             theta = rnorm(N_Part, beta_0, sd_Part),
             mu = exp(theta),
             is_user = rbinom(N_Part, 1, 1 - p_zero),
             visits = 0 + is_user *rpois(N_Part, mu))
}

D_zi <- sim_zi()
D_zi %>%
  ggplot(aes(x = visits)) +
  geom_histogram()
```



```
## [1] "sim_zi" "D_zi"
```

Logistic (aka Binomial) regression (#logistic_regression)

When the outcome variable can be conceived as successes in a fixed number of trials, logistic regression applies. In brief, logistic regression has the following attributes:

1. The outcome variable is bounded at zero and the number of trials k
2. The linear predictors is on a *logistic scale*, with the *logit* being the inverse. However, in @ref(talking-odds) we will see, that using the logarithm results in a convenient way of speaking about the effects.
3. The random component follows a *binomial distribution*.
4. Due to the former, the variance of randomness is largest at $\mu = 0.5$ or $\eta = 1$ and declines towards both boundaries, taking a characteristic cigar shape.

The most simple form of successes-in-trials measure is when there is only one trial. This is called *dichtotomous*, with the following common examples:

- a user is successful at a task, or fails
- a visitor returnsa to a website or doesn't
- a usability problem is discovered or remains unseen
- a driver brakes just in time or crashes
- a customer would recommend a product to a friend or rather not
- a web user starts a search for information by keyword query or by following links

Most dichotomous outcome variables have a more or less clear notion of success and failure (although not necessarily as in the last example). When the outcome casts a positive light on the design, by convention it is coded as 1, otherwise 0.

In computer science jargon, every dichotomous observation accounts to a *bit*, which is the smallest amount of information ever possible. Since in inferential statistics the amount of information is tantamount with the reduction in uncertainty, with dichotomous data one usually needs an abundance of observations to reach reasonably certain conlusions. Because the information of a single observation is so sparse, large samples and repeated measures are important when dealing with dichtomous outcomes.

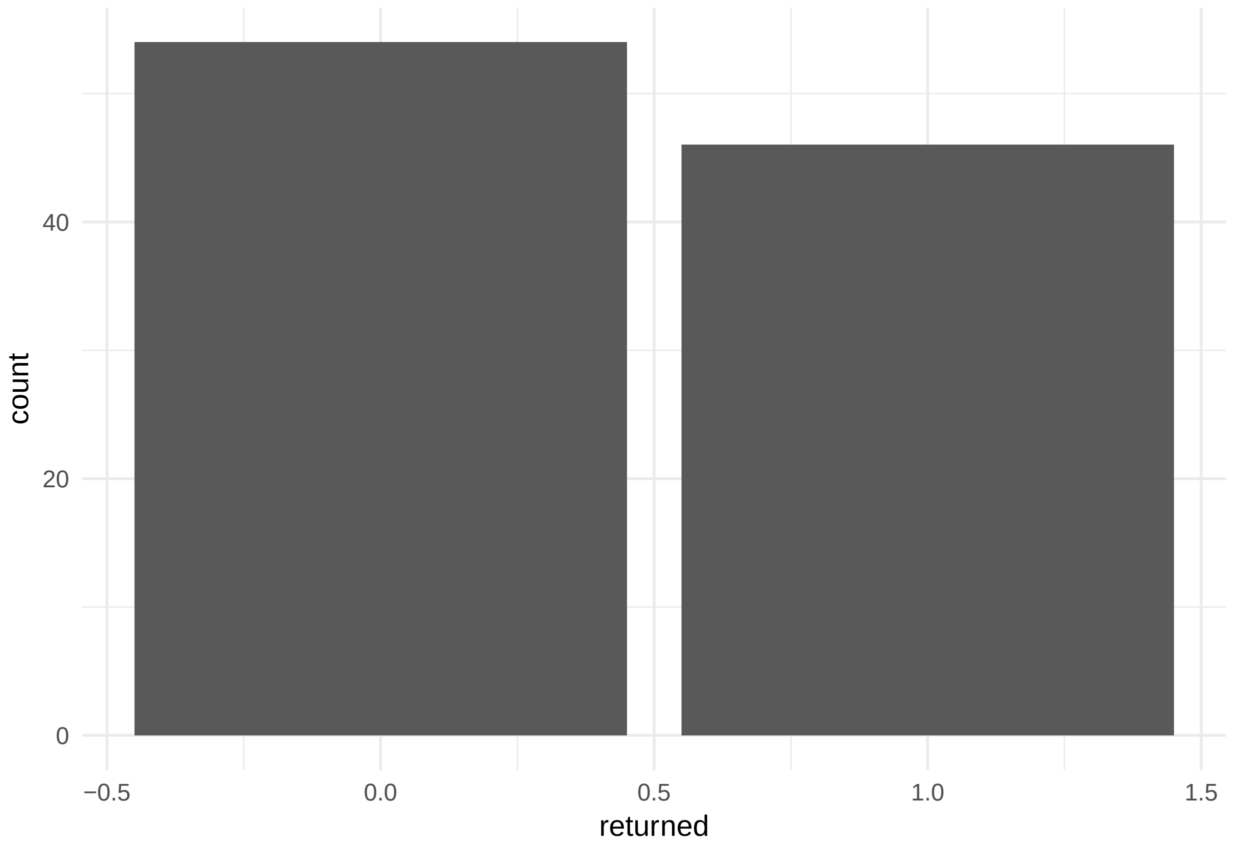
Let us see an example: early research on foraging strategies of web users revealed that they are extremely impatient companions. They scan a page for visual features, rather than reading [REF: high school students information mall]. Visitor of websites build their first judgement in a time as short as 17ms [REF: Tuch presentation time]. For e-commerce that is a highly important fact to know about their customers and practically all commercial websites shine with a pleasing visual appearance, nowadays. But, how would one measure the gratitude of a visitor who actually used the website and may have something to tell beyond visual pleasance.

A simple measure for gratitude is whether a visitor returns. This usually is a highly available measure, too, as any skilled web administrators can distill such data from the server logfiles with little effort. First, all unique visitors are extracted and if the same visitor returns within a given period of time, this is coded as a success (one) otherwise failure (zero). We simulate such a data set:

```r
set.seed(42)
D_ret <- data_frame(visitor = as.factor(1:100),
                returned = rbinom(100, 1, .4))

D_ret %>% sample_n(6) %>% kable()
```

visitor	returned
63	1
22	0
99	1
38	0
91	1
92	0

```r
D_ret %>%
  ggplot(aes(x = returned)) +
  geom_bar()
```



In total, 46% visitors return. In order to estimate the return rate together with a statement on uncertainty, we run a logistic regression grand mean model and inspect the coefficient table. Note how the linear formula is completely common ground, but we explicitly pass the binomial `family` to the regression engine.

```
M_ret <- D_ret %>% stan_glm(returned ~ 1, data = .,
                            family = binomial, iter = iter) # <--
```

```
fixef(M_ret)
```

Table 7: Estimates with 95% credibility limits

model	type	fixef	center	lower	upper
object	fixef	Intercept	-0.148	-0.542	0.211

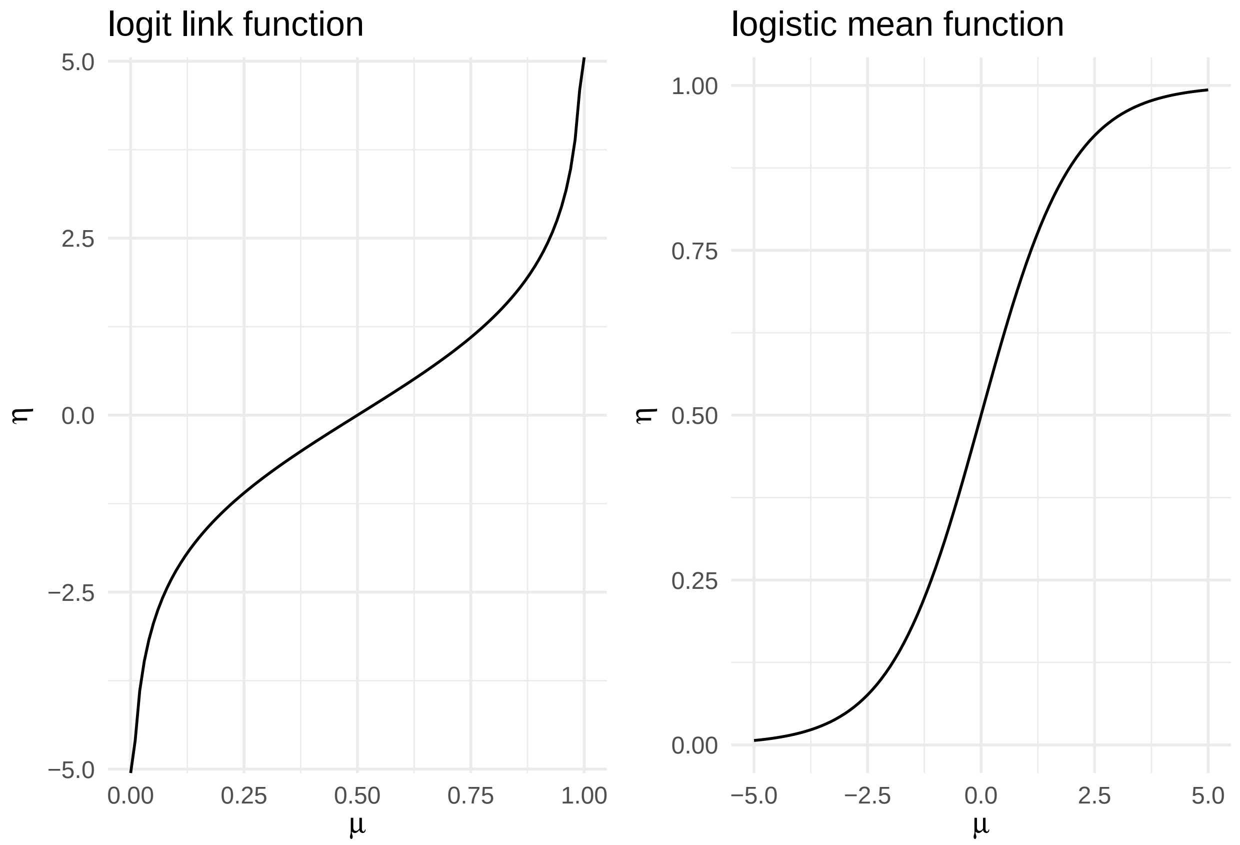
As expected from a GMM we retrieve one parameter that here reflects the average tendency to return to the site. Recall, that the linear model assumes the predictions to be unbounded. However, in case of return rates, we rather speak of *proportions* of users to return. As a side note, I would rather avoid speaking of probabilities in the context of logistic regression. While being mathematically correct, it sometimes causes confusion with certainty or, beware of this, the p-value.

Proportions are on a range from zero to one. Because the quantity of interest is bounded, a link function is needed that stretches the bounded into an unbounded range. For logistic regression, the *logit* functions maps the expected values $\mu_i \in [0;1]$ onto the *linear predictor* scale $\eta_i \in [-\infty;\infty]$:

$$\eta_i = \text{logit}(\mu_i)$$

The inverse function, commonly called the *mean function*, of the logit is the *logistic function*. @ref(logit_logist) shows link and mean functions side-by-side.

```
grid.arrange(
  ggplot(data.frame(mu=c(0, 1)), aes(x = mu)) +
    stat_function(fun = mascutils::logit) +
    xlab(expression(mu)) + ylab(expression(eta)) +
    ggtitle("logit link function"),
  ggplot(data.frame(eta=c(-5, 5)), aes(x = eta)) +
    stat_function(fun = mascutils::inv_logit) +
    xlab(expression(mu)) + ylab(expression(eta)) +
    ggtitle("logistic mean function"),
  nrow = 1)
```



In order to obtain a statement on proportion μ (note that in a GMM, there is only one), we therefore have to perform the mean transformation:

$$\eta = \beta_0 \mu = \text{logist}(\eta)$$

The `fixef` command lets you pass on a mean function. However, ths logistic mean function only is admissable for intercepts and other absolute group means, as we will see in @ref(talking-odds)

```
fixef(M_ret, mean.func = inv_logit)
```

Table 8: Estimates with 95% credibility limits

model	type	fixef	center	lower	upper
object	fixef	Intercept	0.463	0.368	0.553

The apt reader may have noticed that the returners data set has been simulated with an exact return rate of 40%. Despite the sample size of 100, the center estimate seems rather off and hampered by considerable uncertainty. That is precisely because of the low level of information contained in dichotomous variables (one bit). For a reasonably certain estimate one would need many more observations. These can either be obtained by a larger sample or by repeated measures.

Recall the fictional jump-and-run game *smart smurfer* in @ref(poisson_dist): the goal of the game is that players collect items and for the user experience it is crucial that this is neither too difficult nor too easy. Imagine, that for adjusting the difficulty level, the developers conduct a quick evaluation study, where they place a number of items (trials) in the game and the success rate of a single player is observed in a series of 15 game sessions:

```
D_smrf <-
  data_frame(
    Session = 1:15,
    trials = round(runif(15, 0, 25), 0),
    successes = rbinom(15, trials, .4),
    failures = trials - successes) %>%
  mascutils::as_tbl_obs()

D_smrf
```

Table 9: Data set: showing 8 of 15 observations

Obs	Session	trials	successes	failures
1	1	18	7	11
2	2	18	8	10
7	7	19	11	8
9	9	13	4	9
11	11	0	0	0
12	12	9	6	3
13	13	15	6	9
14	14	21	9	12

Per session the player has a number of opportunities for collecting an item, which is a repeated measures situation. One might expect that we need to include random effects into the model. Later, we will see, that this is necessary when the sessions were observed on a sample of players with different abilities. However, as long as one can reasonably assume the chance of catching an item to be constant across all sessions, plain logistic regression can deal with *successes-in-multiple-trials*. In order to estimate a model with more than one trial per observation, it is necessary to add a variable for the number of failures and use a `cbind(successes, failures)` statement for the left-hand-side of the model formula. This may seem inconvenient, but it allows to have a different number of trials per observation.

```
M_smrf <- stan_glm(cbind(successes, failures) ~ 1,# <--
                   family = binomial,
                   data = D_smrf, iter = iter)
```

```
fixef(M_smrf, mean.func = inv_logit)
```

Table 10: Estimates with 95% credibility limits

model	type	fixef	center	lower	upper
object	fixef	Intercept	0.485	0.418	0.559

```
## [1] "D_smrf" "D_ret"
```

We turn now to a real case study, the comparison of two medical infusion pumps (@ref(slope_RE)). On both devices (legacy and novel), 25 nurses completed a set of eight tasks repeatedly over three session. In @ref(slope_RE) a multi-level model was estimated on the workload outcome. It is tempting to apply the same structural model to success in task completion, using binomial random patterns and logit links.

```
completion ~ Design*Session + (Design*Session|Part) + (Design*Session|Task)
```

Such a model is practically impossible to estimate, because dichtomous variables are so scarce in information. Two populations encounter each other in the model: participants and tasks, with 6 observation per combination (6 bit). We should not expect to get reasonably certain estimates on that level and, in fact, the chains will not even mix well. The situation is a little better on the population level: every one of the six coefficients is estimated on 400 bit of raw information. We take a compromise here: estimate the full model on group level and do only intercept random effects, to account for gross differences between participants and tasks.

```
attach(IPump)
```

```
M_cmpl <-
  D_pumps %>%
  stan_glmer(completion ~ Design * Session +
               (1|Part) + (1|Task),
             family = binomial,
             data = ., iter = iter)

sync_CE(IPump, M_cmpl)
```

```
T_cmpl <-
  fixef(M_cmpl)
T_cmpl
```

Table 11: Estimates with 95% credibility limits

fixef	center	lower	upper
Intercept	1.367	0.242	2.497
DesignNovel	0.398	0.116	0.710

fixef	center	lower	upper
Session2-1	0.694	0.155	1.223
Session3-2	-0.062	-0.602	0.492
DesignNovel:Session2-1	-0.281	-1.066	0.520
DesignNovel:Session3-2	0.272	-0.543	1.006

Keep in mind that the estimates are on the scale of the linear predictor η_i. This is a boundless space, where we can freely create linear combinations of effects to obtain group means. To get a group mean prediction on the more meaningful measurement scale $\mu \in [0;1]$, one must *first* do the linear combination, *followed* by the mean function.

- the completion rate in the first legacy session is 0.797
- in novel/session 1: `logist(Intercept + DesignNovel)` = 0.854
- in novel/session 2: `logist(Intercept + DesignNovel + Session2-1 + DesignNovel:Session2-1)` = 0.898
- in legacy/session 3: `logist(Intercept + DesignNovel + Session2-1)` = 0.881

Talking odds

When presenting results of a statistical analysis, the linear predictor is likely to cause trouble, at least when the audience is interested in real quantities. The linear predictor scale has only very general intuition:

- zero marks a 50% chance
- positive values increase the chance, negative decrease
- bigger effects have larger absolute values

That ís sufficient for purely ranking predictors by relative impact (if on a comparable scale of measurement), or plain hypothesis testing, but it does not connect well with quantities a decision maker is concerned with, for example:

1. What is the expected frequency of failure on first use?
2. The novel design reduces failures, but sufficiently?
3. Is frequency of failures reduced to an acceptable level by two training sessions?

Above we have used the mean logistic mean function to elevate the absolute group means to proportions. This is an intuitive scale, but unfortunately, the mean function does not apply to individual effects. It is for example, *incorrect* to apply it like: "the novel pumps proportion of failures in the first session increases by `logist(DesignNovel)` = 0.598".

However, there is another transformation, that does the trick. For a better understanding, we have to first inspect, what the logit actually is. The logit is also called a *log-odds*: $\text{logit}(p) := \log(p(1-p))$. The inner part of the function, the *odds*, are the chance of success divided by the chance of failure. Odds are a rather common way to express ones chances in a game, say:

- odds are 1 against one that the coin flip produces Head. If you place €1 on Head, i put €1 on tail.
- odds are 1 against 12 that Santa wins the dog race. If you place 1€ on Santa, I place €12 against.

If the coefficients are log-odds, than we can extract the odds by the inverse of the logarithm, the exponential function, like in the following call of `fixef`:

```r
T_fixef_cmpl_odds <- fixef(M_cmpl, mean.func = exp)
T_fixef_cmpl_odds
```

Table 12: Estimates with 95% credibility limits

fixef	center	lower	upper
Intercept	3.922	1.274	12.14
DesignNovel	1.489	1.123	2.03
Session2-1	2.001	1.167	3.40
Session3-2	0.940	0.548	1.64
DesignNovel:Session2-1	0.755	0.344	1.68
DesignNovel:Session3-2	1.312	0.581	2.73

But is it legitimate to apply the transformation on individual coefficients in order to speak of changes of odds? The following arithmetic law tells that what is a sum on the log-odds scale, is multiplication on the scale of odds:

$$\exp(x + y) = \exp(x)\exp(y)$$

Consequently, we may speak of changes of odds using *multiplicative language*:

- If you place €100 on failure in the next task with the legacy design in session 1, I place €392.214 on success.
- The odds of success with the novel design increase by *factor* 1.489. Now, I would place 392.214×1.489 = €583.99 on success.
- On success with the novel design in session 2, I would place $392.214 \times 1.489 \times 2.001 \times 0.755 =$ €882.124 on success.

Once, we have transformed the coefficients to the odds scale, we can read coefficients as multipliers and speak of them in hard currency.

```r
detach(IPump)
```

Modelling overdispersion

If you are in a hurry: real data is always overdispersed. If your data is real, prefer the negative binomial family over Poisson and beta-binomial over logistic regression. Or do observation-level random effects.

Poisson and binomial distributions are one-parameter distributions. As there is only one parameter, it is impossible to set location and dispersion separately. In effect, both properties are tightly entangled. For Poisson distributions they are even the same.

$x \sim Pois(\lambda) \implies \mu = \sigma^2 = \lambda$

For binomial variables, mean and variance both depend on probability p and are entangled in cigar shaped form, as the dispersion shrinks when approaching either two boundaries.

The strict variance assumptions of Poisson and binomial models are frequently violated by real data. The violation happens when impact factors have not been included in the likelhood equation. Whenever there is one or more impact factors on the outcome at question that the researcher has not regarded, overdispersion inevitably happens. That means it practically always happens in studies involving objects with complex dynamics, such as the human mind.

Two solutions exist for overdispersed count data: we can either switch to an appropriate two parameter response distribution, that disentangles mean and variance, or introduce an observation-level random effect.

Negative-binomial regression for overdispersed counts

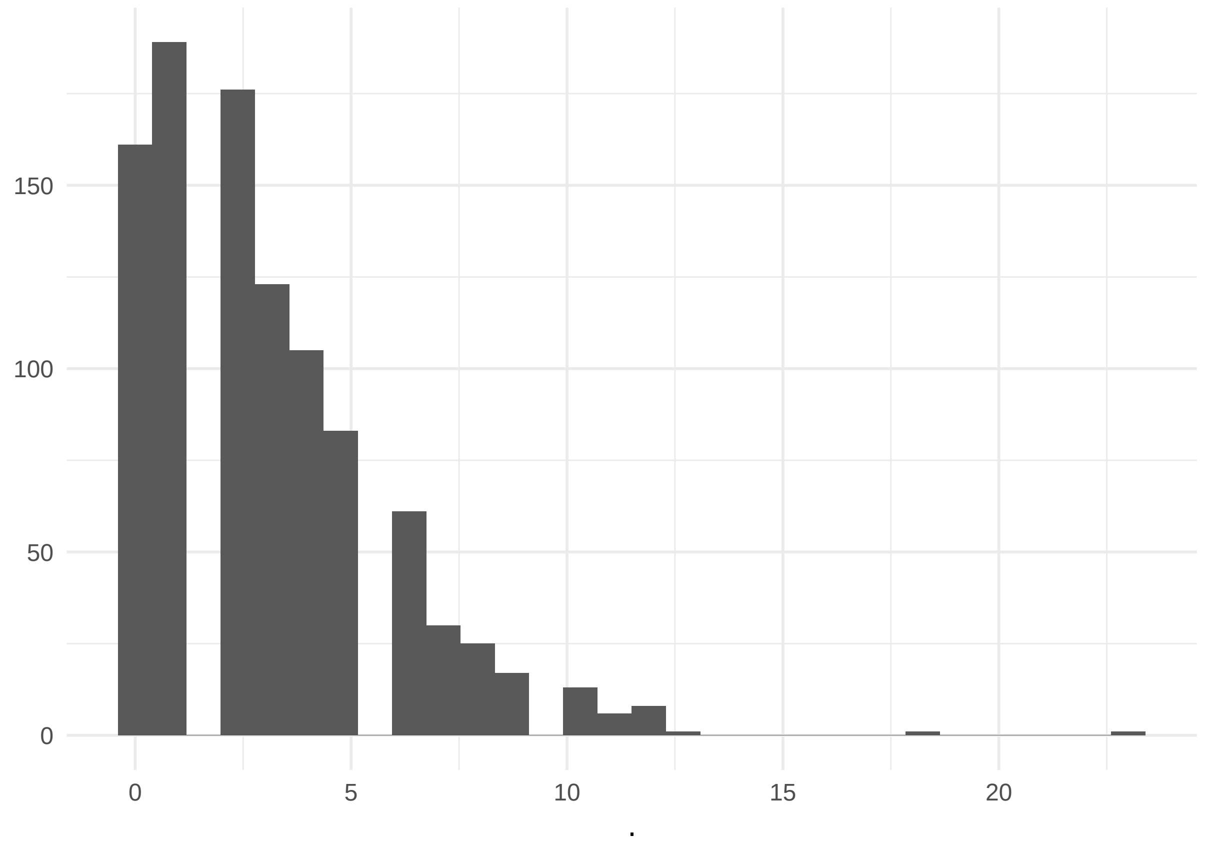
For all three one-parameter distributions, there exists a two-parameter distribution that allows to estimate the amount of random dispersion (almost) independently of the mean.

```
readxl::read_excel("Illustrations/GLM_distributions.xlsx", sheet = "plugin")
```

canonical	generalization	parameters	limiting case
binomial	betabinomial	$\alpha > 0, \beta > 0$	$\alpha, \beta \to \infty$
Poisson	negative binomial	NA	NA
exponential	gamma	rate, shape	NA

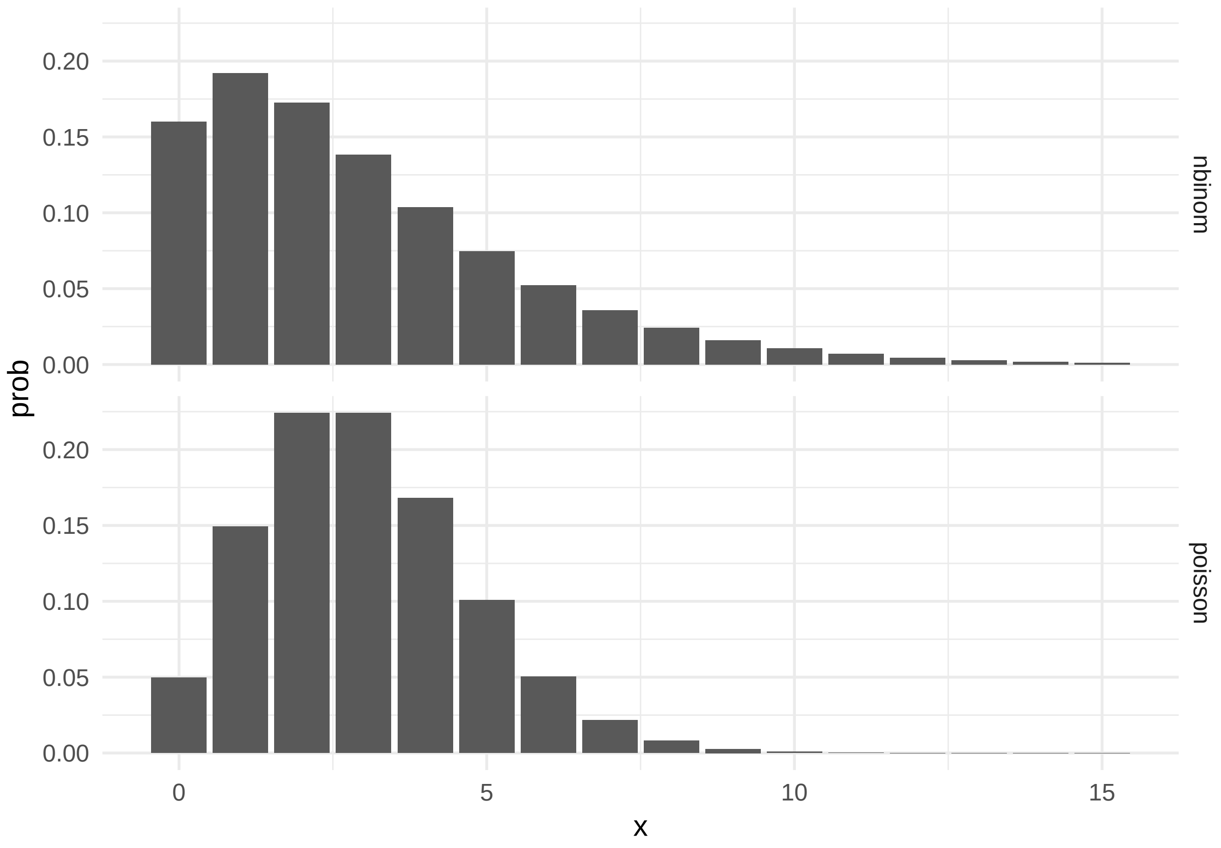
Using Poisson regression for overdispersed count data results in too favorable certainty of estimates, which is a mistake, of course. One solution to the problem is to switch to yet another response distribution that has a second parameter, thereby allowing the variance to vary (almost) freely. For the Poisson case (i.e., counts without an upper limit) that typically is the negative binomial distribution (never mind its name!), for binomial the beta-binomial applies. Both distributions are so-called *mixture distributions*. In mixture distributions, the parameter of the original distribution is not constant, but allowed to vary, typically according to some other distribution. Under this perspective, negative binomial distribution is equivalent to a Poisson distribution, when we let parameter λ follows a certain gamma distribution:

```
rnegbinom <- function(n, mu, size){
  shape = size
  scale = mu/size
  lambda = rgamma(n, shape = shape, scale = scale)
  rpois(n, lambda = lambda)
}

rnegbinom(1000, mu = 3, size = 2) %>%  qplot()
```



The figure below shows a negative binomial distribution and Poisson distribution with the same mean.

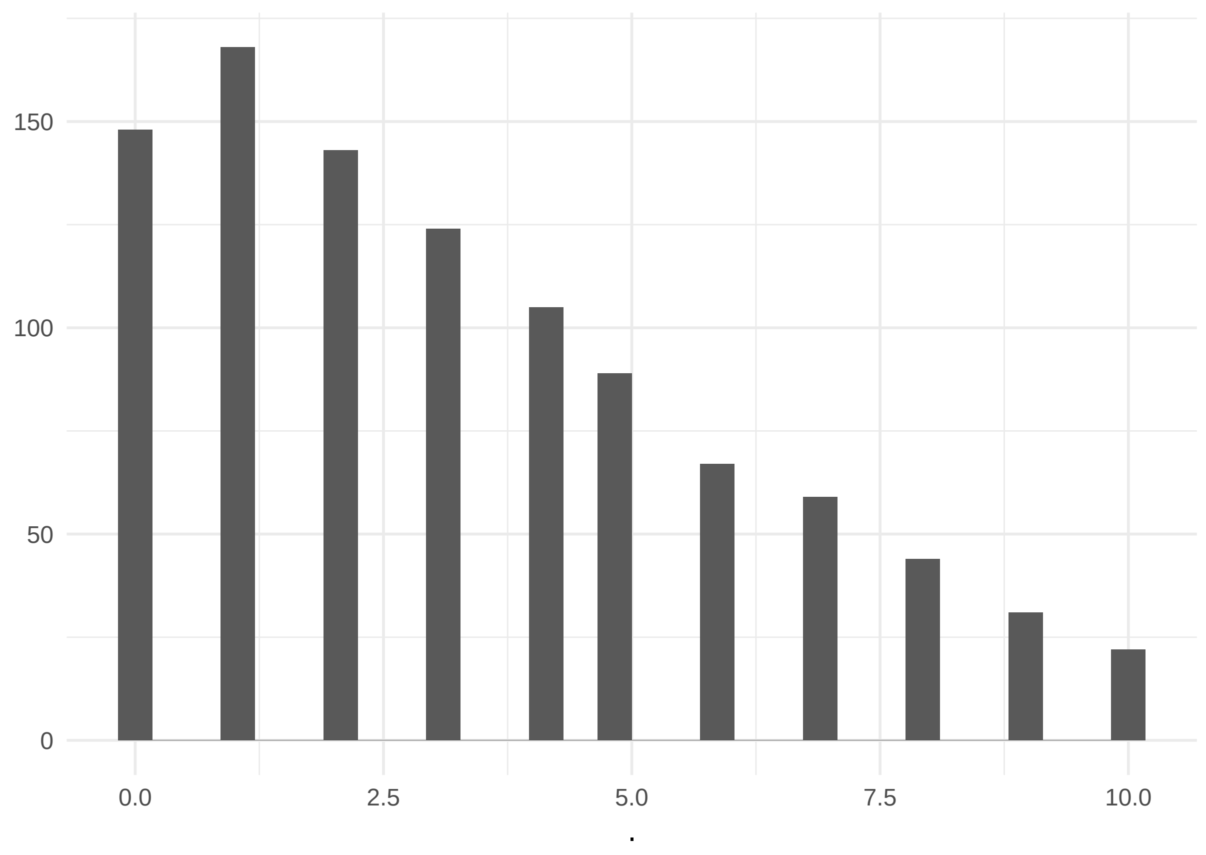
```r
data_frame(x = 0:15,
           nbinom = dnbinom(x, mu = 3, size = 2),
           poisson  = dpois(x, 3)) %>%
  gather(distribution, prob, -x) %>%
  ggplot(aes(x = x, y = prob)) +
  facet_grid(distribution ~ .) +
  geom_col(position = "dodge")
```



Beta-binomial regression for successes in trials

For beta-binomial distributions, the binomial parameter p is mixed from a beta distribution, with parameters a and b:

```r
rbetabinom <- function(n, size, a, b) rbinom(n, size, rbeta(n, a, b))
rbetabinom(1000, 10, 1, 2) %>% qplot()
```



Predictions and interpretation of coefficients of negative-binomial and beta-binomial models are just as with their counterparts, using the same link functions. There is just a tiny difference: a single parameter has been added to the model, which modifies the dispersion. In a standard analysis these parameters have very little meaning, even less than the standard error in a Gaussian model. No misunderstanding: these parameters are *not* the constant standard deviation of residuals. They act as scalers for the "natural" dispersion at any point.

The brms regression engine currently only implements the negative binomial, but not the beta-binomial family. That is a minor problem, because the brms regression engine can be extended. The following code is directly taken from the brms documentation and provides a betabinomial model. The canonical parametrization of the betabinomial distribution takes the parameters a and b from the inner beta distribution. Note, how the author of this code transforms the parameters to obtain an expected value μ and a dispersion parameter ϕ. Like in logistic regression, coefficients are on a logit scale.

```
# define a custom beta-binomial family
beta_binomial2 <- custom_family(
  "beta_binomial2", dpars = c("mu", "phi"),
  links = c("logit", "log"), lb = c(NA, 0),
  type = "int", vars = "trials[n]"
)

# define custom stan functions
bb_stan_funs <- "
  real beta_binomial2_lpmf(int y, real mu, real phi, int N) {
    return beta_binomial_lpmf(y | N, mu * phi, (1 - mu) * phi);
  }
  int beta_binomial2_rng(real mu, real phi, int N) {
    return beta_binomial_rng(N, mu * phi, (1 - mu) * phi);
  }
"

D_betabin <- data_frame(y = rbetabinom(100, 10, 4,2), n = 10)

M_betabin <- D_betabin %>%
  brm(y | trials(n) ~ 1, family = beta_binomial2,
      stan_funs = bb_stan_funs, data = .)
```

```
coef(M_betabin)
```

Table 14: Estimates with 95% credibility limits

parameter	type	fixef	center	lower	upper
b_Intercept	fixef	Intercept	0.876	0.676	1.08
phi	shape	NA	6.283	4.054	10.28

Using observation-level random effects

With the broad implementation of random effects models in Bayesian regression engines, there is a generic procedure to capture the extra variance even with one parameter distributions. The trick is to introduce an *observation-level random effect*. Recall how we regard variation between members of a population as normally distributed deviations from the population mean, by the example of a Poisson grand mean model with a participant-level (p) random effect:

$$\theta_{pi} = \beta_0 + x_p\beta_{0p}\mu_{pi} = \exp(\theta_{pi})\beta_{0p} \sim N(\mu_p, \sigma_p)y_p \sim \text{Pois}(\mu_{ij})$$

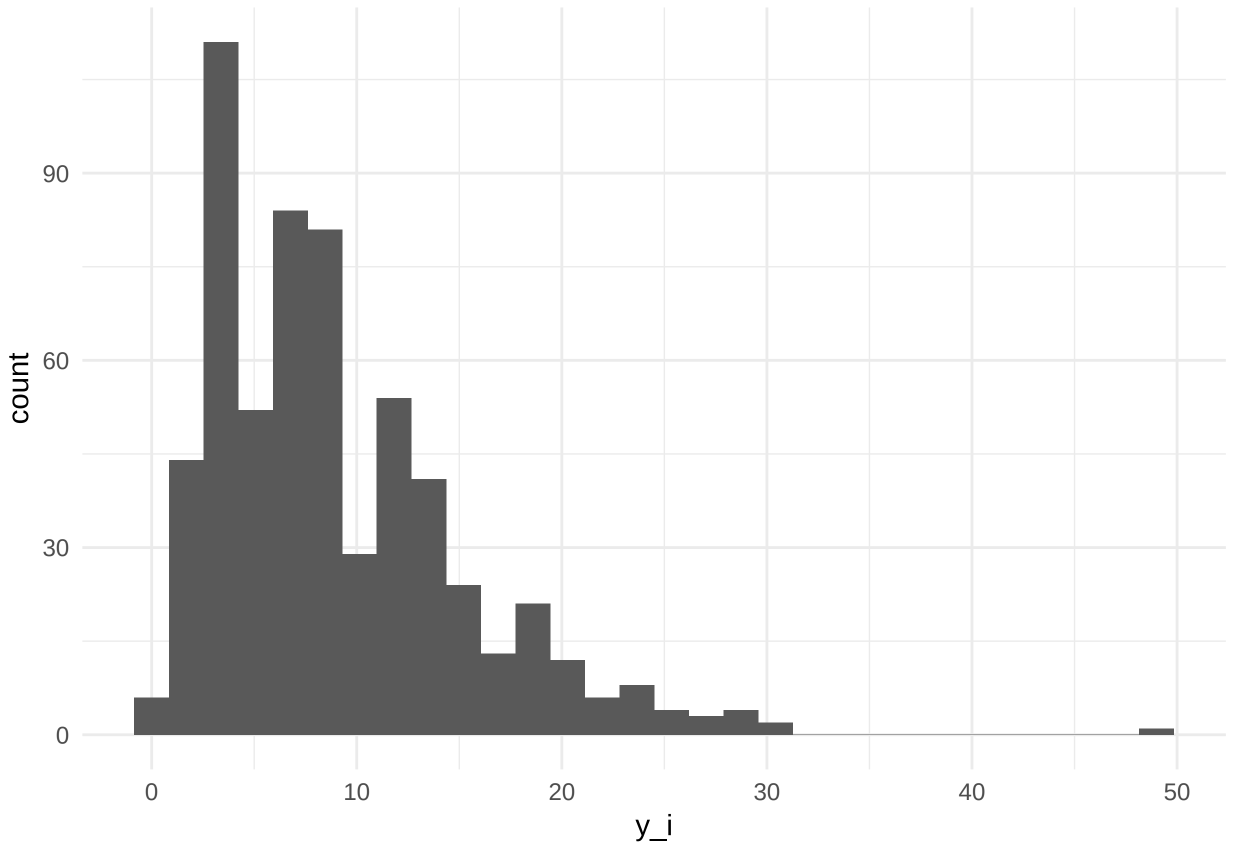
The OLRE is normally distributed but does not cause any bounded-range range, as it is added on the level of the linear predictor, before applying the exponential transformation. Observation-level random effects are completely analogous, except that every observation becomes its own group, in a Poisson grand mean model with added variation:

$$\theta_i = \beta_0 + \beta_i\mu_i = \exp(\theta_i)y_{ij} \sim \text{Pois}(\mu_{ij})$$

See, how β_i is a unique deviation per observation i, and how a variance parameter σ appears in an otherwise purely Poisson model. Observation-level random effects are on the linear predictor level, and therefore additive. Compare this to the negative binomial distribution where variance is scaled up, which is multiplication. We find a resemblance with how sums on the linear predictor become multiplications on the expected values scale.

For demonstration of the concept, we simulate from an overdispersed Poisson grand mean model with participant-level random effects, and recover it via regression.

```
sim_ovdsp <- function(
  beta_0 = 2,    # mu = 8
  sd_Obs = .3,
  sd_Part   = .4,
  N_Part = 30,
  N_Rep  = 20,
  N_Obs =  N_Part * N_Rep,
  seed = 42){
  set.seed(seed)
  Part <- data_frame(Part = 1:N_Part,
                     beta_0p = rnorm(N_Part, 0, sd_Part)) ## participant-level RE
  D <- data_frame(Obs  = 1:N_Obs,
                    Part = rep(1:N_Part, N_Rep),
                    beta_0i = rnorm(N_Obs, 0, sd_Obs),   ## observeration-level RE
                    beta_0 = beta_0) %>%
    left_join(Part) %>%
    mutate(theta_i = beta_0 + beta_0p + beta_0i,
           mu_i    = exp(theta_i),               ## inverse link function
           y_i     = rpois(N_Obs, mu_i))
  D %>% as_tbl_obs()
}

D_ovdsp <- sim_ovdsp()

D_ovdsp %>%
  ggplot(aes(x = y_i)) +
  geom_histogram()
```



```
## [1] "sim_ovdsp" "D_ovdsp"
```

```r
M_ovdsp <-
  D_ovdsp %>%
  stan_glmer(y_i ~ 1 + (1|Part) + (1|Obs), data = .,
             family = poisson, iter = iter)
```

Random effect variation is accurately recovered from the simulated data. The following two plots show, the participant latent scores can be recovered and even the observation levels themselves. Every observation gets an accurate measure of how much it had been pushed by unrecorded sources of variation. Practically, we obtain residuals which can be used for model criticism. For example, extreme outliers can be identified and relations between random variation and predicted values (or groups) are open to scrutiny.

```r
grpef(M_ovdsp)
```

Table 15: Estimates with 95% credibility limits

re_factor	center	lower	upper
Obs	0.305	0.264	0.350
Part	0.536	0.403	0.719

Frequently, I reminded the reader to interpret parameters quantitatively, by translating their magnitude to statements of practical relevance. For random effects variance this isn't always straight forward. One possible way is to make comparative statements on the sources of variance *"the variance due to individual differences exceeds all other sources of variation taken together"*. OLREs are on the same scale as all other random effects in the model, which makes it a good default reference. A non-default comparison of sources of variance is the one of Dennis Egan, that people cause more variance than designs do. With GLMM, the marriage of LMM and GLM this claim is testable.

From LMM we borrow a surprisingly simple and general solution, observation-level random effects. So, most of the time we won't need one of those twisted two parameter random distribution to account for overdispersion. With OLRE models we get an estimate that is very similar to a *residuals*, which have proven very useful in model criticism.

```
## [1] "sim_ovdsp" "D_ovdsp"
```

Exercises:

Measures of time

Time is a highly accessible measure, as clocks are all around us: on your wrist, in transport stations, in your computers and a very big one at Physikalisch-Technischen Bundesanstalt in Braunschweig (Germany). Temporal variables often carry useful information. *Reaction time (RT)* measures are prime in experimental cognitive studies and have revealed fascinating phenomena of the human mind, such as the Stroop effect and priming. In user studies and design research *time-on-task (ToT)* is a common measure for efficiency, with quicker being the better.

Temporal variables are practically continuous (as long as one measures with sufficient precision), but have lower bounds. A large number of statistical distributions are routinely used to model temporal variables. However, those do not always apply well to ToT or RT data, as they assume a lower bound of zero, which is unrealistic. Still, we begin with two of such models, exponential and gamma regression, and present a candidate for ToT data with offset as third (exgaussian regression).

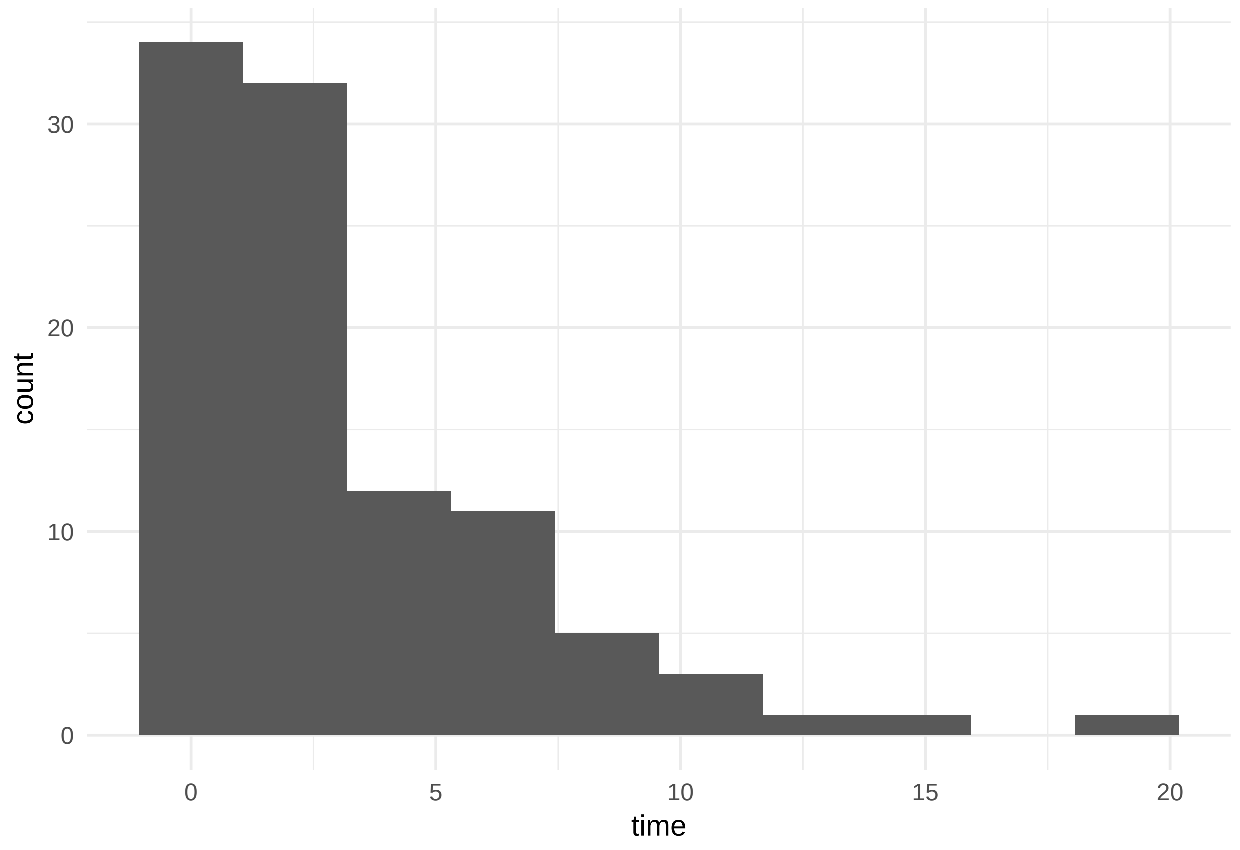
Exponential regression

Exponentially distributions arise from random processes under some very idealized conditions. First, the lower boundary must be zero and second, the waiting time of any event in a series is completely independent, i.e. not predictable, from how long one has been waiting so far. This is also called the property of *being memoryless*. In physics memoryless processes are observed only in the simplest systems, such as the time between two nuclei of a radioactive isotope to decay. Examples of memoryful processes are plenty, such as:

- earthquakes are essentially relaxations in the earth crust. Once it happened, it is less likely to reoccur in near future.
- participants learn with every trial or task, making shorter times more likely

Reconsider the subway smurfer example, where players collect items in a jump-and-run game. We have already seen how collection counts can be modelled using Poisson or binomial regression. Another way to look at it is the time between two events of item collection. For demonstration only, we assume such idealized conditions in the subway smurfer example and generate a data set. Exponential distributions are determined by one parameter, the *rate* parameter λ, which is strictly positive. The mean of an exponential distribution is the inverse $\mu = 1/\lambda$ and the variance is $\text{Var} = 1/\lambda^2$

```
set.seed(20)
D_exp <-
  data_frame(Obs = 1:100,
  time = rexp(100, rate = 1/3))

D_exp %>%
  ggplot(aes(x = time)) +
  geom_histogram(bins = 10)
```



```
mean(D_exp$time)
```

```
## [1] 3.29
```

```
var(D_exp$time)
```

```
## [1] 12.4
```

As the `stan_glm` engine does not support exponential response distributions, we use `brm`, instead, and recover the parameter.

```
M_exp <- brm(time ~ 1,
             family = "exponential",
             data = D_exp)
```

```
fixef(M_exp, mean.func = exp)
```

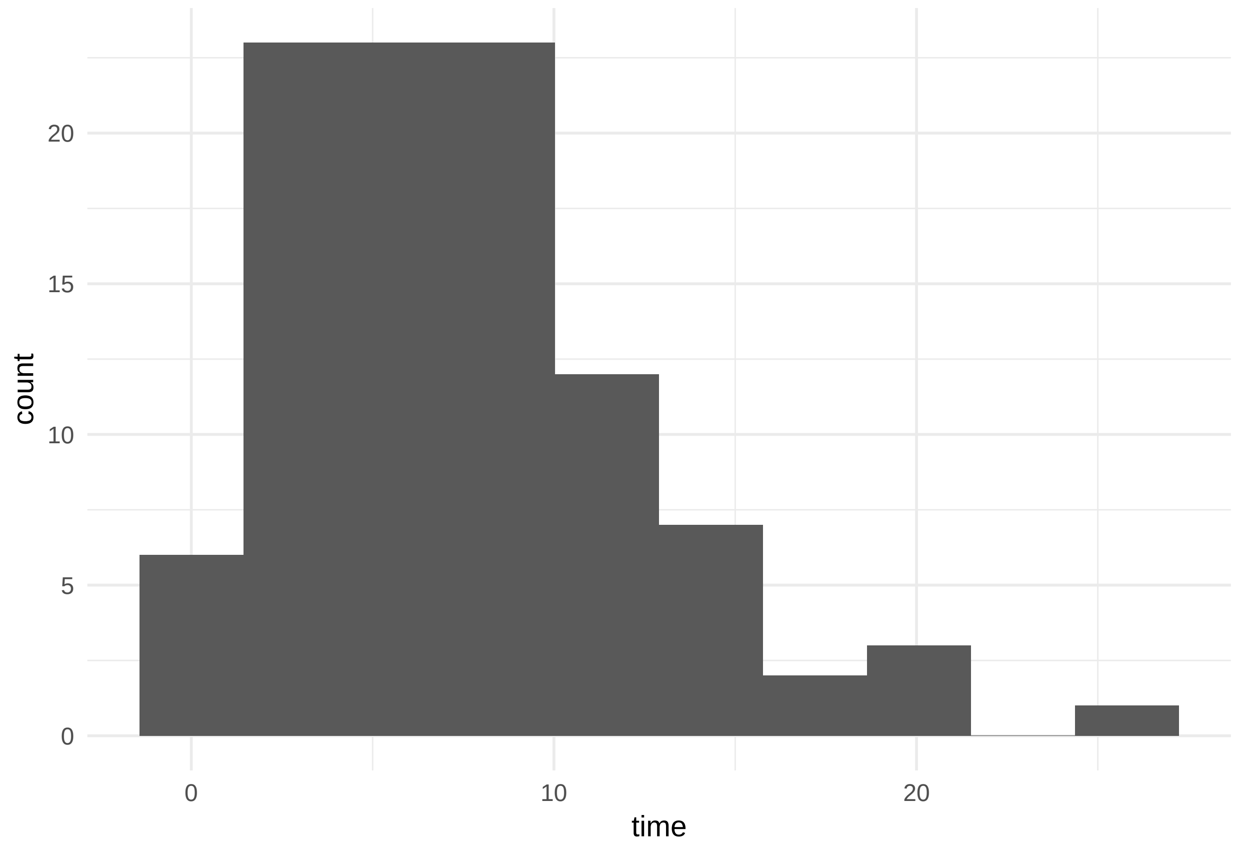
Table 16: Estimates with 95% credibility limits

type	fixef	center	lower	upper
fixef	Intercept	3.29	2.73	4

Gamma regression

Exponential regression has a single parameter and therefore has the same problem as seen with Poisson and binomial regression before. Only if all events have the same probability to occur, will an exponential distribution arise, which for behavioural research means: never. Again, one could solve this by introducing an observation-level random effect. Instead, here we will tackle the problem by using a continuous, zero-bounded distribution with two parameters, the gamma family of distributions. While the two parameters rate and shape do not directly translate into location and dispersion as with Gaussian, it provides the extra degree of freedom to set them almost independently. The only limitation is that variances rises with the mean, but as we have argued in @ref(assume-constant-variance), this is rather a desired feature than a problem. In the following, we simulate gamma distributed observations.

```r
set.seed(20)
D_gam <-
  data_frame(Obs = 1:100,
  time = rgamma(100, rate = 1/3, shape = 2))

D_gam %>%
  ggplot(aes(x = time)) +
  geom_histogram(bins = 10)
```



```r
mean(D_gam$time)
```

```
## [1] 7.61
```

In comparison to the exponential distribution above, a significant difference is that the mode of the gamma distribution (its peak) is not fixed at zero, but can move along the x-axis. That makes it appear a much more realistic choice for temporal data in behavioural research. We estimate a simple gamma GMM on the simulated data. For historical reasons, `brm` uses the inverse link function ($\theta = 1/\mu$) for gamma regression per default, but that does not actually serve the purpose of link functions to stretch μ into the range of real numbers. Instead, we resort to the common log link.

```
M_gam <- brm(time ~ 1,
             family = Gamma(link = log),
             data = D_gam)

M_gam
```

```
fixef(M_gam, mean.func = exp)
```

Table 17: Estimates with 95% credibility limits

type	fixef	center	lower	upper
fixef	Intercept	7.64	6.7	8.71

Both, the exponential and the gamma distributions support the range of real numbers, including zero. The weak point of both models is that they have zero as their natural starting point. For the exponential distribution that even goes to the extreme, that zero always is the point of highest density, i.e. the most likely outcome. As we will see in the following section, that assumption is usually violated with RT and ToT data, and exponential and gamma regression should be avoided. So, what are they good for, after all? These two models are routinely used for the *time intervals (TI)* between events that are triggered independently. In nuclear physics the individual triggers are atoms, each one *deciding on their own* when to emit a neutron. If you measure the interval between two emissions the time interval is exponentially distributed. (And if you count the neutrons per time interval, the result is a Poisson distribution). An analogue situation arises for customer support systems. Customers are like atoms in that their decision to file a request is independent from each other, usually. By chance it can happen that the whole center is idle for 20 minutes, but it is equally possible that 20 customers call within a minute and some of them practically at the same moment. Overwhelmed hotline queues does not make people nhappy, when they have technical problems. When planning a support system, the risk of angry customers has to be weighed against the costs of over-staffing. A good design would hit a certain sweet spot and in the ideal case there would be a predictive model of inflow rate of customers. Whatever predictors such a model would have, the response distribution would probably be very much a gamma distribution. In contrast, when the events are the moments of completion in successive tasks performed by one user, the triggers are not independent and the measure cannot be arbitrarily small (unless, perhaps, you kill seven flies with a single strike).

ExGaussian regression

The problem with the two temporal models discussed so far is that they assume a RT or ToT of zero to be possible. In the case of exponential regression, this even is the most likely region. This assumption is not realistic in most cases, as any task uses up a minimum time to complete. For example, the table below shows the minimum reaction times for finding the academic calendar on ten university websites (case Egan). This varies a lot between designs, but is never close to zero. The last column puts the minimum observed ToT in relation to the observed range. On two of the websites, the offset was even larger than the obvserved range itself, hence the problem of positive lower boundaries is real in user studies.

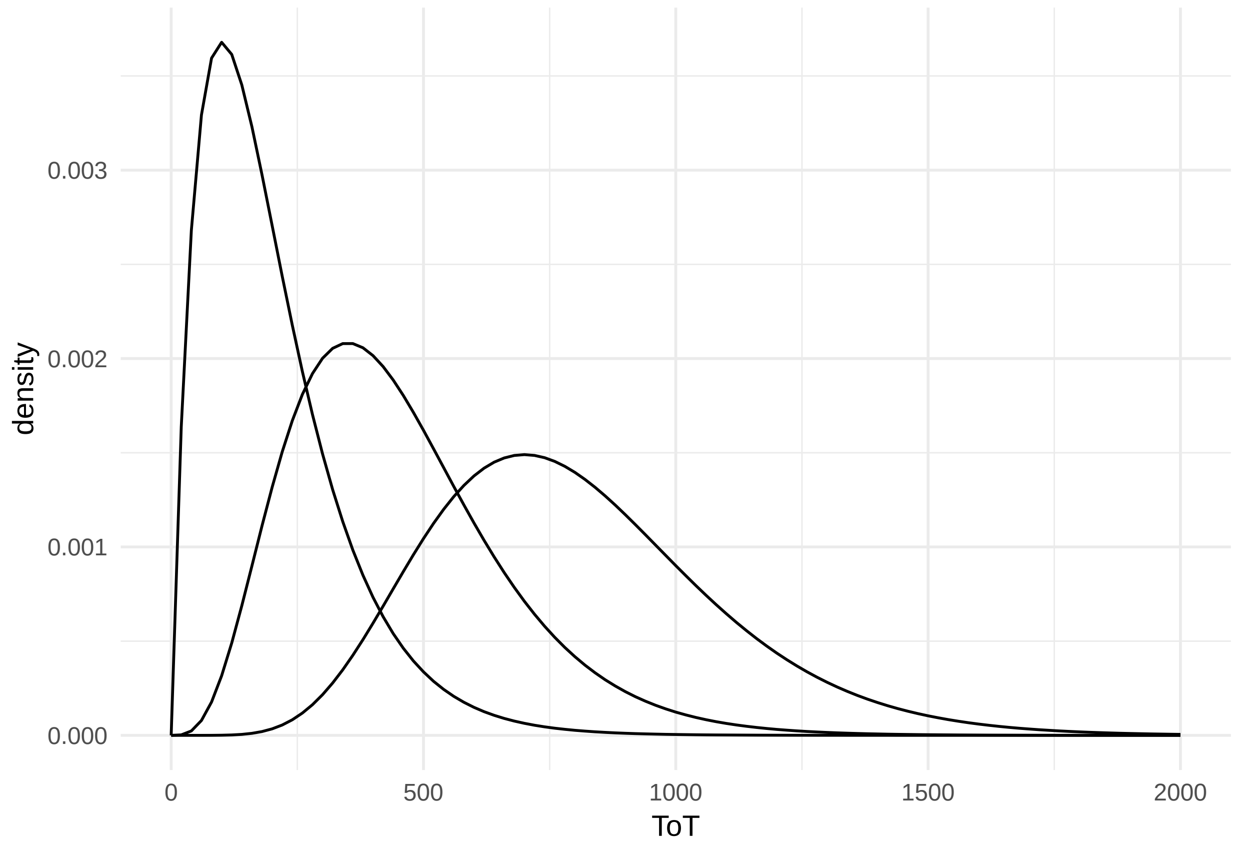
```r
attach(Egan)
```

```r
D_egan %>%
  filter(success,
         Task == "academic calendar") %>%
  group_by(Task, Design) %>%
  summarize(min_time = min(ToT),
            range = max(ToT) - min_time,
            min_time/range) %>%
  kable()
```

Task	Design	min_time	range	min_time/range
academic calendar	VU Brussel	21	130	0.162
academic calendar	KU Leuven	52	40	1.300
academic calendar	UGent	8	70	0.114
academic calendar	University of Antwerp	3	7	0.429
academic calendar	UHasselt	21	48	0.438
academic calendar	Leiden University	130	181	0.718
academic calendar	VU Amsterdam	207	188	1.101
academic calendar	RUG	119	132	0.902
academic calendar	University Tilburg	24	39	0.615

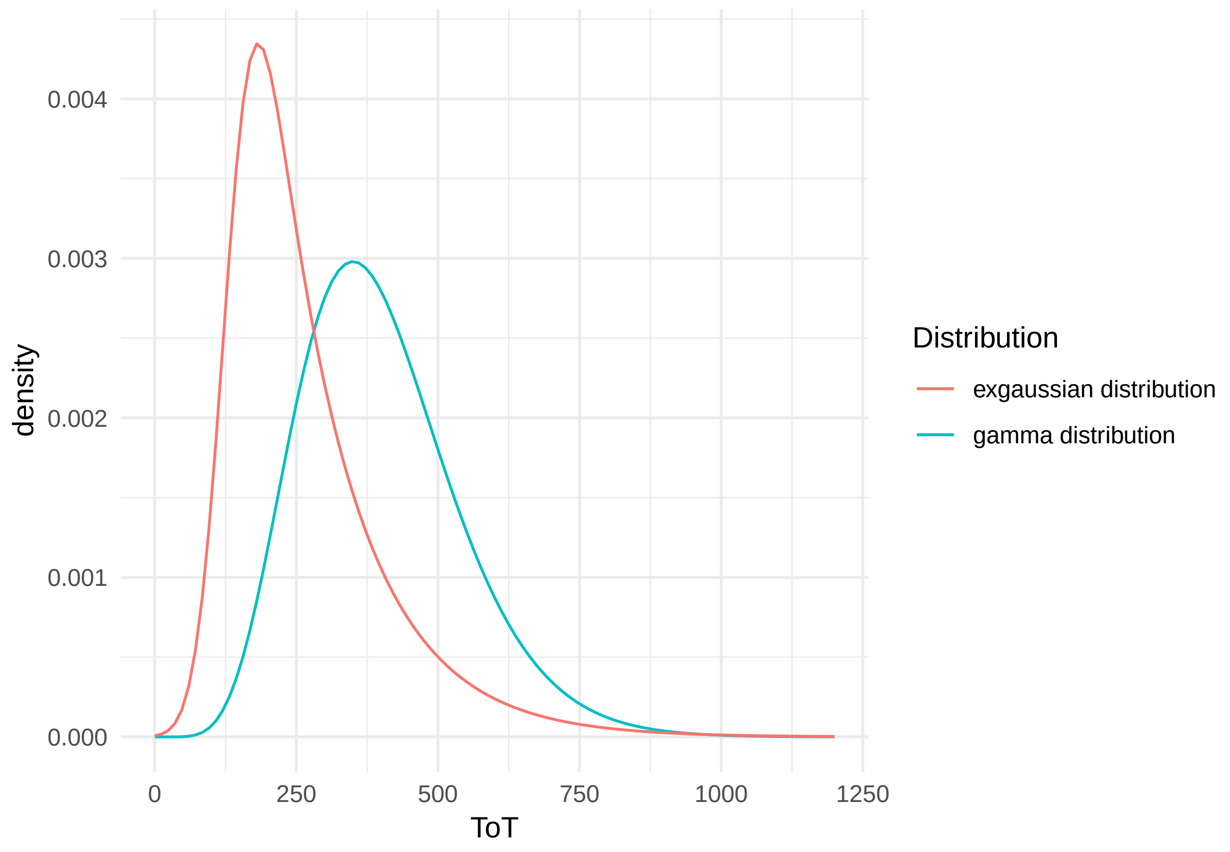
On the first glance, that does not seem to pose a major problem for gamma regression, as the mode can move along the x-axis. However, when a theoretical gamma distribution moves to the right, it inevitably becomes more symmetric, i.e. the skewness is reduced (and we may eventually use a Gaussian distribution, instead). As there is no separate parameter controlling the skewness of the curve it may happen that the random component captures the amount of variance, but overdoes the left tail, which introduces a bias on the coefficients. The following graphic illustrates that with a bunch of gamma distributions that move from left to right (`M`), keeping the variance constant (`V`):

```r
M = c(200, 300, 400)
V = 20000

## gamma
rate = M/V
shape = rate^2 * V

ggplot(data.frame(x = c(0, 2000)), aes(x = x)) +
  stat_function(fun = dgamma,
                args = list(rate = rate[1], shape = shape[1])) +
  stat_function(fun = dgamma,
                args = list(rate = rate[1], shape = shape[2])) +
  stat_function(fun = dgamma,
                args = list(rate = rate[1], shape = shape[3])) +
  labs(x = "ToT", y = "density")
```



We have seen so far, that distributions with one parameter (Poisson, binomial, exponential) have a fixed relationship between location and dispersion. In order to vary location and dispersion independently, a second parameter is needed (Gamma, Gaussian). It seems logical that only three-parameter distributions can do the trick of setting skewness separately. The exponentially modified Gaussian (exgaussian) distribution is a convolution of a normal distribution and an exponential distribution and has three parameters, μ, σ and rate β. Very roughly, the Gaussian component controls location and dispersion whereas the exponential part introduces the skewness. When β is large in comparison to μ, the distribution is more left skewed. By this additional degree of freedom it becomes possible to simulate (and estimate) distributions that are far to the right have strong dispersion *and* strong skewness. The following plot shows the density of an exgaussian and gamma distribution with the same mean and variance.

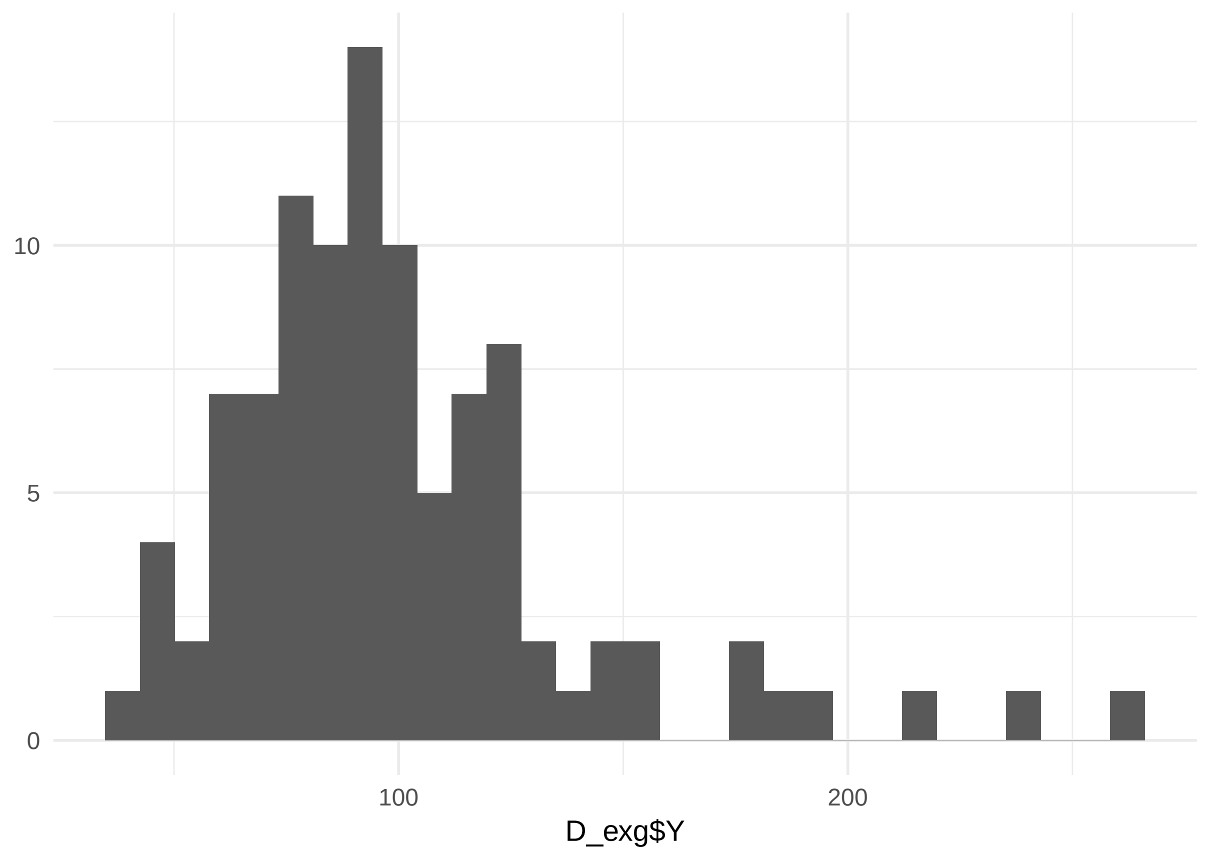
```
M = 400
V = 20000

## exgauss
beta = 135
mu = M - beta
sigma = sqrt(V - beta^2)

## gamma
rate = M/V
shape = rate^2 * V

ggplot(data.frame(x = c(0, 1200)), aes(x = x)) +
  stat_function(fun = dgamma,
                args = list(rate = rate, shape = shape),
                mapping = aes(colour = "gamma distribution")) +
  stat_function(fun = brms::dexgaussian,
                args = list(mu = mu,
                            sigma = sigma,
                            beta = beta),
                mapping = aes(colour = "exgaussian distribution")) +
  labs(colour="Distribution", x = "ToT", y = "density")
```



The gamma distribution in this example starts approaching a bell curved form, almost resembling a Gaussian distribution. In contrast, the exgaussian distribution takes a steep left climb followed by a long right tail, which is caused by its pronounced exponential component. We do the usual exercise to simulate a grand mean model and recover the parameters with the help of the fabulous `brm` engine:

```
attach(Chapter_GLM)
```

```
D_exg <- data_frame(Y = rexgaussian(100, mu = 100, sigma = 20, beta = 30))
qplot(D_exg$Y)
```



```
M_exg <- brm(Y ~ 1,
             family = exgaussian,
             data = D_exg)
```

```
fixef(M_exg)
```

Table 19: Estimates with 95% credibility limits

type	fixef	center	lower	upper
fixef	Intercept	99.4	92.9	107

Noteworthy, the brm engine uses the identity link function by default. While this is rather convenient for interpretation, it could theoretically lead to impossible predictions. As we will see later, the exgaussian is not immune, but *robust to impossible predictions* because of its tiny left tail. Any linear impact factor, like an experimental treatment can push it 150 ms to the left with insignificant risk of impossible predictions.

Modelling reaction times

In experimental studies, the *inertia of the nervous system* sets a limit larger than zero for reaction times. This is due to some hard electrochemical and biomechanical facts of the peripheral systems. Nerve cells and muscle fibers are slow working horses. The same goes for our minds. Arguably, they are blazingly fast at complex tasks, such as recognizing written words in the faintest colors and the bizarrest advertisements.

Still, there is a minimum time to retrieve an idea from the memories and activate the surrounding nodes, too.

As swift and enthusiastic most people are with words, the more clumsy and desinterested many are with computers. Today's consumer computing devices are unmatched in usability and most people don't need to think harder than they like, when hunting for the best online prices, stream movies and enjoy their communications. However, there is a minority of computer users, who call themselves the geek. The hypothetical geek personality feels attracted to the inner workings of a computer system itself, rather than the applications and media it delivers. A geek person seeing a computer is more likely to have certain memories or associations, for example, remembering how it was to build your first own computer, or the intellectual joy of learning a new programming language. If this were true, we thought, than showing a word that is related to how geeks perceive computers (e.g. "explore", "play", "create") should create a brief nostalgic moment, resulting in a delayed response. As a response we had choden the Stroop task, and in order to make this more likely, participants were primed by a picture shown before the Stroop task. These pictures were from two conditions: either showing computers in a geekish way (for example, an open case or programming code on the screen) or as regular product images. Furthermore, we theorized that the least one can say is that geeks like to think hard and therefore used the need-for-cognition scale as a predictor. It was expected that participants with high NCS scores would recognize computers as a source of delightful hard thinking and hence have slower reaction times, when priming image and target word are both from the category Geek.

What would be a suitable response distribution for reaction times in the semantic Stroop task? In the following, we run three models with the same predictor term, but with exgaussian, gamma or Gaussian random components.

```r
attach(Hugme)
```

```r
D_hugme <-
  filter(D_hugme, correct) %>%
  select(Obs, Part, zNCS, WordGeek, PrimeGeek, RT) %>%
  as_tbl_obs()
D_hugme
```

Table 20: Data set: showing 8 of 4152 observations

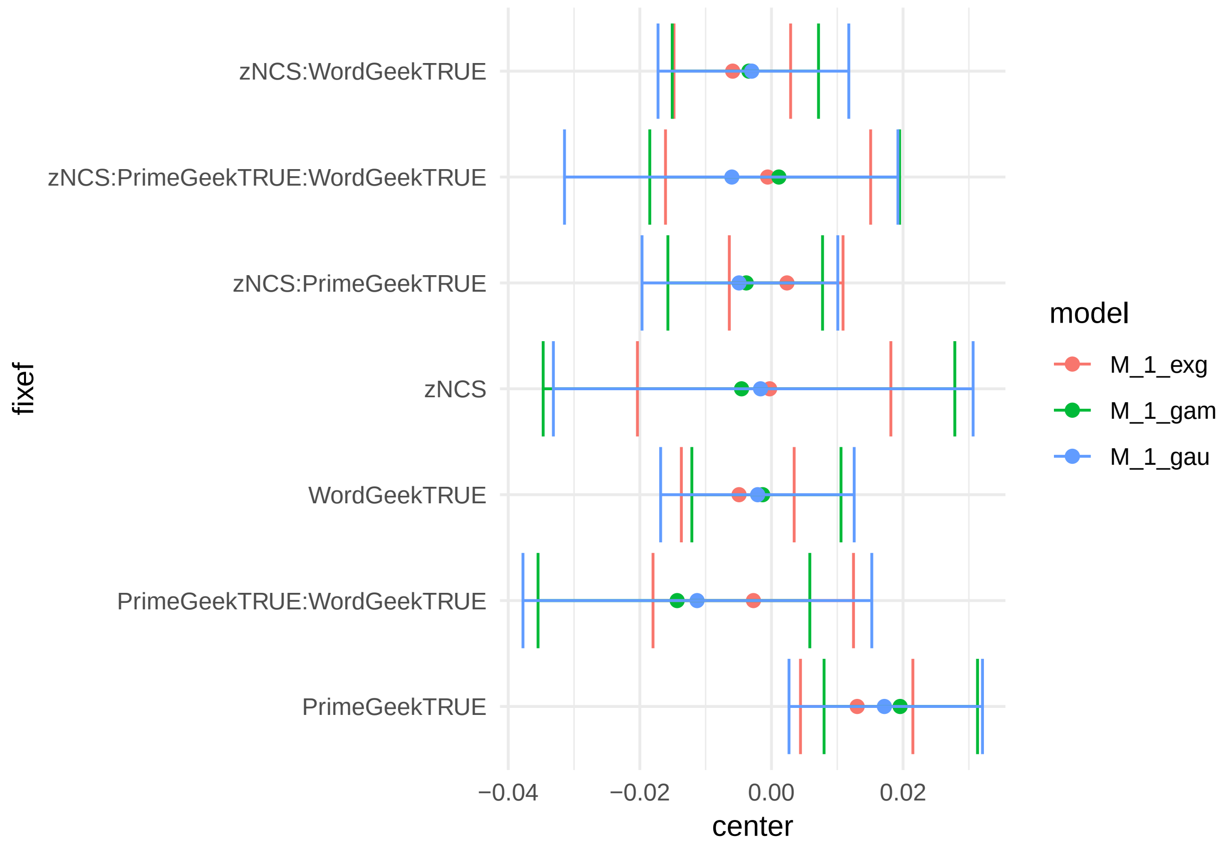
Obs	Part	zNCS	WordGeek	PrimeGeek	RT
3	1	0.318	FALSE	FALSE	0.656
1771	26	0.703	FALSE	FALSE	1.066
1885	28	0.382	FALSE	FALSE	0.798
2194	32	1.281	TRUE	FALSE	0.500
2798	54	-1.801	FALSE	FALSE	0.475
3595	66	-0.260	TRUE	FALSE	0.813
3608	66	-0.260	FALSE	FALSE	0.688
3996	78	-0.324	FALSE	TRUE	0.645

```r
F_1 <- formula(RT ~ zNCS*PrimeGeek*WordGeek + (1|Part))

M_1_gau <- D_hugme %>%
  brm(F_1,
      family = gaussian,
      data = .)
```

```r
M_1_exg <- D_hugme %>%
  brm(F_1,
      family = exgaussian,
      data = .)

M_1_gam <- D_hugme %>%
  brm(F_1,
      family = Gamma(link = identity),
      data = .)

P_1 <- bind_rows(
  posterior(M_1_gau),
  posterior(M_1_gam),
  posterior(M_1_exg)
)

T_1_predict <-
  bind_rows(
    post_pred(M_1_gau, thin = 5),
    post_pred(M_1_gam, thin = 5),
    post_pred(M_1_exg, thin = 5)
  ) %>%
  predict()
```

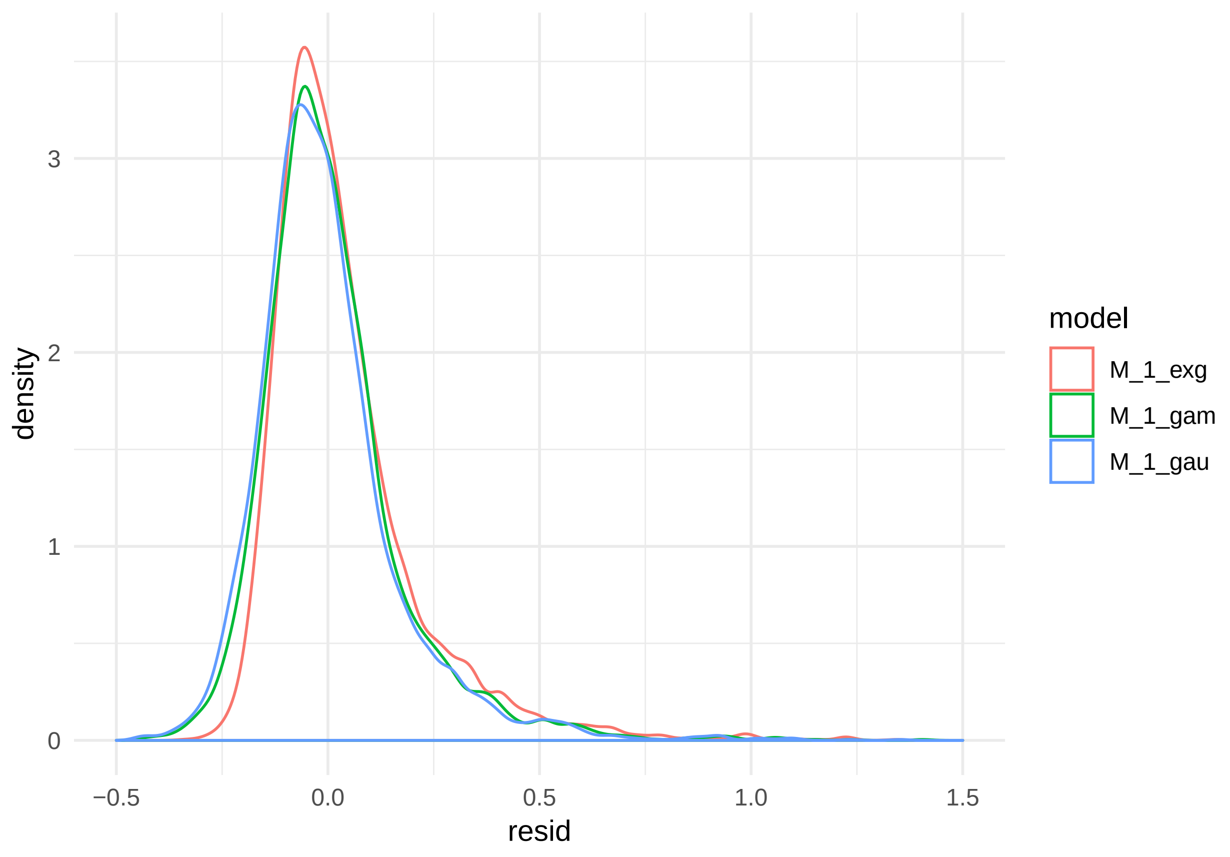
The following plot shows the fixed effects for the three random components:

```r
T_1_fixef <- fixef(P_1)

T_1_fixef %>%
  filter(fixef != "Intercept") %>%
  ggplot(aes(y = fixef, x = center, xmin = lower, xmax = upper, color = model, group = model)) +
  geom_point(size = 2) +
  geom_errorbarh()
```



None of the effects have considerable impact. Nevertheless, it seems that the Exgaussian model produces much tighter credibility limits, i.e. better degrees of certainty. In any case, if there is a reason to prefer the exgaussian model, we should primarily see that in how the residuals are shaped. In the following plot it can be seen, that the extra flexibility of the exgaussian is employed, indeed. Both, Gaussian and gamma are unable to accomodate the steep left climb and are producing a visible drag to the left.

```
D_hugme <- D_hugme %>%
  left_join(T_1_predict) %>%
  mutate(resid = RT - center)

D_hugme %>%
  ggplot(aes(x = resid, color = model)) +
  geom_density() +
  xlim(-.5,1.5)
```



Modelling Time-on-task

Although experimental psychologists call the Stroop task a complex one, the minimal processing time is rather short in comparison to tasks usually administered in usability studies, such as finding information on websites or renting cars online. We compare the three patterns of randomness on the CUE8 data set, which contains ToT measures on five tasks on a car rental website. In this study 14 professional teams took part with two conditions: remote and moderated sessions. As we will see in a later section, the remote condition is contaminated with cheaters. Therefore, we only use the moderated sessions. In addition, it is interesting to compare the impact of the chosen distribution on effects estimates. For this reason only, we include the factor Task as a fixed effect (with treatment contrasts), despite this not being very meaningful.

The comparison draws upon the effects, as well as residual distributions. For the latter, the predictive posterior distribution is required. With several hundred observations, this results in a very large object. To prevent running into the memory limit, we crank it up (`memory.limit`) and thin out the number of posterior predictive samples by factor 5. Finally, we combine the three posterior predictive distributions and examine the differences.

```
attach(CUE8)
```

```
D_cue8_mod <- D_cue8 %>%
  filter(Condition == "moderated", !is.na(ToT)) %>%
  as_tbl_obs()
```

```
memory.limit(16000)
```

```r
F_4 <- formula(ToT ~ 1 + Task + (1|Part) + (1|Team))

M_4_gau <- D_cue8_mod %>%
  brm(F_4,
      family = gaussian,
      data = .)

M_4_exg <- D_cue8_mod %>%
  brm(F_4,
      family = exgaussian,
      data = .)

M_4_gam <- D_cue8_mod %>%
  brm(F_4,
      family = Gamma(link = identity),
      data = .)

P_4 <- bind_rows(
  posterior(M_4_gau),
  posterior(M_4_gam),
  posterior(M_4_exg)
)


T_4_predict <- bind_rows(
  post_pred(M_4_gau, thin = 5),
  post_pred(M_4_gam, thin = 5),
  post_pred(M_4_exg, thin = 5)) %>%
  predict()
```

```r
fixef(P_4)
```

Table 21: Estimates with 95% credibility limits

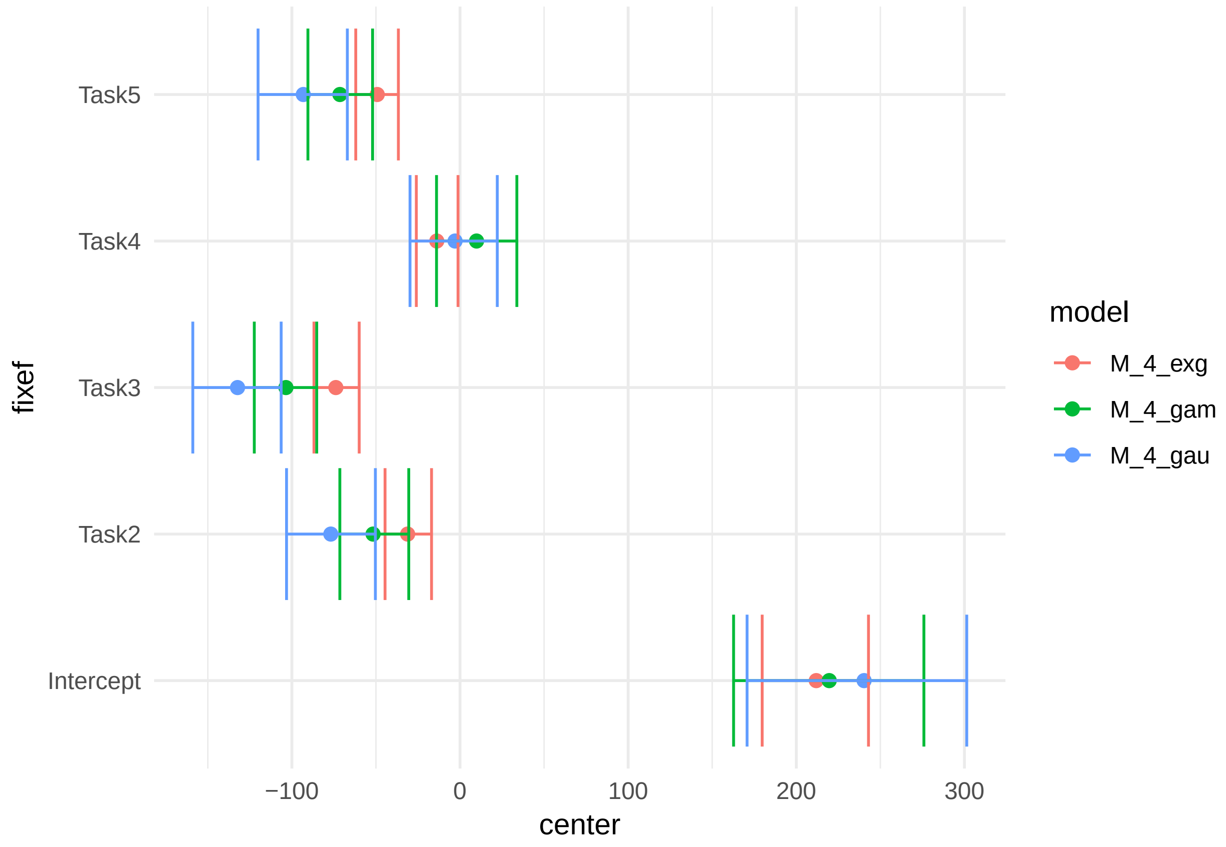
model	fixef	center	lower	upper
M_4_exg	Intercept	211.87	179.7	242.93
M_4_exg	Task2	-31.15	-44.6	-16.94
M_4_exg	Task3	-73.86	-86.9	-59.97
M_4_exg	Task4	-13.82	-26.0	-1.18
M_4_exg	Task5	-49.23	-62.0	-36.65
M_4_gam	Intercept	219.58	162.7	275.89
M_4_gam	Task2	-51.72	-71.5	-30.49
M_4_gam	Task3	-103.55	-122.4	-85.23
M_4_gam	Task4	9.84	-14.0	33.81
M_4_gam	Task5	-71.43	-90.5	-52.00
M_4_gau	Intercept	240.33	170.7	301.38
M_4_gau	Task2	-76.84	-103.2	-50.34
M_4_gau	Task3	-132.31	-158.9	-106.38
M_4_gau	Task4	-2.94	-29.7	22.16
M_4_gau	Task5	-93.21	-120.1	-67.02

```
grpef(P_4)
```

Table 22: Estimates with 95% credibility limits

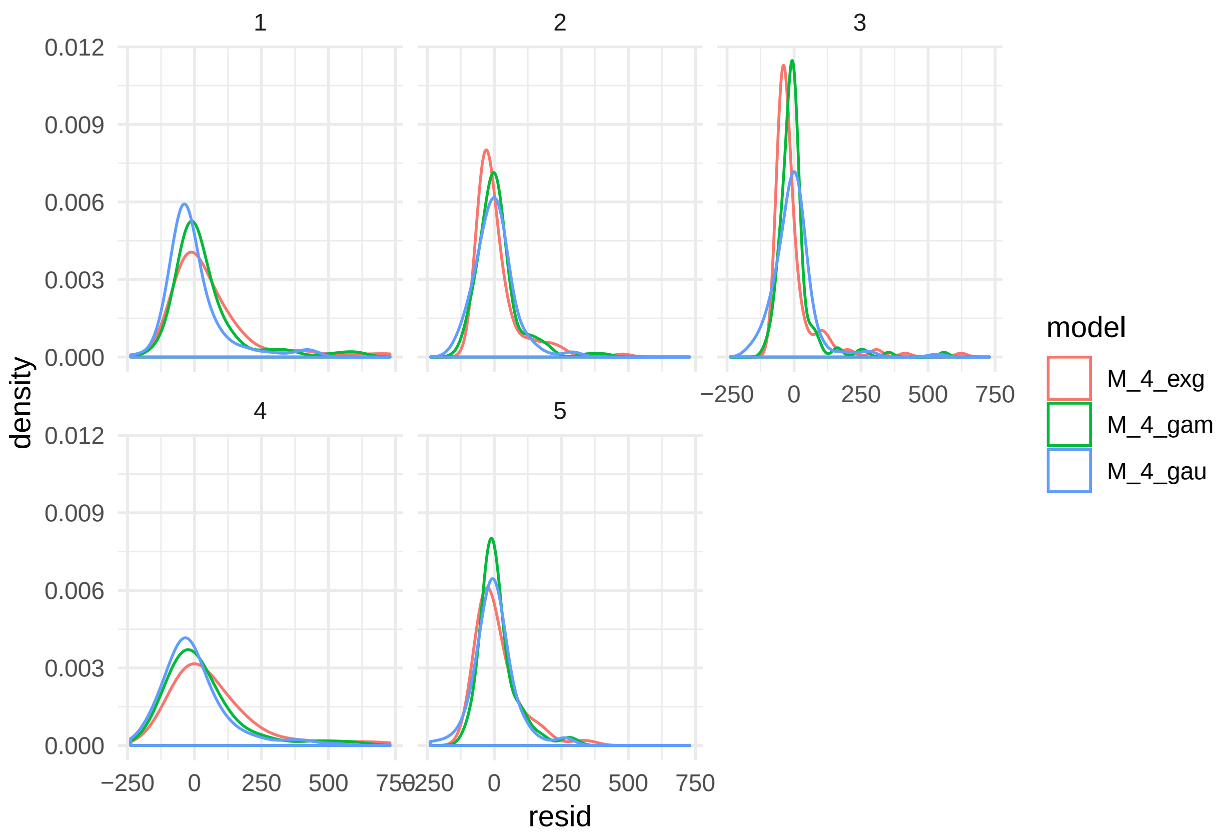
model	re_factor	center	lower	upper
M_4_exg	Part	23.4	16.2	31.5
M_4_exg	Team	37.3	21.4	76.5
M_4_gam	Part	40.2	29.3	52.0
M_4_gam	Team	71.6	42.0	141.5
M_4_gau	Part	65.2	52.4	80.2
M_4_gau	Team	82.2	47.3	157.0

```
fixef(P_4) %>%
  ggplot(aes(y = fixef, x = center, xmin = lower, xmax = upper, color = model)) +
  geom_point(size = 2) +
  geom_errorbarh()
```



As with reaction times, the three models produce rather different fixed effects estimates and with the tendency that the Gaussian, followed by the gamma model, exaggerates the effects. Again, the exgaussian model produces estimates of superior certainty.

```
D_cue8_mod %>%
  left_join(T_4_predict) %>%
  mutate(resid = ToT - center) %>%
  ggplot(aes(x = resid, color = model)) +
  facet_wrap(~Task) +
  geom_density(adjust = 2)
```



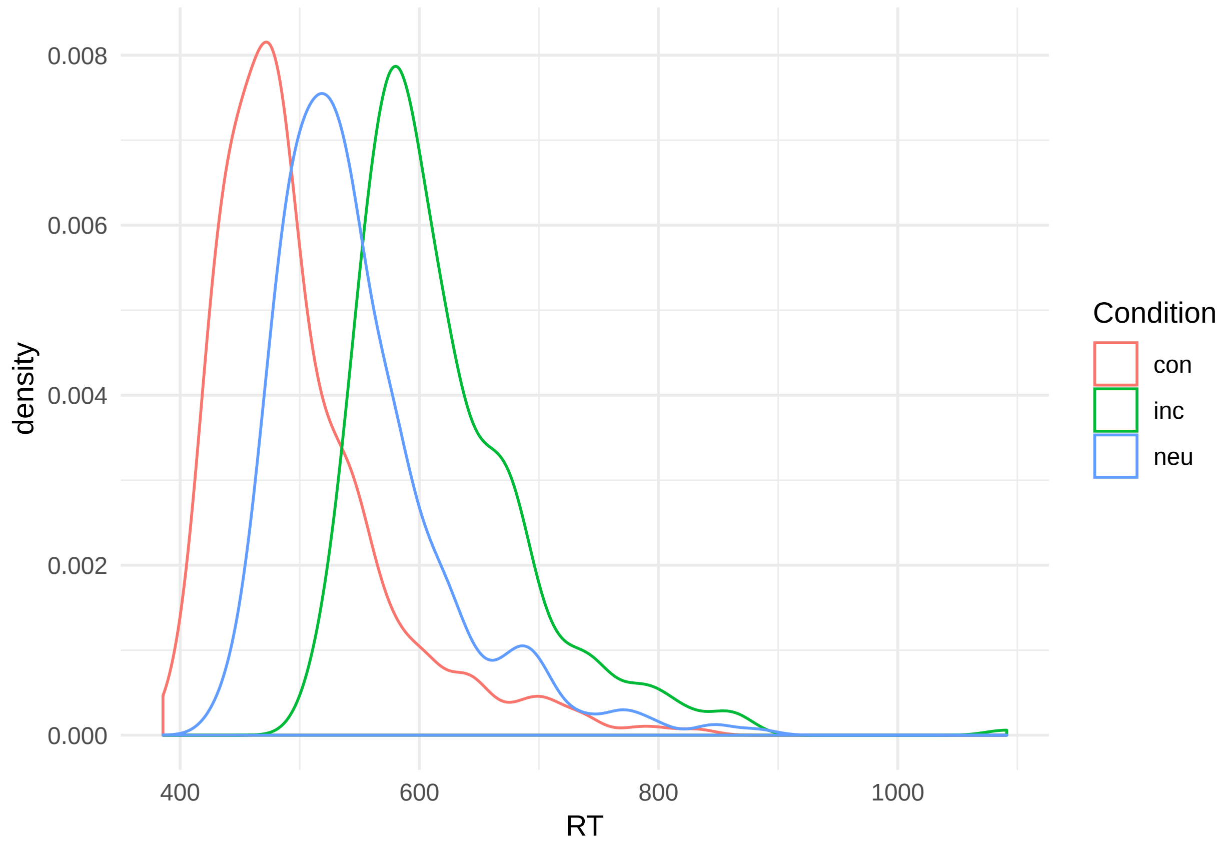
Inspecting the residual distributions yields a different pattern as with RT: generally, the left skewness is much less pronounced and Gaussian and gamma even tend to be right skewed. Strikingly, the residuals of the exgaussian models sit much tighter around the center, which corresponds with the narrower credibility intervals for the fixed effects.

In general, it seems that the exgaussian model for RT and ToT accomodates left skewness better and produces estimates that are more conservative and certain at the same time. Could it be true, that Gaussian and gamma models overestimate group mean differences for left skewed RT and ToT responses? We examine this possibility by simulating a well-known experiment using an exgaussian distribution.

```
sim_Stroop <- function(beta_0 = 500, # congruent
                       beta_1 = 50,  # neutral
                       beta_2 = 120, # incongr
                       sigma = 20,
                       beta = 70,
                       N = 400,      # obs per condition
                       seed = 42){
  set.seed(seed)
  data_frame(Condition = rep(c("con", "neu", "inc"), N),
             mu = beta_0 + beta_1 * (Condition == "neu") + beta_2 * (Condition == "inc"),
             RT = rexgaussian(N * 3, mu, sigma, beta)) %>%
    as_tbl_obs()
  }

D_stroop <- sim_Stroop()

D_stroop %>%
  group_by(Condition) %>%
  summarize(mean(RT)) %>%
  kable()
```

Condition	mean(RT)
con	497
inc	619
neu	549

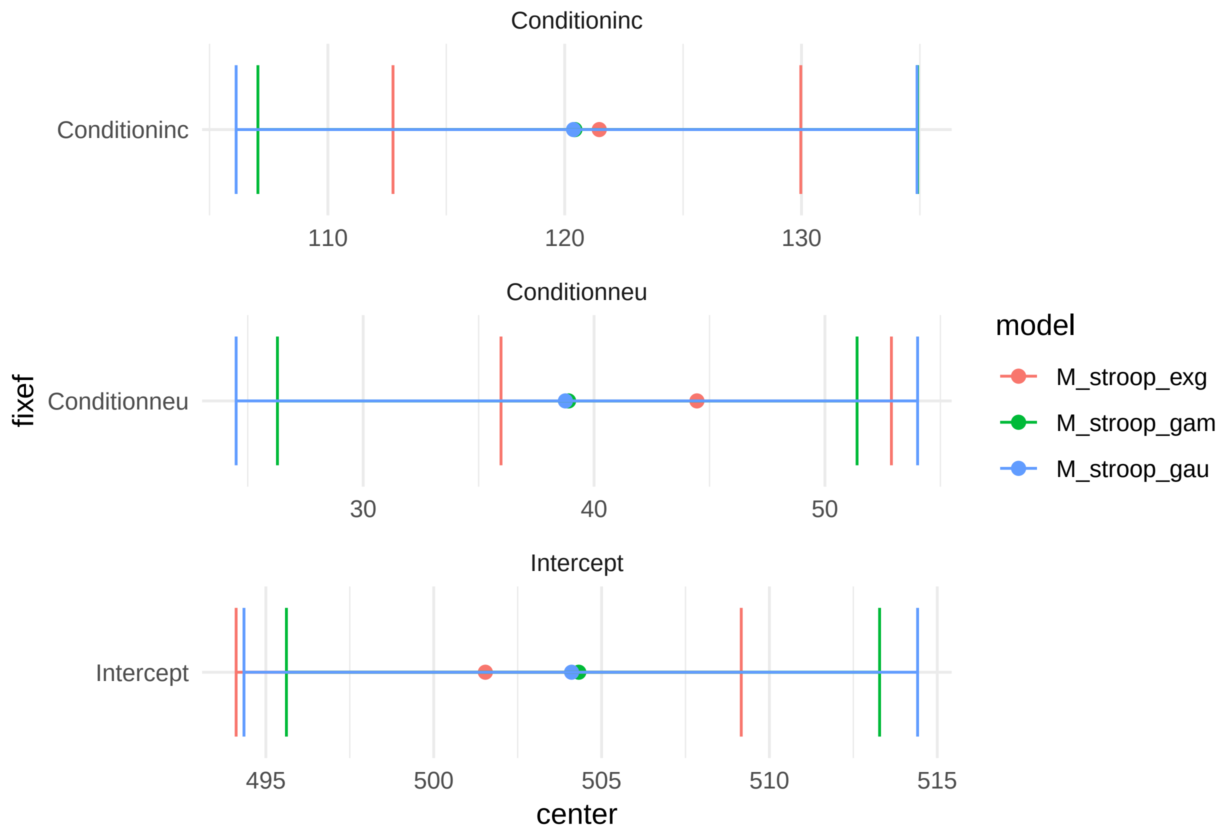
```
D_stroop %>%
  ggplot(aes(x = RT, col = Condition)) +
  geom_density()
```



In the same way as above, we recover the effects by three models that have the same likelihood, but differ in their response distribution.

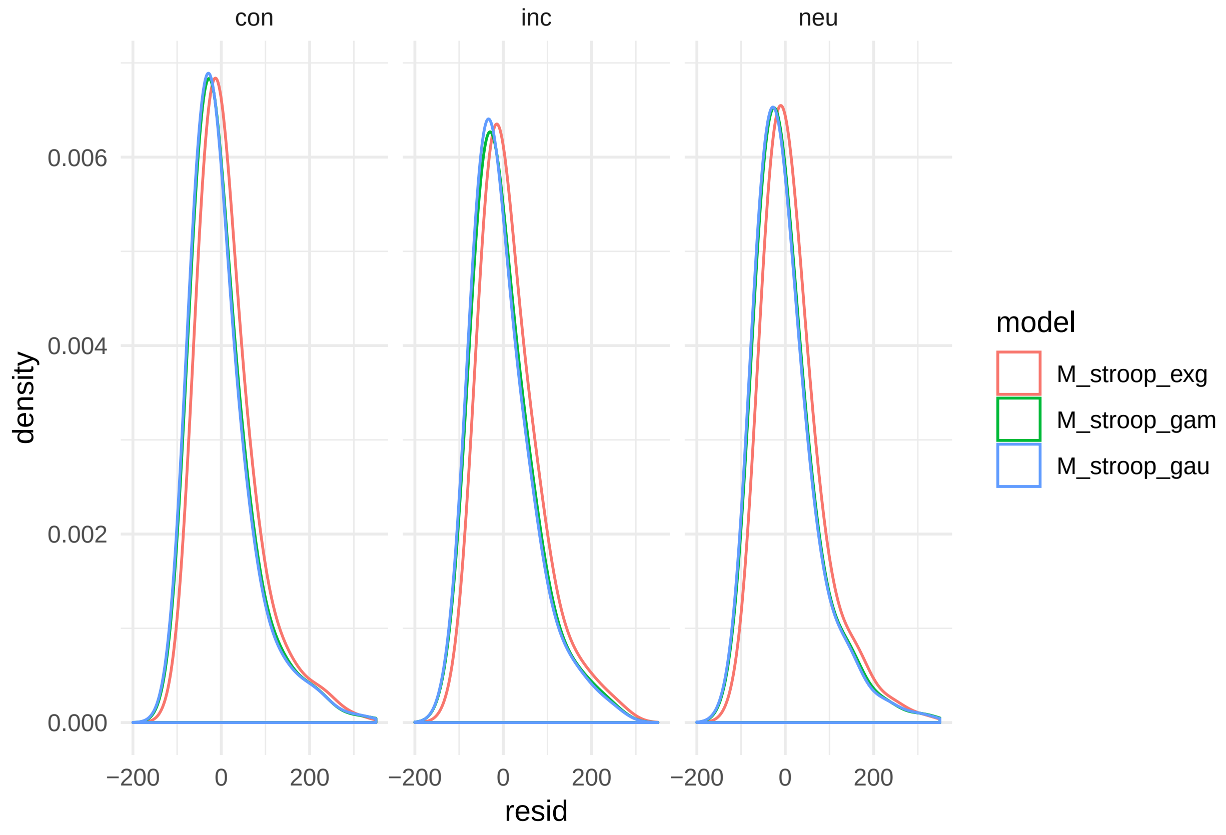
```r
F_stroop <- formula(RT ~ Condition)

M_stroop_gau <- D_stroop %>%
  brm(F_stroop,
      family = gaussian,
      data = .)

M_stroop_exg <- D_stroop %>%
  brm(F_stroop,
      family = exgaussian,
      data = .)

M_stroop_gam <- D_stroop %>%
  brm(F_stroop,
      family = Gamma(link = identity),
      data = .)

P <- bind_rows(
  posterior(M_stroop_gau),
  posterior(M_stroop_gam),
  posterior(M_stroop_exg)
)


T_stroop_predict <- bind_rows(
  post_pred(M_stroop_gau, thin = 4),
  post_pred(M_stroop_gam, thin = 4),
  post_pred(M_stroop_exg, thin = 4)
) %>%
  predict()
```

```r
fixef(P_stroop) %>%
  ggplot(aes(y = fixef, x = center, xmin = lower, xmax = upper, color = model)) +
  facet_wrap(~fixef, ncol = 1, scales = "free") +
  geom_point(size = 2) +
  geom_errorbarh()
```



What is confirmed by the simulation is that the exgaussian model, when it is the true one, produces more certain estimates.

```
D_stroop  %>%
  left_join(T_stroop_predict) %>%
  mutate(resid = RT - center) %>%
  ggplot(aes(x = resid, color = model)) +
  facet_wrap(~Condition) +
  geom_density(adjust = 2) +
  xlim(-200, 350)
```



Different to what has been observed above, the shape of residual distributions do not differ much in shape, except for a shift offset to the right. What could be accountable for that is that the simulation only contained three homogenous groups, rather than the many groups in the previous multi-level data sets (random factors). It remains to be clarified what precisely the biases and drags are caused by ill-specified response distribution for RT and ToT in complex research designs. Despite these question marks, it has been confirmed that the superior certainty of estimates is not just an artifact of the exgaussian model, but is real and likely to make quantitative inference from RT and ToT data more efficient.

One last issue remains to get clarified: using the identity link for exgaussian models is very convenient and is probably much safer as compared to Gaussian models with their longer left tails. But, what risk is there to get impossible, i.e. negative, predictions? We check this on the posterior predictive distributions of both studies, CUE8 and Hugme. The following table shows the proportion observations, that get a negative 2.5% credibility limit assigned:

```
bind_rows(Hugme$T_1_predict, CUE8$T_4_predict) %>%
  group_by(model) %>%
  summarize(mean(lower < 0)) %>%
  kable()
```

model	mean(lower < 0)
M_1_exg	0.000
M_1_gam	0.000
M_1_gau	0.000
M_4_exg	0.029
M_4_gam	0.000
M_4_gau	0.714

For our RT data, impossible predictions is not a big issue with any of the models, as all 2.5% quantiles are positive. That is different for ToT: while the gamma model is inherently immune to negative predictions, the exgaussian model produced a few impossible lower 2.5% limits (around 3%). The Gaussian model is extremely off: more than 70% of all predictions have impossible lower 2.5% limits.

In the scientific literature, the coverage on what random pattern to use for RT and ToT data is meager at this moment. Probably, that is due to the lack of user-friendly engines supporting the more exotic GLM family members, gamma or exgaussian regression. The brms engine covers a much broader set of distributions than any other implementation before and researchers have the choice. This chapter attempted to provide theoretical arguments as well as empirical indications that the exgaussian regression is a better choice than Gaussian and gamma. First of all, it accomodates the strong left skew of RT and ToT much better than the gamma, which takes a too symmetric form when far from the left boundary. Second, it is reasonably robust to impossible predictions, even when using the convenient identity link function. Third, and that is almost too good to be true, it massively improves certainty in predictors. Possibly, exgaussian models are more efficient for carving out delicate cognitive effects in comparison to Gaussian models (not to mention non-parametric tests).

However, as the discussion has not even fully started, to declare it settled would be premature. In contrast, the aim of this chapter was to illustrate a semi-formal approach that reseachers can follow to choose among the candidate models for their specific RT and ToT data. Data from other RT paradigms might take different shapes. For example, when measuring RT by events in EEG signals (rather than actual key presses), motor time plays a much smaller role, pushing RTs closer to the left boundary. Then, the exgaussian model might produce higher rates of impossible predictions and the gamma model could sufficiently accomodate the left skewness. Note that even using a log link on the exgaussian model can produce visits to the negative range. When both accomodate the left skew equally well, the gamma model is to be preferred as it never produces impossible predictions and is more parsimomous.

That being said, the brms engine offers even more opportunities. First, it supports two more distributions with an offset component: the shifted log-normal and the Wiener distribution. Interestingly, the latter grounds on one of the few formally specified cognitive process models, the diffusion model for simple choice tasks. All four parameters of the Wiener distribution are directly linked to individual elements of the cognitive process. This brings us to the second relevant extension of brms, which I will not fully cover, but is worth mentioning: *distributional models*. The vast majority of statistical analysis capitalizes on the location parameters. We ask whether an increase in a continuous predictor causes an increase in the outcome or if one group has a higher average than the other.

Only in the analysis of random effects have we drawn conclusions from dispersion parameters, such as to test Egans claim. In design research, the variance in performance is a crucial issue. To give another example: reportedly, several areas of cognitive functioning deteriorate with age, on average, but variance typically increases. It was the very idea of Dennis Egan that designs should not just improve performance on average, but also keep variance at a minimum. Hence, linking variance to predictors, such as design and age, can be a fruitful endeavour under the paradigm of robust designs. For RT the beforementioned Wiener distribution matches RTs in simple choice tasks and every parameter corresponds with an element in the so called diffusion model. In design research, such ideas are almost unexplored. Perhaps, one day a researcher finds that the gaussian and the exponential component are influenced by different design features.

Literature

Exercises:

1. Review the literature on reaction times. What is the shortest time length you can find?

2. The user can only do things one after the other and therefore, RT and ToT will never come close to zero. Conceive examples of independently triggered events that *happen* to users and effect user satisfaction.

Rating scales

In classic design research of the last millenium, die-hard Human Factors researchers have mainly been asking objectively sounding questions, like:

- Can a user achieve accurate results with the system?
- Can they do so in less time?
- Is the number of errors reasonably confined?

For professional, and especially critical, systems, these are highly valid questions, indeed. The purpose of a medical infusion pump is to improve the health status of a patient by accurately and reliably delivering medication into the bloodstream and the extent to that this is happening can be measured dircetly.

However, starting with the 1990s, wave after wave of novel electronic entertainment systems and digital gadgets rolled over the comsumer mass market. The purpose of a video recorder or a smartphone is to deliver joy … and to be sold in large batches. The sole purpose of a commercial website is to sell and nothing else. With the new millenium, design researchers began to recognize what consumer psychologists had discovered two decades earlier: users are not rational decision makers in a utilitarian sense. When people decide to adopt (or buy) a new system, this is only partly driven by their expectation of productivity. These additional expectations are commonly called *hedonistic values* and cover a broad class of human needs, such as:

- positive emotions
- expression of self
- social connectedness
- aesthetic perception
- personal growth

Whether or not these concepts are well-defined from a psychological point-of-view is beyond the scope of this book. What matters is that these concepts are so elusive that the most sincere researchers have not yet found objective criteria to measure them. Instead, almost everyone resorts to use of *self-report rating scales*, like this one:

How beautiful do you perceive the user interface to be?

unattractive 1 – 2 – 3 – 4 – 5 a piece of art

If you use a 5 point rating scale like this one to measure perceived beauty, participants have to convert their guts feeling into a number, which involves the following three processes somewhere in their minds:

1. anchoring
2. introspection
3. binning

By *anchoring* participants establish an idea of how ugly or beautiful something has be to get an extreme rating of 1 or 5. These imaginary endpoints define the *absolute range* of the rating scale. The researcher might early on give explicit or implicit cues to let the participant guess the range the researcher has in mind. If an experiment is overtly about web design, then probably "very ugly" means the least attractive commercial website the participant can think of. However, participants old enough to remember web design in its infancy (say the early attempts of disney.com), they may end up with a lower anchor than today's kids. If too few cues are given upfront, participant will probably adjust their anchors to the stimuli they see throughout the experiment. Probably, it will make a difference for what 1 or 5 mean, when the set of stimuli contain just websites, or websites *and* impressionist paintings *and* screenshots from 1980 splatter movies.

By *introspection* participants intuitively assess the intensity of their *real feelings* as compared to the anchors. Reportedly, feelings are influenced by:

1. visual simplicity
2. prototypicality
3. second exposure
4. Gestalt principles
5. fluency of processing
6. attribute substitution heuristics
7. color aesthetics
8. fashion
9. previous stimuli
10. current mood
11. a person's history
12. and cultural background

By *binning* the participant mentally divides the absolute range into five categories that are either fuzzy or defined by stereotypes, like "It must look at least as elegant as the website of Mapple to get a 4."

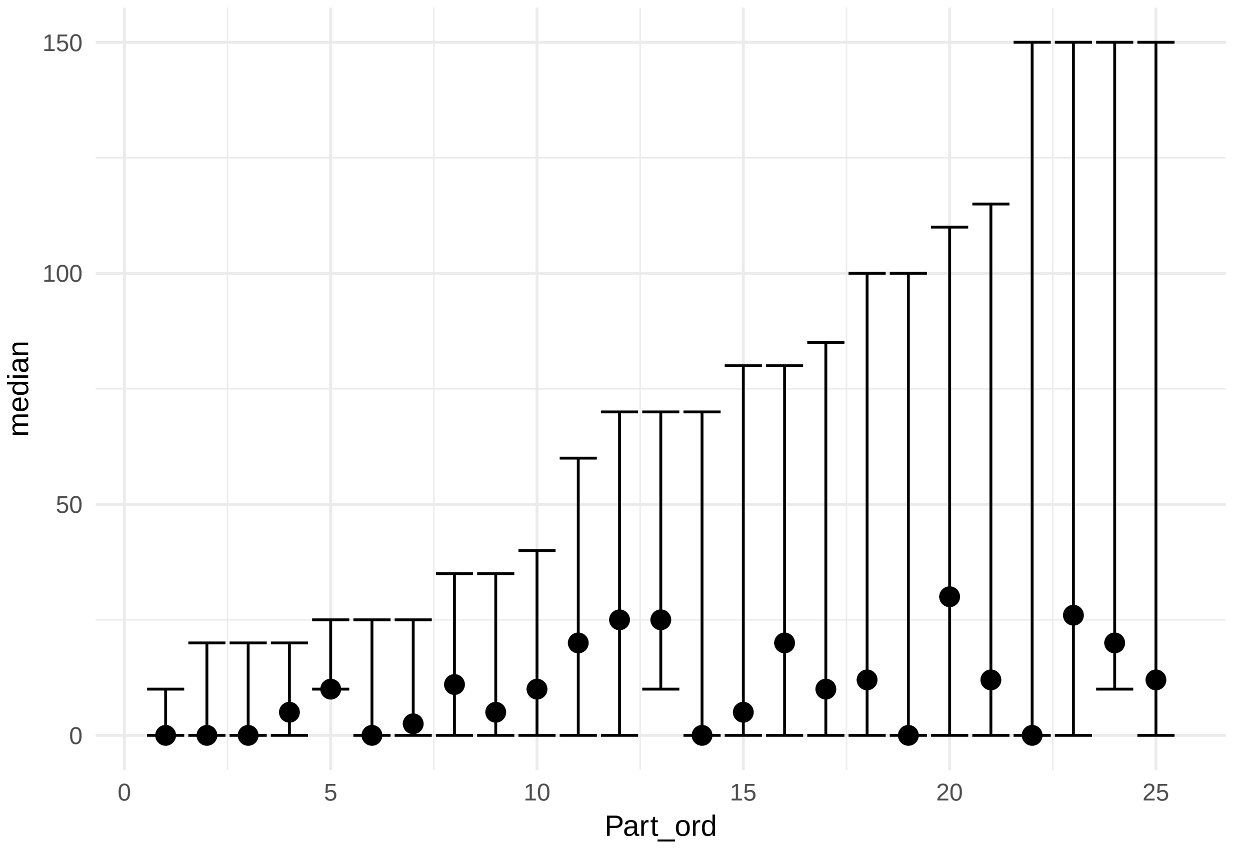
As the outcome of anchoring, introspection and binning are not under the control of the researcher, the response patterns can vary between participants. Let's consider a few possible patterns of participants (and their dramatic stories):

1. A is undecisive and stays in the center region
2. B has a crush on the experimenter and responds slightly more positive
3. C politely avoids the negative extremes
4. D is a human rights activist and habitually treats the seven bins equally.
5. E is annoyed by the experiment (rightly so) and falls into a dichotomous response pattern: 1 or 5
6. F is a surrealist and has a completely unique way to "look at things".

Many unkowns are in the game. Only one special cases we can alleviate with the multilevel modelling tools in our hands. Anchoring can (but not necessarily does) result in a constant *shift* between participants. Compare participants A and B: A collects almost all stimuli in categories 2, 3 and 4, whereas B uses 3, 4 and 5. This is not much else than a participant-level intercept random effect. Unfortunately, the situation can be more difficult than that. When participants differ in how extreme they set their endpoints, like C and D, than their responses will differ in variance. The maximum variance, however, will be found in participant E.

To speak of a real case: In the IPump study, a single-item rating scale was used to measure mental workload. The results suggest that all participants used the lower range of the scale, but differed vastly in where they set their upper point. Figure XY orders participants by the maximum value they used. This is obviously related to variance, but seemingly not so much with location. It does not suffice to use a response distribution with mean-variance relationship, as we used to. All these issues make rating scales peculiar and we should not pretend they have the same neat arithmetic properties as objective measures.

```r
attach(IPump)

D_pumps %>%
  group_by(Part) %>%
  summarize(min = min(workload),
            max = max(workload),
            median = median(workload)) %>%
  mutate(Part_ord = rank(max, ties.method = "first")) %>%
  ggplot(aes(x = Part_ord, ymax = max, ymin = min, y = median)) +
  geom_errorbar() +
  geom_point(size = 3)
```



```r
detach(IPump)
```

Setting the idiosyncracies rating scales responses aside, how does a common rating scale appear in our framework of link functions and patterns of randomness? Rating scales are bounded on two sides and we already know what that means: a suitable model for rating scales will likely contain a logit link function and a distribution of randomness that is bounded on two sides.

A real problem with rating scales is that they often are discrete. Most scales force participants to give their answer as a choice between five or seven ordered levels. When the response variable has just a few levels, *ordinal regression* is a good choice. Ordinal regression itself is a generalization of logistic regression.

However, with most properly designed self-report instruments, a scale comprises several items, because only that can sufficiently reduce measurement error and allow for in-depth psychometric assessments. Take the well-known Cronbach α, which assesses reliability of a scale by correlating every items score with the sum score. Obviously, that only makes sense when there are multiple items. While frokm a psychometric perspective, single-item scales are susceptible, there can be situations where a researcher may use a validated single item scale for pragmatic reasons. Especially, when measures happen in situ, such as during a usability test or even a real operation, being brief and unobtrusive might be more important than good quality of measures.

With multi-item rating scales, one also has the possibility to build a psychometric multi-level model, where items are considered a sample of a population of possible items. That is actually a very good idea, as the item-level random effects control for differences in item location. For example, the following item is likely to produce generally lower beauty ratings than the one shown earlier, because the anchors have been moved downwards:

How beautiful do you perceive the user interface?

like a screenshot from a splatter movie 1 – 2 – 3 – 4 – 5 quite attractive

Unless one builds such a psychometric multi-level model, ordinal regression is not very suitable for multi-item scales and here is why: The sum (or mean) score The sum score is still binned, but more finely grained so. A sum score over three seven-binned items already has 21 bins, which would result in an inflation of number of parameters in ordinal regression.

As a rescue one might well regard a measure with 21 bins as continuous. Furthermore, there actually is no strong reason to use binned rating scales, at all. So called *visual analog scales* let participants make continuous choices by either drawing a cross on a line or move a slider control. For sum scores and visual analogue scales, the problem of choice reduces to a logit link function (they still have two boundaries) and a continuous distribution bounded on both sides. That is precisely what is behind *beta regression* and, as we shall see, this distribution is flexible enough to smooth over several of the rating scale pathologies that were just discussed.

Ordered logistic regression

When the ordinal response has a low number of response categories (between 4 and 7), ordinal regression applies. Recall logistic regression: the response falls into one of two categories, which are coded as 0 and 1. Although not in a strict sense, the two category can often be thought of as in an order: success is better than failure, presence more than absence and a return better than bailing out. Instead of two categories, we can also conceive the situation as a *threshold* between the categories, that needs force to jump over it. Any positive impact factor x_i can then be thought of as such a force that pushes a responses probability to the higher category, by the amount β_i (on logit scale). At the same time, the intercept β_0 represents the basic log-odds of falling into category 1 in a default state, that is $x_i = 0$.

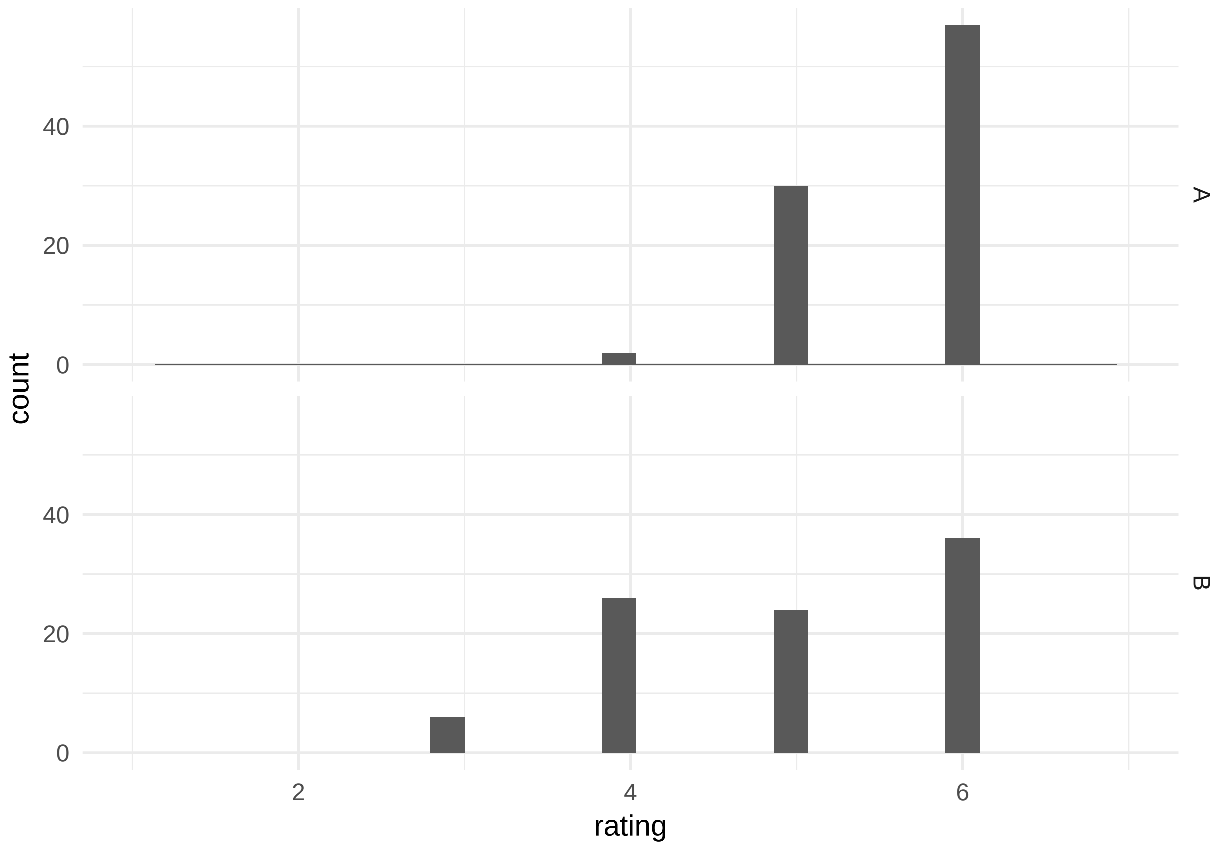
In ordinal regression, this idea extends to cases with more than two ordered response categories. The only arising complication is that with two categories, we have one *threshold* to overcome, whereas with three categories there are two thresholds and generally, with c categories, there are $c - 1$ thresholds. Ordinal regression deals with the problem by estimating $c - 1$ intercept estimates $\beta_{0[k]}$. Each threshold intercept $\beta_{0[k]}$ represents the probability (on logit scale) that the response falls into category k *or lower*, or formally:

$$\text{logit}(P(y_i \leq k)) = \beta_{0[k]}$$

Let's see this at the example of the BrowsingAB case, first. User ratings have been simulated with seven levels:

```
attach(BrowsingAB)
```

```
BAB1 %>%
  ggplot(aes(x = rating)) +
  facet_grid(Design~.) +
  geom_histogram() +
  xlim(1,7)
```



The brms regression engine implements ordinal regression by the family `cratio` (cumulative odds ratio) with a default logit link function.

```r
M_ord_1 <-
  BAB1 %>%
  brm(rating ~ Design,
      family = "cratio",
      data = .)
```

```r
fixef(M_ord_1)
```

Table 25: Estimates with 95% credibility limits

fixef	center	lower	upper
NA	-12.753	-47.631	-5.870
NA	-12.979	-53.096	-5.817
NA	-4.087	-4.999	-3.260
NA	-2.263	-2.825	-1.802
NA	-1.118	-1.566	-0.744
NA	1.322	0.847	1.924
DesignB	-0.865	-1.339	-0.443

The six intercepts correspond with the thresholds between the seven levels. It is no coincidence that the intercept estimates increase by order, as they are cumulative (the "c" in cratio). The first intercept estimate represents (the logit of) the proportion of responses $y_i \leq 1$, the second $y_i \leq 2$ etc. The Design effect has the usual interpretation as compared to logistic regression, an increase in logit. The only difference is that it refers to all six reference points. The expected proportion of responses equal to or smaller than 2 for design A is:

$$\pi(y_i \leq 2|A) = \text{logit}^{-1}(\beta_{0[2]}) = \text{logit}^{-1}(-13) = 2.26 \times 10^{-6}$$

The expected proportion of responses equal to or smaller than 2 for design B we get by the usual linear combination:

$$\pi(y_i \leq 2|B) = \text{logit}^{-1}(\beta_{0[2]} + \beta_1) = \text{logit}^{-1}(-13.9) = 9.19 \times 10^{-7}$$

All coefficients are shifting all threshold by the same amount (on the linear predictor scale). You can picture this as a single puppetier controlling multiple puppets by just one stick, making them dance in sync. As long as the ordinal scale has only a low number of bins, that keeps the number of parameters at a reasonable level. Just imagine, you were estimating an ordinal multilevel model and all participant-level effects were five or sevenfolded, too. However, the equidistancy of effects on bin thresholds is an assumption by itself, and in the presence of response styles on rating scales, it cannot be taken for granted.

Besides that, the ordinal model appears very snug to the structure of the data. It does not wipe over the fact that the response is discrete and the thresholds represent the order. Conveniently, effects are represented by a single estimate, which one can use to communicate direction and certainty of effects. On the downside, communicating absolute performance (that is, including the intercept) is more complicated. When presenting predictions from an ordinal model one actually has to present all thresholds, rather than a single mean. In practice that probably is less relevant than one might think at first, because predictions on self-report scales is less useful than metric performance data. Ordinal data also does not lend itself so much to further calculations. For example, you can use ToT measures on infusion pumps in calculating the required staffing of an intensive care unit, because seconds are metric and can be summed and divided. In contrast, it does not make sense to calculate the cognitive workload of a team of nurses by summing their self-report scores. The only possibility is to compare the strengths of predictors, but that does not require predictions.

```
detach(BrowsingAB)
```

Beta regression

One of the most futile discussions in methodology research to my mind is whether one should use a four, five or seven binned Likert scale. From a pure measurement point of view, more bins give better resolution, the ultimate consequence being to bin at all, that is using continuous rating scales. At the same time, many rating responses come from multiple item scales, which multiplies the number of bins. Speaking of ordinal regression, it seems reasonable to have seven intercepts for a single item scale, but who would want 14 or 21 for a two or three-item scale? And most scales have more items than that, which is good from a psychometric perspective.

In fact, psychometric research in the process of developing rating scales routinely uses a method called *confirmatory factor analysis*, which derives from the Gaussian linear model and inherits its assumptions. Not surprisingly, most research applying the very same instruments also use plain linear models. It seems fair enough to take a multi-item scale as a continuous measure, but given the framework of GLM, it is unnecessary (to put it mildly) to go along with the assumptions of Normality and linearity. While the link function for a double bounded response variable is simply the logit, the only missing ingredient is a double bounded error distribution. Enter beta distribution!

We demonstrate beta regression on rating scales at the example of the CUE8 study. This study aimed at assessing whether remote usability testing arrives at the same ToT measures as in moderated sessions. As we have seen in [CROSSREF], the difference is marginal. But, rating scales are susceptible for all kinds of cognitive and social biases. For that reason, a golden rule for user test moderators is to constantly remind participants to not blame themselves for errors. Reportedly, test moderators also do help participants (after counting to 10) in order to minimize frustration (and maximize information flow). What could the presence or absence of a moderator do to satisfaction ratings? Perhaps, remote participants feel the lack of assurance and support as higher levels of frustration. Furthermore, it is not unlikely that satisfaction ratings are sensitive to idiosyncratics in the process and setting of the user test, such that we could even expect differences between teams.

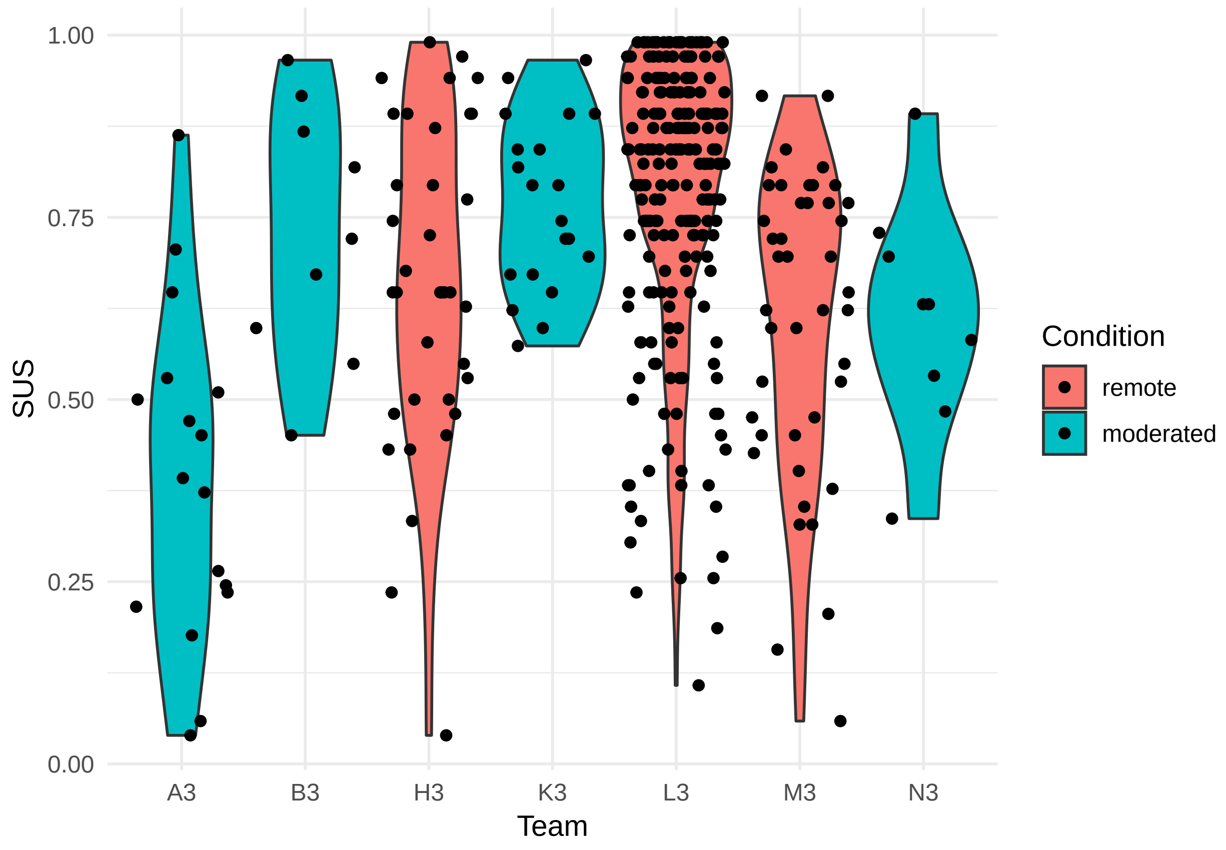
Before we build the model, there are two issues to regard: first, the boundaries are 0 and 1, which requires a rescaling of responses into this interval. The SUS scores are on a scale from 0 to 100 and a divisor of 100 would produce the desired interval. Not just so, because second, the responses must actually lie *strictly between 0 and 1*, excluding the boundaries. On (quasi)continuous scales, it seems not very likely to have 0 or 1 as response, but it can happen. Indeed, participants in the CUE8 study have responded with a satisfaction rating of 100 quite often.

A practical solution is to scale the responses in such a way as to avoid the two boundaries, which is what the following hack does.

1. add a tiny value to all responses
2. create a divisor by adding double that value to the maximum value the responses can take
3. divide all responses by that divisor

You may find it inappropriate to mangle a response variable in such an arbitrary way. However, keep in mind that the levels of ordinal responses are highly arbitrary. In terms of measurement theory, all transformations that maintain the order are permitted for ordinal scales. For the following analysis, the data set was further reduced by averaging the scores across tasks and excluding probable cheaters with a ToT < 30s.

```r
attach(CUE8)

D_cue8_SUS <-
  D_cue8 %>%
  filter(!is.na(SUS)) %>%
  group_by(Part, Team, Condition) %>%
  dplyr::summarize(ToT = sum(ToT),
            SUS = mean(SUS)) %>%
  ungroup() %>%
  filter(ToT > 30) %>%
  mutate(SUS = (SUS + 1)/(100 + 2)) %>% ## rescaling to ]0;1[
  as_tbl_obs()

D_cue8_SUS %>%
  ggplot(aes(x = Team, y = SUS, fill = Condition)) +
  geom_violin() +
  geom_jitter()
```



```
M_5_bet <-
  D_cue8_SUS %>%
  brm(SUS ~ Condition + (1 | Team),
      family = Beta(link = "logit"), iter = 0, chains = 1,
      data = .)

M_5_bet <-
  D_cue8_SUS %>%
  brm(fit = M_5_bet, data = .)

sync_CE(M_5_bet, Env = CUE8)
```

```
M_5_bet
```

```
##  Family: beta
##   Links: mu = logit; phi = identity
## Formula: SUS ~ Condition + (1 | Team)
##    Data: . (Number of observations: 363)
## Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
##          total post-warmup samples = 4000
##
## Group-Level Effects:
## ~Team (Number of levels: 7)
##               Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat
## sd(Intercept)     0.81      0.39     0.34     1.95        297 1.02
```

```
##
## Population-Level Effects:
##                     Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat
## Intercept               0.79      0.52    -0.51     1.78        385 1.00
## Conditionmoderated     -0.34      0.70    -1.70     1.11        967 1.00
##
## Family Specific Parameters:
##     Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat
## phi     4.13      0.30     3.56     4.74       3362 1.00
##
## Samples were drawn using sampling(NUTS). For each parameter, Eff.Sample
## is a crude measure of effective sample size, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

```
fixef(M_5_bet)
```

Table 26: Estimates with 95% credibility limits

fixef	center	lower	upper
Intercept	0.798	-0.506	1.78
Conditionmoderated	-0.343	-1.699	1.11

```
grpef(M_5_bet)
```

Table 27: Estimates with 95% credibility limits

type	fixef	re_factor	center	lower	upper
grpef	Intercept	Team	0.71	0.344	1.95

Do participants in remote sessions feel less satisfied? There seems to be a slight disadvantage, but we cannot confirm this with sufficient certainty. In contrast, the variation between teams is substantial, which indicates that SUS ratings are not independent of the particular setting. That is rather concerning for a widely used, an allegedly validated rating scale.

Is that a realistic model for the SUS responses? Another glance at the violin plot suggests another pathology: the teams seem to differ in variation. In the closing section I will briefly demonstrate how to deal with differences in variance (rather than mean) by a *distributional model*.

Distributional models

The framework of GLM, as flexible as it has proven to be up to this point, has one major limitation: it renders the relationship between predictors and the location of the response. We only think in terms of impact factors that improve (or damage) average response times, error rates, satisfaction ratings etc. one would think that multi-level models deal with variance to a good extent, and they do. But, they only give us the variance of a certain effect on a set of objects. That is absolutely not the same as asking: do teams in CUE8 differ in the variation of responses?

That brings me to the final feature of modern regression modelling in the scope of this book: GLM greatly enhanced the scope of modelling by giving us the choice of response distributions and linearizing functions. Still, all models introduced so far establish an association between predictors and the expected value μ, only.

However, all but the one-parameter distributions come with additional parameters that capture a family of distributions in its whole variety of shapes. Strong variance can become a real problem, because this implies that extremely poor performance becomes more likely. Under the perspectives of safety in hazardous environments and universal usability, variance is a crucial parameter by itself. We should track carefully, that an improvement on average is not accompanied by more variance (other than the mean-variance relationship prescribed by the error distribution).

As a first illustration, imagine two versions of a continuous rating scale for visual beauty that differ in how their extreme levels are labelled:

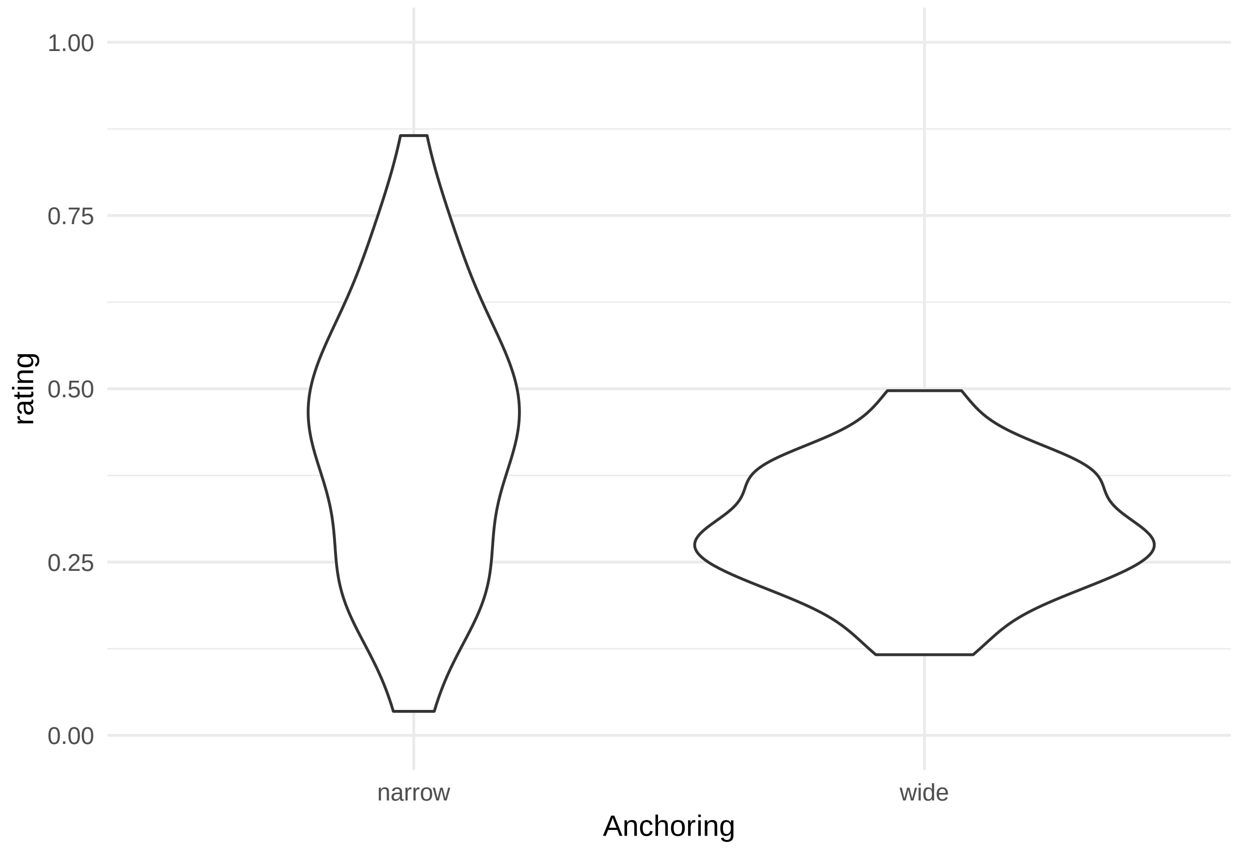
1. like the ugliest website I have ever seen: 0 ——- 1 like the most beautiful website
2. distgusting as a screenshot from a splatter movie: 0 ——- 1 like the most beautiful sunset I have seen

The second scale has the lower and upper anchors moved to more extremes. Two questions arise:

1. Is the overall location of the scale untouched, that is, have both anchors been moved by the same distance outwards?
2. What range do websites cover as compared to all thinkable visual impressions?

For the sake of simplicity (not for a strong research design), let's assume that one participant has rated a randomized sample of 100 websites in two conditions: narrow anchoring and wide anchoring. The following simulates data as if there were just a minor positive shift of the wider condition, accompanied by an immense up-scaling.

```r
set.seed(42)

N = 100

Conditions <-
  frame_data(~Anchoring, ~mu, ~phi,
             "wide", .3, 18,
             "narrow", .4, 6) %>%
  mutate(a = mu * phi,
         b = phi - mu * phi)

D_Anchor <-
  data_frame(Obs = 1:N,
             Anchoring = rep(c("wide", "narrow"), N/2)) %>%
  left_join(Conditions) %>%
  mutate(rating = rbeta(N, a, b))

D_Anchor %>%
  ggplot(aes(x = Anchoring, y = rating)) +
  geom_violin() +
  ylim(0,1)
```

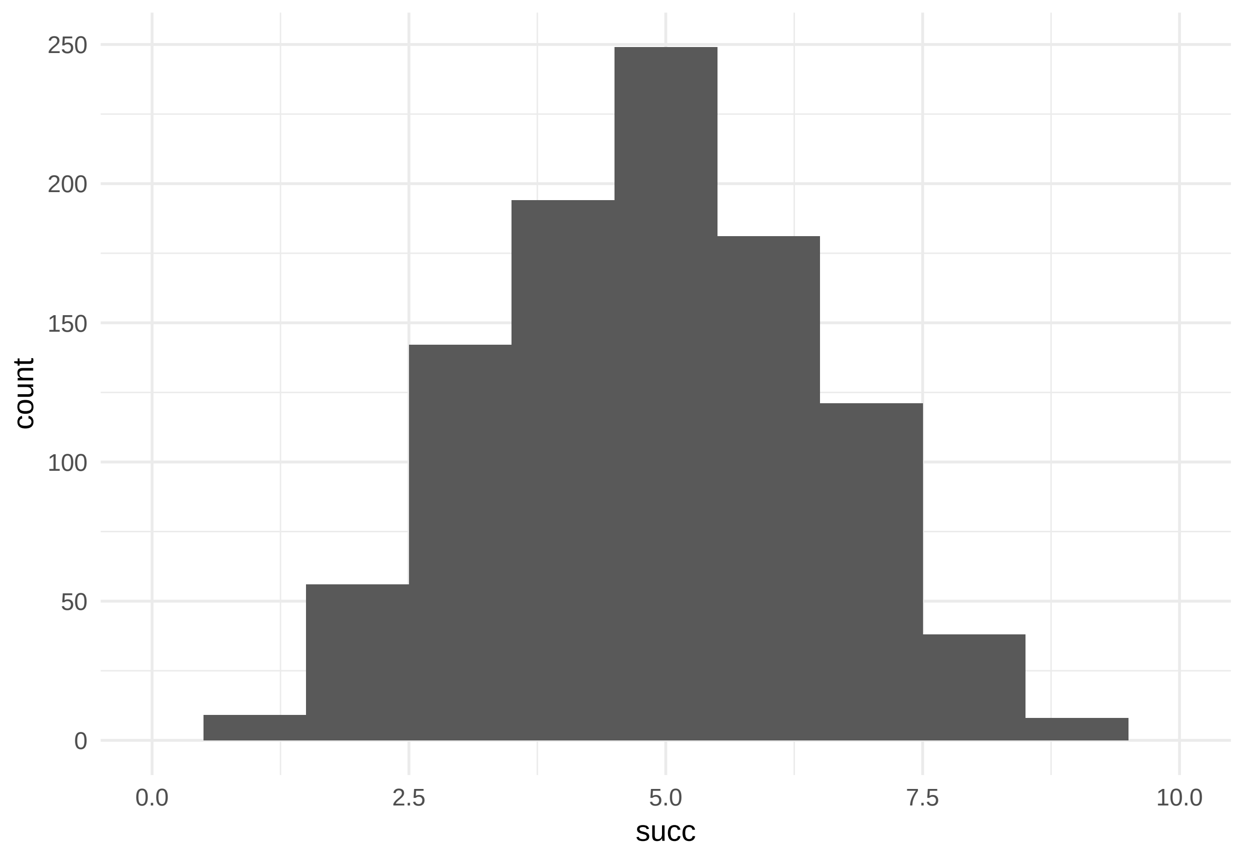


The two conditions have about the same location, but a more narrow anchoring produces a wider dispersion of responses. How would we confirm this statistically?

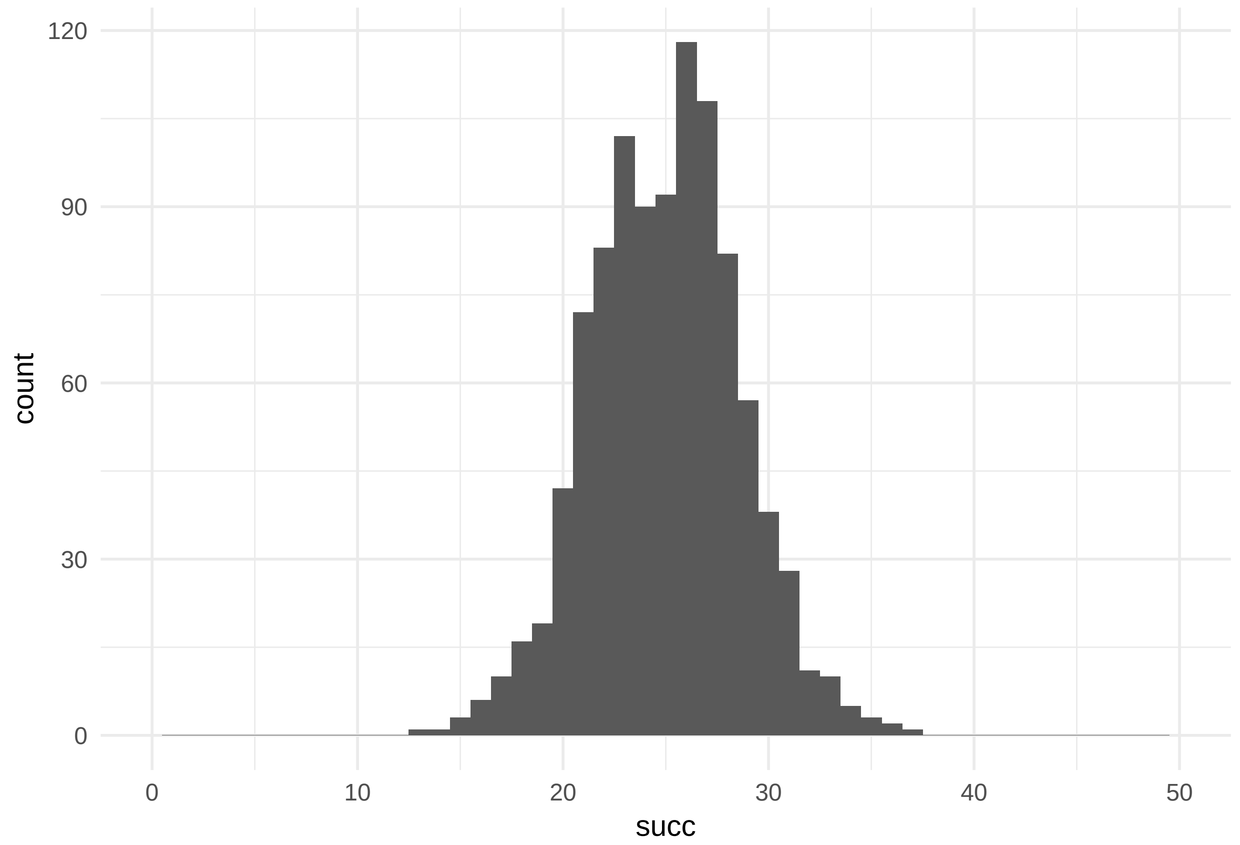
Models that contain predictors linked to any distribution parameter other than μ are called *distributional models* and have only recently been implemented in the brms engine. They have an immense potential as they relax another assumption of GLM, namely that all parameters, but μ, are constant across observations or follow the mean-variance relationship. Here we aim to estimate the difference in variance by experimental condition.

The brms engine uses a parametrization of the beta distribution (other than the more common a, b parametrization), where μ is the location and *phi* is a *scale* parameter. Take great care: "scale" does not refer to dispersion itself. Rather, it is comparable to the number of trials in a binomial process. The more trials there are, the tighter the distribution becomes, *relative* to the boundaries:

```
plot_rbinom <- function(N, size, p) {
  data_frame(succ = rbinom(N, size, p)) %>%
  ggplot(aes(x = succ)) +
  geom_histogram(bins = size + 1) +
  xlim(0, size)
}

plot_rbinom(1000, 10, .5)
```



```r
plot_rbinom(1000, 50, .5)
```



In effect, increasing ϕ results in reduced dispersion and accordingly, when used in a distributional model, positive efefcts decrease variance and negative increase. This all works on top of to the mean-variance relationship of the beta distribution.

When estimating dispersion or scale parameters, we have to regard that these are positive, strictly. When linking a linear term to such a parameter, predictions are generated for the variance and these should never become negative. The brm engine simply extends the principle of link functions to parameters other the μ and sets a default log link for ϕ. In order to estimate the changes in μ and ϕ simultanously, the brm engine receives two regression formulas, which is done by the command `bf()`.

```
M_beta <- brm(bf(rating ~ 1 + Anchoring,
                 phi ~ 1 + Anchoring),
             family = Beta(),
             data = D_Anchor)

M_beta <- brm(fit = M_beta, data = D_Anchor)
```

The coefficient table shows the effect of anchoring on both parameters of the response distribution: the widely anchored item produces slightly less favorable ratings, but dramatically reduces on dispersion.

```
fixef(M_beta)
```

Table 28: Estimates with 95% credibility limits

fixef	center	lower	upper
Intercept	-0.318	-0.544	-0.095
NA	1.630	1.247	1.986
Anchoringwide	-0.529	-0.788	-0.274
NA	1.504	0.968	2.023

Back to the CUE8 study. Do teams differ in how much variance arises, as the violin plot suggests? Before we test this by a distributional model, recall one again the principle of mean-variance relation. Beta distributions have variance tied to the mean in much the same way as binomial distribution. When moving along the range between 0 and 1, variance is largest in the center and decreases towards the boundaries. That does not seem to be the case in CUE8. Compare the distributions of Teams B and K to H and L. They all are close to the upper boundary, but show inflated variance. It could be the case, that somehow some teams trigger more extreme responses, inflating variance. The following model tests the effect of testing condition and teams on the location and dispersion of responses simultaneously.

```
F_unequal_var <- bf(SUS ~ 1 + Condition + (1 | Team),
                    phi ~ 1 + Condition + (1 | Team))

M_6_bet <-
  D_cue8_SUS %>%
  brm(F_unequal_var,
      family = Beta(), iter = 1, chains = 1,
      data = .)

M_6_bet <-
  D_cue8_SUS %>%
  brm(fit = M_6_bet, data = .,
      chains = 6,
      iter = 4000,
      warmup = 2000)

sync_CE(M_6_bet, Env = CUE8)
```

```
T_fixef <-
  brms::fixef(M_6_bet)[,c(1,3,4)] %>%
  as_data_frame(rownames = "fixef") %>%
  dplyr::rename(center = Estimate)
T_fixef
```

fixef	center	Q2.5	Q97.5
Intercept	0.751	-0.247	1.86
phi_Intercept	1.087	-0.632	1.88
Conditionmoderated	-0.211	-1.723	1.15
phi_Conditionmoderated	0.701	-0.277	2.82

The default behaviour of brm is that the scale parameter ϕ is on a log scale. As usual, lifting it to original scale by exponantiation makes it a multiplier. By exp(0.701) = 2.015, we see that there is just a small difference between the two conditions. But, are there other differences between teams? The following table shows the scale multipliers for individual teams. All multipliers are closely arranged around 1, which means there is little differences. The SUS scale can safely be adminstsred in remote and moderated usability testing.

```
T_ranef <-
  ranef(M_6_bet) %>%
  filter(nonlin == "phi") %>%
  mutate_if(is.numeric, exp) %>%
  discard_redundant()
T_ranef
```

re_entity	center	lower	upper
A3	0.830	0.323	1.32
B3	0.965	0.384	1.71
H3	0.967	0.485	6.75
K3	1.151	0.720	2.95
L3	1.029	0.608	7.78
M3	1.112	0.669	9.87
N3	1.015	0.573	2.41

```
detach(CUE8)
```

Exercises

1. The IPump study took repeated measure of workload on a one-item quasi-continuous rating scale. Examine the effect of training and Design on workload. Then take a closer look at how participants used the scale. Build a distributional model.