

# exercise\_sheet\_10\_Immanuel\_Albrecht

May 11, 2023

## 1 Exercise sheet 10

### 1.1 NWO grant applications

#### 1.1.1 Exercise 1

For this exercise, you will need to load the dataset NWOGrants from the rethinking package. This dataset reports on the funding outcomes of the Netherlands Organisation for Scientific Research (NWO) grant applications over the 2010-2012 period. One study used that dataset to investigate gender bias in the funding awards: <https://www.pnas.org/content/112/40/12349>. You can read there that a response to this paper has been formulated, as briefly discussed at the beginning of lecture 9. Note that in general less than half applications are awarded funding.

Address the same question as the one in the paper by Lee and Ellemers by using binomial GLM to investigate potential gender bias on awards. Quantify the contrast between male and female applicants. In a second step, condition on the discipline as well. What are your conclusions? Should the NWO take specific measures for gender equity in general and across disciplines? Is there any excess variance in the data? If yes, can you elaborate on the nature of possible unaccounted sources?

```
[1]: library(rethinking)
      data(NWOGrants)
      d <- NWOGrants
```

Lade nötiges Paket: rstan

Lade nötiges Paket: StanHeaders

rstan version 2.26.16 (Stan version 2.26.1)

For execution on a local, multicore CPU with excess RAM we recommend calling `options(mc.cores = parallel::detectCores())`.

To avoid recompilation of unchanged Stan programs, we recommend calling `rstan_options(auto_write = TRUE)`

For within-chain threading using ``reduce_sum()`` or ``map_rect()`` Stan functions, change ``threads_per_chain`` option:

```
rstan_options(threads_per_chain = 1)
```

Do not specify '-march=native' in 'LOCAL\_CPPFLAGS' or a Makevars file

Lade nötiges Paket: cmdstanr

This is cmdstanr version 0.5.3

- CmdStanR documentation and vignettes: [mc-stan.org/cmdstanr](https://mc-stan.org/cmdstanr)
- CmdStan path: D:/Users/Immanuel/Documents/.cmdstan/cmdstan-2.31.0
- CmdStan version: 2.31.0

A newer version of CmdStan is available. See `?install_cmdstan()` to install it.  
To disable this check set option or environment variable  
`CMDSTANR_NO_VER_CHECK=TRUE`.

Lade nötiges Paket: parallel

rethinking (Version 2.31)

Attache Paket: 'rethinking'

Das folgende Objekt ist maskiert 'package:rstan':

stan

Das folgende Objekt ist maskiert 'package:stats':

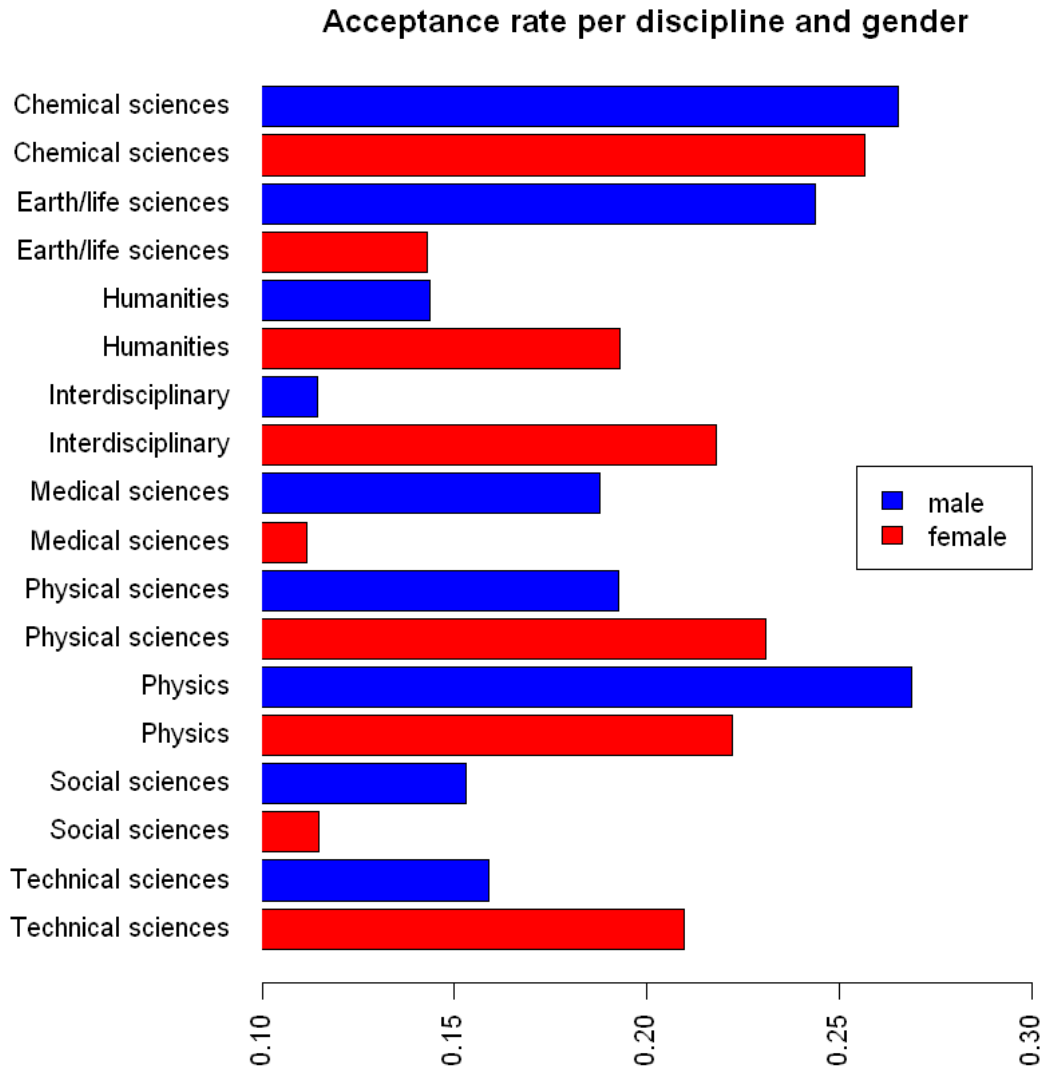
rstudent

```
[2]: d$male <- as.integer(d$gender) - 1
d$field <- as.integer(d$discipline)
d$accept <- d$awards / d$applications
d <- d[order(d$field), ]
d$accept.scaled <- scale(d$accept)
d
```

		discipline <fct>	gender <fct>	applications <int>	awards <int>	male <dbl>	field <int>	accept <dbl>	ac <dbl>
	1	Chemical sciences	m	83	22	1	1	0.2650602	1.4
	2	Chemical sciences	f	39	10	0	1	0.2564103	1.2
	13	Earth/life sciences	m	156	38	1	2	0.2435897	1.0
	14	Earth/life sciences	f	126	18	0	2	0.1428571	-0.0
	7	Humanities	m	230	33	1	3	0.1434783	-0.0
	8	Humanities	f	166	32	0	3	0.1927711	0.0
	11	Interdisciplinary	m	105	12	1	4	0.1142857	-1.0
	12	Interdisciplinary	f	78	17	0	4	0.2179487	0.5
	17	Medical sciences	m	245	46	1	5	0.1877551	-0.0
	18	Medical sciences	f	260	29	0	5	0.1115385	-1.0
	3	Physical sciences	m	135	26	1	6	0.1925926	0.0
	4	Physical sciences	f	39	9	0	6	0.2307692	0.7
	5	Physics	m	67	18	1	7	0.2686567	1.4
	6	Physics	f	9	2	0	7	0.2222222	0.6
	15	Social sciences	m	425	65	1	8	0.1529412	-0.0
	16	Social sciences	f	409	47	0	8	0.1149144	-1.0
	9	Technical sciences	m	189	30	1	9	0.1587302	-0.0
	10	Technical sciences	f	62	13	0	9	0.2096774	0.3

A data.frame: 18 × 8

```
[3]: par(mar = c(4, 9, 2, 2))
barplot(rev(d$accept), names.arg = rev(d$discipline), las=2, xlim = c(0.10, 0.
↪30), xpd = FALSE, horiz = TRUE, col = ifelse(d$male, "red", "blue"))
title("Acceptance rate per discipline and gender")
legend("right", c("male", "female"), fill = c("blue", "red"))
```



So male applicants are more likely to get accepted in humanities, interdisciplinary, physical and technical sciences. Female applicants are more likely to get accepted in chemical, earth/life, medical and social sciences and in physics.

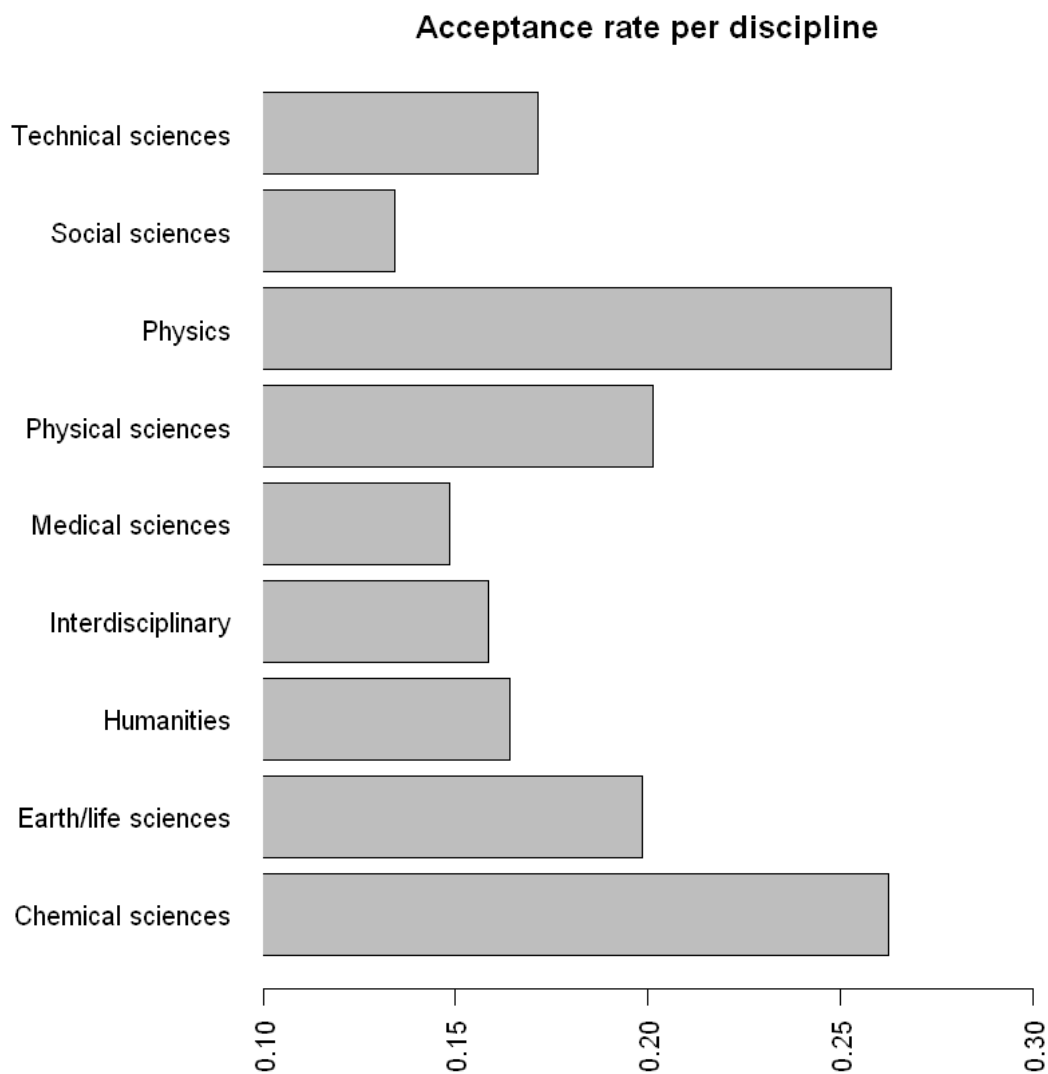
```
[4]: e <- data.frame(discipline = character(), applications = integer(), awards =
  ↪integer(), field = integer(), accept = double())
for (field in 1:max(d$field)) {
  dat <- d[d$field == field, ]
  discipline <- as.character(dat$discipline[1])
  applications <- sum(dat$applications)
  awards <- sum(dat$awards)
  accept <- awards / applications
  e[nrow(e) + 1, ] <- list(discipline, applications, awards, field, accept)
```

```
}  
e
```

A data.frame: 9 × 5

	discipline <chr>	applications <int>	awards <int>	field <int>	accept <dbl>
1	Chemical sciences	122	32	1	0.2622951
2	Earth/life sciences	282	56	2	0.1985816
3	Humanities	396	65	3	0.1641414
4	Interdisciplinary	183	29	4	0.1584699
5	Medical sciences	505	75	5	0.1485149
6	Physical sciences	174	35	6	0.2011494
7	Physics	76	20	7	0.2631579
8	Social sciences	834	112	8	0.1342926
9	Technical sciences	251	43	9	0.1713147

```
[5]: par(mar = c(4, 9, 2, 2))  
barplot(e$accept, names.arg = e$discipline, las=2, xlim = c(0.10, 0.30), xpd =  
  FALSE, horiz = TRUE)  
title("Acceptance rate per discipline")
```

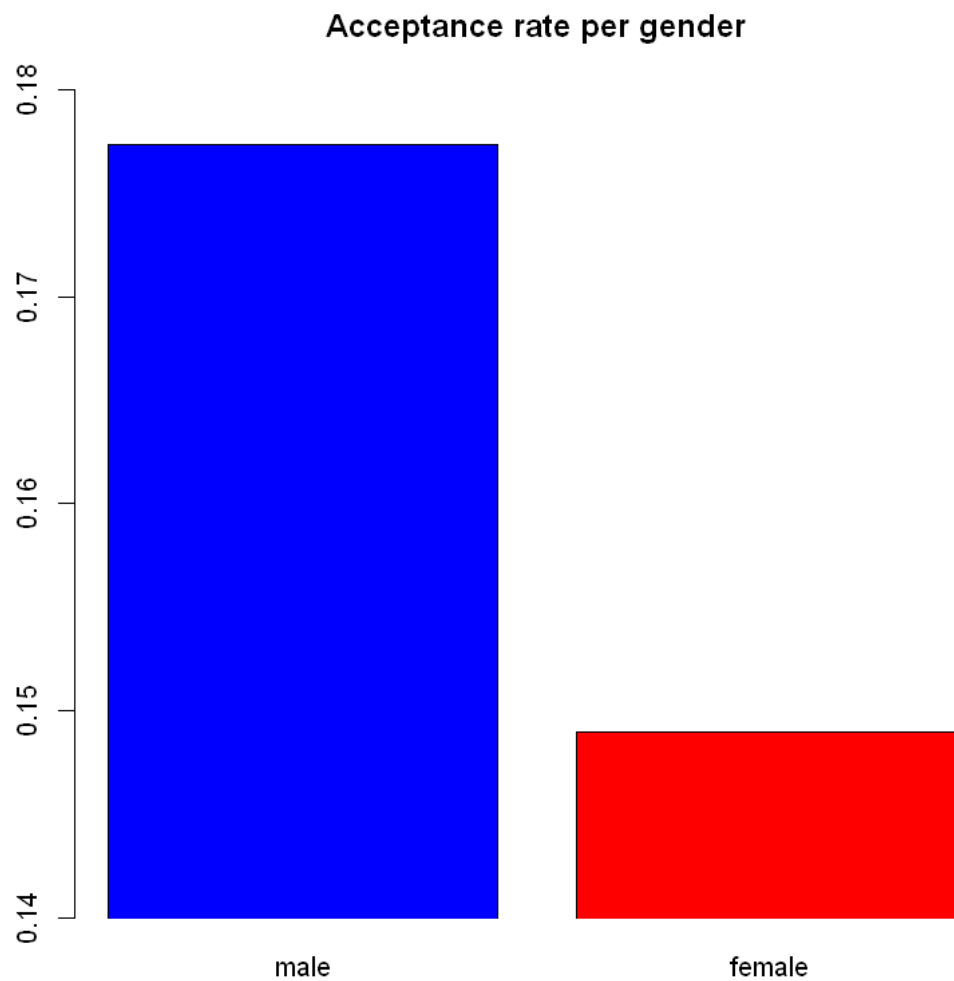


```
[6]: male_applications <- sum(d[d$male == 1, ]$applications)
female_applications <- sum(d[d$male == 0, ]$applications)
male_awards <- sum(d[d$male == 1, ]$awards)
female_awards <- sum(d[d$male == 0, ]$awards)
male_accept <- male_awards / male_applications
female_accept <- female_awards / female_applications

barplot(c(male_accept, female_accept), names.arg = c("male", "female"), ylim =
  ↪c(0.14, 0.18), xpd = FALSE, col = c("blue", "red"))
title("Acceptance rate per gender")

mean(male_accept) - mean(female_accept)
```

0.0283801315911408



So in the data there is a difference between the male and female acceptance rate in the data. But is it statistically significant? We construct different models and compare them.

```
[7]: # A single mean over all the data
model1 <- map(
  alist(
    awards ~ dbinom(applications, p),
    logit(p) <- a,
    a ~ dnorm(0, 10)
  ),
  data = d
)
```

```
model1_parameter_amount <- 1 # 1
```

```
[8]: # One mean for male and one mean for female
model_male <- map(
  alist(
    awards ~ dbinom(applications, p),
    logit(p) <- a + a_male * male,
    a ~ dnorm(0, 10),
    a_male ~ dnorm(0, 10)
  ),
  data = d
)
model_male_parameter_amount <- 1 + 1 # 2
```

```
[9]: # A model where we dont distinguish between male and female, but the department
      ↳ is relevant
model_field <- map(
  alist(
    awards ~ dbinom(applications, p),
    logit(p) <- a[field],
    a[field] ~ dnorm(0, 10)
  ),
  data = d
)
model_field_parameter_amount <- nrow(e) # 9
```

```
[10]: # Each field has its own mean but the change if a participant is male is global
model_field_male <- map(
  alist(
    awards ~ dbinom(applications, p),
    logit(p) <- a[field] + a_male * male,
    a[field] ~ dnorm(0, 10),
    a_male ~ dnorm(0, 10)
  ),
  data = d
)
model_field_male_parameter_amount <- nrow(e) + 1 # 10
```

```
[11]: # We have the same mean for all fields, but the influence if the participant is
      ↳ male is unique for each field
model_male_field <- map(
  alist(
    awards ~ dbinom(applications, p),
    logit(p) <- a + a_male[field] * male,
    a ~ dnorm(0, 10),
    a_male[field] ~ dnorm(0, 10)
  ),
  data = d
)
```



```

      data = d
    )
    model_male_field_parameter_amount <- 1 + nrow(e) # 10

```

```

[12]: # Both the mean and the offset for a male participant is different for each
      ↪ department
    model_field_male_field <- map(
      alist(
        awards ~ dbinom(applications, p),
        logit(p) <- a[field] + a_male[field] * male,
        a[field] ~ dnorm(0, 10),
        a_male[field] ~ dnorm(0, 10)
      ),
      data = d
    )
    model6_field_male_field_parameter_amount <- nrow(e) + nrow(e) # 18

```

```

[13]: compare(model1, model_male, model_field, model_field_male, model_male_field,
      ↪ model_field_male_field)

```

		WAIC <dbl>	SE <dbl>	dWAIC <dbl>	dSE <dbl>	pWAIC <dbl>	weight <dbl>
A compareIC: 6 × 6	model_field_male_field	114.1189	3.323187	0.000000	NA	8.916445	0.9780
	model_male_field	121.8910	7.573247	7.772083	5.880442	7.050472	0.0200
	model_field_male	128.4570	8.013722	14.338031	6.176659	12.589328	0.0007
	model_field	129.1645	9.418417	15.045598	7.314806	12.477572	0.0005
	model_male	130.1521	8.867268	16.033179	7.403613	4.998377	0.0003
	model1	130.1852	12.900592	16.066222	11.779835	2.702629	0.0003

So we see that the model that is able to distinguish between male and female and also between departments is able to fit the data the best, obviously.

Now we quantify the contrast while disregarding the field the participants come from. These are the two models `model_male` and `model1`. Because the latter is gender independent, we only have to do this discussion one for the first model.

```

[14]: # The relative scale, which in most cases can be disregarded.
      summary(model1)
      summary(model_male)

```

A precis: 1 × 4	mean <dbl>	sd <dbl>	5.5% <dbl>	94.5% <dbl>
a	-1.61835	0.05065213	-1.699302	-1.537398

A precis: 2 × 4	mean <dbl>	sd <dbl>	5.5% <dbl>	94.5% <dbl>
a	-1.7424160	0.08146995	-1.87262075	-1.6122113
a_male	0.2081389	0.10405967	0.04183145	0.3744463

```
[15]: # Better to compare the models with an information criterion
compare(model1, model_male)
```

	WAIC <dbl>	SE <dbl>	dWAIC <dbl>	dSE <dbl>	pWAIC <dbl>	weight <dbl>
A compareIC: 2 × 6						
model_male	129.9961	8.736106	0.0000000	NA	4.900122	0.5569528
model1	130.4537	13.016595	0.4576087	6.713701	2.867156	0.4430472

We see that the inclusion of the male parameter makes a difference, although its not that significant. Next we look at the contrast between the number of male and female awardees in the second model.

```
[16]: post <- extract.samples(model_male)
p.award.male <- logistic(post$a + post$a_male)
p.award.female <- logistic(post$a)
diff.award <- p.award.male - p.award.female
quantile(diff.award, c(0.025, 0.5, 0.975))
```

```
2.5\%    0.000513055530130447 50\%    0.0286093141054553 97.5\%    0.0556196194455272
```

We see that as in the data, the model generated a gap between male and female of 0.028, which means that males are 3 percent more likely to be awarded than females. Next we also include the field of study. We consider the model `model_field_male_field`.

```
[17]: post <- extract.samples(model_field_male_field)
p.award.male <- logistic(post$a + post$a_male)
p.award.female <- logistic(post$a)
diff.award <- p.award.male - p.award.female

means <- c()
names <- c()
for (index in 1:ncol(diff.award)) {
  means <- append(means, mean(diff.award[, index]))
  names <- append(names, e[e$field == index, ]$discipline)
}

par(mar = c(4, 9, 2, 2))
bp <- barplot(means, names.arg = names, las=2, xpd = FALSE, horiz = TRUE, xlim = c(-0.11, 0.11))
title("Award probability gender difference per discipline")
text(bp, 0, means)
```

### Award probability gender difference per discipline

