

## Repeated measures analysis

## Repeated measures by profile analysis

- ▶ More than one response *measurement* for each subject. Might be
  - ▶ measurements of the same thing at different times
  - ▶ measurements of different but related things
- ▶ Generalization of matched pairs (“matched triples”, etc.).
- ▶ Variation: each subject does several different treatments at different times (called *crossover design*).
- ▶ Expect measurements on same subject to be correlated, so assumptions of independence will fail.
- ▶ Called *repeated measures*. Different approaches, but *profile analysis* uses Manova (set up right way).
- ▶ Another approach uses *mixed models* (random effects).

# Packages

```
library(car)  
library(tidyverse)  
library(lme4) # for mixed models later
```

## Example: histamine in dogs

- ▶ 8 dogs take part in experiment.
- ▶ Dogs randomized to one of 2 different drugs.
- ▶ Response: log of blood concentration of histamine 0, 1, 3 and 5 minutes after taking drug. (Repeated measures.)
- ▶ Data in `dogs.txt`, column-aligned.

## Read in data

```
my_url <- "http://ritsokiguess.site/datafiles/dogs.txt"  
dogs <- read_table(my_url)
```

## Setting things up

dogs

```
# A tibble: 8 x 7
```

	dog	drug	x	lh0	lh1	lh3	lh5
	<chr>	<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>
1	A	Morphine	N	-3.22	-1.61	-2.3	-2.53
2	B	Morphine	N	-3.91	-2.81	-3.91	-3.91
3	C	Morphine	N	-2.66	0.34	-0.73	-1.43
4	D	Morphine	N	-1.77	-0.56	-1.05	-1.43
5	E	Trimethaphan	N	-3.51	-0.48	-1.17	-1.51
6	F	Trimethaphan	N	-3.51	0.05	-0.31	-0.51
7	G	Trimethaphan	N	-2.66	-0.19	0.07	-0.22
8	H	Trimethaphan	N	-2.41	1.14	0.72	0.21

```
response <- with(dogs, cbind(lh0, lh1, lh3, lh5))  
dogs.1 <- lm(response ~ drug, data = dogs)  
response
```

lh0 lh1 lh3 lh5

# The repeated measures MANOVA

Get list of response variable names; we call them times. Save in data frame.

```
times <- colnames(response)
times
```

```
[1] "lh0" "lh1" "lh3" "lh5"
```

```
times.df <- data.frame(times=factor(times))
times.df
```

	times
1	lh0
2	lh1
3	lh3
4	lh5

## Fitting the model

```
dogs.2 <- Manova(dogs.1,  
  idata = times.df,  
  idesign = ~times  
)
```



# The output (some: there is a lot)

```
summary(dogs.2)
```

Type II Repeated Measures MANOVA Tests:

-----

Term: (Intercept)

Response transformation matrix:

(Intercept)

lh0	1
lh1	1
lh3	1
lh5	1

Sum of squares and products for the hypothesis:

(Intercept)

(Intercept)	285.366
-------------	---------

Multivariate Tests: (Intercept)

	Df	test	stat	approx	F	num	Df	den	Df	Pr(>F)
Pillai	1	0.763467	19.36642			1	6	0.0045648	**	
Wilks	1	0.236533	19.36642			1	6	0.0045648	**	
Hotelling-Lawley	1	3.227738	19.36642			1	6	0.0045648	**	
Roy	1	3.227738	19.36642			1	6	0.0045648	**	

---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

-----

Term: drug

Response transformation matrix:

(Intercept)

lh0	1
-----	---

# What there is here

- ▶ three sets of tests, for
  - ▶ times
  - ▶ drug
  - ▶ their interaction
- ▶ two *types* of test for each of these:
  - ▶ multivariate
  - ▶ univariate
- ▶ multivariate is the same as MANOVA
- ▶ univariate is more powerful *if* it applies

# Sphericity

- ▶ The thing that decides whether the univariate tests apply is called “sphericity”.
- ▶ This holds if the outcomes have equal variance (to each other) and have the same (positive) correlation across subjects.
- ▶ Tested using Mauchly's test (part of output)
- ▶ If sphericity rejected, there are adjustments to the univariate P-values due to Huynh-Feldt and Greenhouse-Geisser.  
Huynh-Feldt better if responses not actually normal (safer).

# Univariate tests

```
summary(dogs.2)$sphericity.tests
```

	Test statistic	p-value
times	0.12334	0.084567
drug:times	0.12334	0.084567

```
summary(dogs.2)$pval.adjustments
```

	GG eps	Pr(>F[GG])	HF eps	Pr(>F[HF])
times	0.5261798	3.744618e-06	0.6822614	1.843418e-07
drug:times	0.5261798	2.348896e-03	0.6822614	7.307096e-04

attr("na.action")

(Intercept)	drug
1	2

attr("class")

[1] "omit"

```
summary(dogs.2)$univariate.tests
```

	Sum Sq	num Df	Error SS	den Df	F value	Pr(>F)
(Intercept)	71.342	1	22.1026	6	19.3664	0.004565 **
drug	11.520	1	22.1026	6	3.1272	0.127406
times	26.160	3	2.2534	18	69.6546	4.215e-10 ***
drug:times	5.111	3	2.2534	18	13.6095	7.050e-05 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

## Comments

- ▶ The sphericity test for the interaction is almost significant
- ▶ The H-F adjusted P-value for the interaction is a bit bigger than the univariate one, but still strongly significant.
- ▶ Therefore any lack of sphericity does not affect our conclusion: there is an interaction between drug and time
- ▶ ie that the effect of time on log-histamine is different for the two drugs.

## Comments

- ▶ Here, univariate test with Huynh-Feldt correction to P-value for interaction was 0.00073.
- ▶ Significant interaction *is* the conclusion here.
- ▶ If the interaction had not been significant:
  - ▶ cannot remove interaction with time
  - ▶ so look at univariate (better, especially if adjusted for sphericity) tests of main effects in *this* model

## Next

- ▶ Interaction significant. Pattern of response over time different for the two drugs.
- ▶ Want to investigate interaction.

# The wrong shape

- ▶ But data frame has several observations per line (“wide format”):

```
dogs %>% slice(1:6)
```

```
# A tibble: 6 x 7
```

	dog	drug	x	lh0	lh1	lh3	lh5
	<chr>	<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>
1	A	Morphine	N	-3.22	-1.61	-2.3	-2.53
2	B	Morphine	N	-3.91	-2.81	-3.91	-3.91
3	C	Morphine	N	-2.66	0.34	-0.73	-1.43
4	D	Morphine	N	-1.77	-0.56	-1.05	-1.43
5	E	Trimethaphan	N	-3.51	-0.48	-1.17	-1.51
6	F	Trimethaphan	N	-3.51	0.05	-0.31	-0.51

- ▶ Plotting works with data in “long format”: one response per line.
- ▶ The responses are log-histamine at different times, labelled lh-something. Call them all lh and put them in one column, with the time they belong to labelled.



## Running pivot\_longer, try 1

```
dogs %>% pivot_longer(starts_with("lh"),  
                      names_to = "time", values_to = "lh")
```

```
# A tibble: 32 x 5
```

	dog	drug	x	time	lh
	<chr>	<chr>	<chr>	<chr>	<dbl>
1	A	Morphine	N	lh0	-3.22
2	A	Morphine	N	lh1	-1.61
3	A	Morphine	N	lh3	-2.3
4	A	Morphine	N	lh5	-2.53
5	B	Morphine	N	lh0	-3.91
6	B	Morphine	N	lh1	-2.81
7	B	Morphine	N	lh3	-3.91
8	B	Morphine	N	lh5	-3.91
9	C	Morphine	N	lh0	-2.66
10	C	Morphine	N	lh1	0.34

```
# i 22 more rows
```

## Getting the times

Not quite right: for the times, we want just the numbers, not the letters lh every time. Want new variable containing just number in time: `parse_number`.

```
dogs %>%  
  pivot_longer(starts_with("lh"),  
               names_to = "timex", values_to = "lh") %>%  
  mutate(time = parse_number(timex))
```

```
# A tibble: 32 x 6
```

	dog	drug	x	timex	lh	time
	<chr>	<chr>	<chr>	<chr>	<dbl>	<dbl>
1	A	Morphine	N	lh0	-3.22	0
2	A	Morphine	N	lh1	-1.61	1
3	A	Morphine	N	lh3	-2.3	3
4	A	Morphine	N	lh5	-2.53	5
5	B	Morphine	N	lh0	-3.91	0
6	B	Morphine	N	lh1	-2.81	1
7	B	Morphine	N	lh3	-3.91	3
8	B	Morphine	N	lh5	-3.91	5
9	C	Morphine	N	lh0	-2.66	0
10	C	Morphine	N	lh1	0.34	1

```
#> # A tibble: 32 x 6
```

## What I did differently

- ▶ I realized that `pivot_longer` was going to produce something like `lh1`, which I needed to do something further with, so this time I gave it a temporary name `timex`.
- ▶ This enabled me to use the name `time` for the actual numeric time.
- ▶ This works now, so next save into a new data frame `dogs.long`.

## Saving the pipelined results

```
dogs %>%  
  pivot_longer(starts_with("lh"),  
               names_to = "timex", values_to = "lh") %>%  
  mutate(time = parse_number(timex)) -> dogs.long  
dogs.long
```

# A tibble: 32 x 6

	dog	drug	x	timex	lh	time
	<chr>	<chr>	<chr>	<chr>	<dbl>	<dbl>
1	A	Morphine	N	lh0	-3.22	0
2	A	Morphine	N	lh1	-1.61	1
3	A	Morphine	N	lh3	-2.3	3
4	A	Morphine	N	lh5	-2.53	5
5	B	Morphine	N	lh0	-3.91	0
6	B	Morphine	N	lh1	-2.81	1
7	B	Morphine	N	lh3	-3.91	3
8	B	Morphine	N	lh5	-3.91	5
9	C	Morphine	N	lh0	-2.66	0
10	C	Morphine	N	lh1	-0.34	1

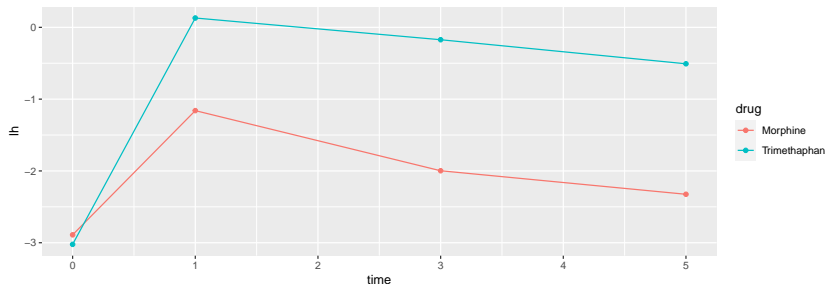
## Comments

This says:

- ▶ Take data frame `dogs`, and then:
- ▶ Combine the columns `lh0` through `lh5` into one column called `lh`, with the column that each `lh` value originally came from labelled by `timex`, and then:
- ▶ Pull out numeric values in `timex`, saving in `time` and then:
- ▶ save the result in a data frame `dogs.long`.

# Interaction plot

```
ggplot(dogs.long, aes(x = time, y = lh,  
                      colour = drug, group = drug)) +  
  stat_summary(fun = mean, geom = "point") +  
  stat_summary(fun = mean, geom = "line")
```



## Comments

- ▶ Plot mean 1h value at each time, joining points on same drug by lines.
- ▶ drugs same at time 0
- ▶ after that, Trimethaphan higher than Morphine.
- ▶ Effect of drug not consistent over time: significant interaction.

## Take out time zero

- ▶ Lines on interaction plot would then be parallel, and so interaction should no longer be significant.
- ▶ Go back to original “wide” dogs data frame.

```
response <- with(dogs, cbind(lh1, lh3, lh5)) # excl time 0
dogs.1 <- lm(response ~ drug, data = dogs)
times <- colnames(response)
times.df <- data.frame(times=factor(times))
dogs.2 <- Manova(dogs.1,
  idata = times.df,
  idesign = ~times
)
```



# Results (univariate)

```
summary(dogs.2)$sphericity.tests
```

	Test statistic	p-value
times	0.57597	0.25176
drug:times	0.57597	0.25176

```
summary(dogs.2)$pval.adjustments
```

	GG eps	Pr(>F[GG])	HF eps	Pr(>F[HF])
times	0.7022305	0.0003752847	0.8520467	0.0001117394
drug:times	0.7022305	0.1078608639	0.8520467	0.0942573437

```
attr("na.action")
```

(Intercept)	drug
1	2

```
attr("class")
```

```
[1] "omit"
```

```
summary(dogs.2)$univariate.tests
```

	Sum Sq	num Df	Error SS	den Df	F value	Pr(>F)
(Intercept)	24.2607	1	20.1874	6	7.2106	0.03628 *
drug	16.2197	1	20.1874	6	4.8207	0.07053 .
times	3.3250	2	0.7301	12	27.3251	3.406e-05 ***
drug:times	0.3764	2	0.7301	12	3.0929	0.08254 .

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

## Comments

- ▶ sphericity: no problem (P-value 0.25)
- ▶ univariate test for interaction no longer significant (P-value 0.082)
- ▶ look at main effects:
  - ▶ strong significance of time, even after taking out time 0
  - ▶ actually *not* significant drug effect, despite interaction plot

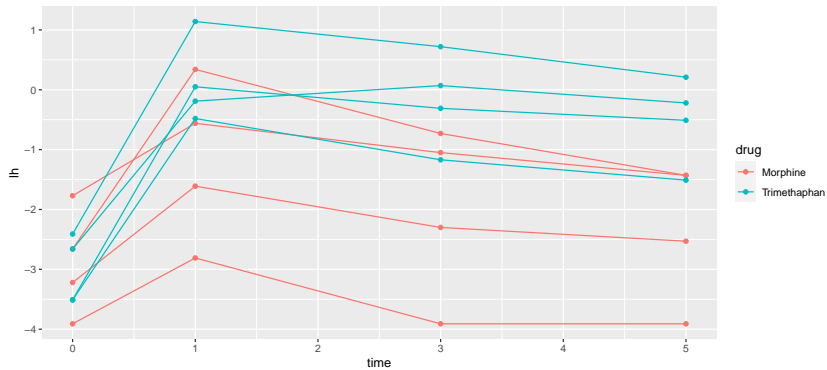
## Is the non-significant drug effect reasonable?

- ▶ Plot *actual data*: lh against days, labelling observations by drug: “spaghetti plot”.
- ▶ Uses long data frame (confusing, yes I know):
- ▶ Plot (time,lh) points coloured by drug
- ▶ and connecting measurements for each *dog* by lines.
- ▶ This time, we want `group = dog` (want the measurements for each *dog* joined by lines), but `colour = drug`:

```
ggplot(dogs.long, aes(x = time, y = lh,  
  colour = drug, group = dog)) +  
  geom_point() + geom_line() -> g
```

# The spaghetti plot

g



## Comments

- ▶ For each dog over time, there is a strong increase and gradual decrease in log-histamine. The gradual decrease explains the significant time effect after we took out time 0.
- ▶ The pattern is more or less the same for each dog, regardless of drug. This explains the non-significant interaction.
- ▶ Most of the trimethaphan dogs (blue) have higher log-histamine throughout (time 1 and after), and some of the morphine dogs have lower.
- ▶ *But* two of the morphine dogs have log-histamine profiles like the trimethaphan dogs. This ambiguity is probably why the drug effect is not quite significant.

# Mixed models

- ▶ Another way to fit repeated measures
- ▶ Subjects (on whom repeated measures taken) are *random sample of all possible subjects* (random effects)
- ▶ Times and treatments are *the only ones we care about* (fixed effects)
- ▶ Use package lme4 function lmer (like lm in some ways)
- ▶ Uses long-format “tidy” data

## Fitting the model (uses lme4)

```
# dogs.long including time zero  
dogs.3 <- lmer(lh~drug*time+(1|dog), data=dogs.long)
```

- note specification of random effect: each dog has “random intercept” that moves log-histamine up or down for that dog over all times

# What can we drop?

► using drop1:

```
drop1(dogs.3, test="Chisq")
```

Single term deletions

Model:

```
lh ~ drug * time + (1 | dog)
```

	npair	AIC	LRT	Pr(Chi)
<none>		113.26		
drug:time	1	114.21	2.9534	0.0857 .

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

► Interaction again not significant, but P-value smaller than before



## Re-fit without interaction

```
dogs.4 <- update(dogs.3, .~.-drug:time)
drop1(dogs.4, test="Chisq")
```

Single term deletions

Model:

```
lh ~ drug + time + (1 | dog)
```

	npars	AIC	LRT	Pr(Chi)
<none>		114.21		
drug	1	115.57	3.3560	0.06696 .
time	1	114.96	2.7501	0.09725 .

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

- ▶ This time neither drug nor (surprisingly) time is significant.
- ▶ MANOVA and lmer methods won't agree, but both valid ways to approach problem.

## The exercise data

- ▶ 30 people took part in an exercise study.
- ▶ Each subject was randomly assigned to one of two diets (“low fat” or “non-low fat”) and to one of three exercise programs (“at rest”, “walking”, “running”).
- ▶ There are  $2 \times 3 = 6$  experimental treatments, and thus each one is replicated  $30/6 = 5$  times.
- ▶ Nothing unusual so far.
- ▶ However, each subject had their pulse rate measured at three different times (1, 15 and 30 minutes after starting their exercise), so have repeated measures.

## Reading the data

Separated by *tabs*:

```
url <- "http://ritsokiguess.site/datafiles/exercise2.txt"
exercise.long <- read_tsv(url)
exercise.long
```

# A tibble: 90 x 5

	id	diet	exertype	pulse	time
	<dbl>	<chr>	<chr>	<dbl>	<chr>
1	1	nonlowfat	atrest	85	min01
2	1	nonlowfat	atrest	85	min15
3	1	nonlowfat	atrest	88	min30
4	2	nonlowfat	atrest	90	min01
5	2	nonlowfat	atrest	92	min15
6	2	nonlowfat	atrest	93	min30
7	3	nonlowfat	atrest	97	min01
8	3	nonlowfat	atrest	97	min15
9	3	nonlowfat	atrest	94	min30
10	4	nonlowfat	atrest	80	min01

## Making wide format

- ▶ `pivot_wider` needs: a column that is going to be split, and the column to make the values out of:

```
exercise.long %>% pivot_wider(names_from=time,  
                             values_from=pulse) -> exercise.wide  
exercise.wide %>% sample_n(5)
```

# A tibble: 5 x 6

	id	diet	exertype	min01	min15	min30
	<dbl>	<chr>	<chr>	<dbl>	<dbl>	<dbl>
1	29	lowfat	running	94	135	130
2	17	lowfat	walking	103	109	90
3	2	nonlowfat	atrest	90	92	93
4	6	lowfat	atrest	83	83	84
5	5	nonlowfat	atrest	91	92	91

- ▶ Normally `pivot_longer` `min01`, `min15`, `min30` into one column called `pulse` labelled by the number of minutes. But `Manova` needs it the other way.

## Setting up the repeated-measures analysis

- ▶ Make a response variable consisting of min01, min15, min30:

```
response <- with(exercise.wide, cbind(min01, min15, min30))
```

- ▶ Predict that from diet and exertype and interaction using lm:

```
exercise.1 <- lm(response ~ diet * exertype,  
  data = exercise.wide  
)
```

- ▶ Run this through Manova:

```
times <- colnames(response)  
times.df <- data.frame(times=factor(times))  
exercise.2 <- Manova(exercise.1,  
  idata = times.df,  
  idesign = ~times)
```

## Sphericity tests

```
summary(exercise.2)$sphericity.tests
```

	Test statistic	p-value
times	0.92416	0.40372
diet:times	0.92416	0.40372
exertype:times	0.92416	0.40372
diet:exertype:times	0.92416	0.40372

No problem with sphericity; go to univariate tests.

# Univariate tests

```
summary(exercise.2)$univariate.tests
```

	Sum Sq	num Df	Error SS	den Df	F value	Pr(>F)	
(Intercept)	894608	1	2085.2	24	10296.6595	< 2.2e-16	***
diet	1262	1	2085.2	24	14.5238	0.0008483	***
exertype	8326	2	2085.2	24	47.9152	4.166e-09	***
diet:exertype	816	2	2085.2	24	4.6945	0.0190230	*
times	2067	2	1563.6	48	31.7206	1.662e-09	***
diet:times	193	2	1563.6	48	2.9597	0.0613651	.
exertype:times	2723	4	1563.6	48	20.9005	4.992e-10	***
diet:exertype:times	614	4	1563.6	48	4.7095	0.0027501	**

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

- ▶ The three-way interaction is significant
  - ▶ the effect of diet on pulse rate over time is different for the different exercise types

## Making some graphs

- ▶ Three-way interactions are difficult to understand. To make an attempt, look at some graphs.
- ▶ Plot time trace of pulse rates for each individual, joined by lines, and make *separate* plots for each diet-exertype combo.
- ▶ ggplot again. Using *long* data frame:

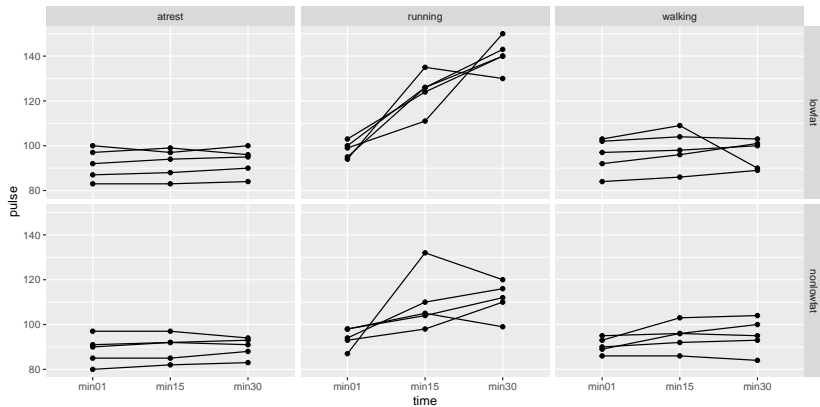
```
g <- ggplot(exercise.long, aes(  
  x = time, y = pulse,  
  group = id  
)) + geom_point() + geom_line() +  
  facet_grid(diet ~ exertype)
```

- ▶ `facet_grid(diet~exertype)`: do a separate plot for each combination of diet and exercise type, with diets going down the page and exercise types going across. (Graphs are usually landscape, so have the factor `exertype` with more levels going across.)



# The graph(s)

09



## Comments on graphs

- ▶ For subjects who were at rest, no change in pulse rate over time, for both diet groups.
- ▶ For walking subjects, not much change in pulse rates over time. Maybe a small increase on average between 1 and 15 minutes.
- ▶ For both running groups, an overall increase in pulse rate over time, but the increase is stronger for the lowfat group.
- ▶ No consistent effect of diet over all exercise groups.
- ▶ No consistent effect of exercise type over both diet groups.
- ▶ No consistent effect of time over all diet-exercise type combos.

## “Simple effects” of diet for the subjects who ran

- ▶ Looks as if there is only any substantial time effect for the runners. For them, does diet have an effect?
- ▶ Pull out only the runners from the wide data:

```
exercise.wide %>%  
  filter(exertype == "running") -> runners.wide
```

- ▶ Create response variable and do MANOVA. Some of this looks like before, but I have different data now:

```
response <- with(runners.wide, cbind(min01, min15, min30))  
runners.1 <- lm(response ~ diet, data = runners.wide)  
times <- colnames(response)  
times.df <- data.frame(times=factor(times))  
runners.2 <- Manova(runners.1,  
  idata = times.df,  
  idesign = ~times  
)
```

## Sphericity tests

```
summary(runners.2)$sphericity.tests
```

	Test statistic	p-value
times	0.81647	0.4918
diet:times	0.81647	0.4918

► No problem, look at univariate tests.

# Univariate tests

```
summary(runners.2)$univariate.tests
```

	Sum Sq	num Df	Error SS	den Df	F value	Pr(>F)	
(Intercept)	383522	1	339.2	8	9045.3333	1.668e-13	***
diet	1920	1	339.2	8	45.2830	0.0001482	***
times	4714	2	1242.0	16	30.3644	3.575e-06	***
diet:times	789	2	1242.0	16	5.0795	0.0195874	*

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

- ▶ Interaction still significant
  - ▶ dependence of pulse rate on time still different for the two diets

## How is the effect of diet different over time?

- ▶ Table of means. Only I need long data for this:

```
runners.wide %>%  
  pivot_longer(starts_with("min"),  
               names_to = "time", values_to = "pulse") %>%  
  group_by(time, diet) %>%  
  summarize(  
    mean = mean(pulse),  
    sd = sd(pulse)  
  ) -> summ
```

- ▶ Result of summarize is data frame, so can save it (and do more with it if needed).

# Understanding diet-time interaction

## ► The summary:

```
summ
```

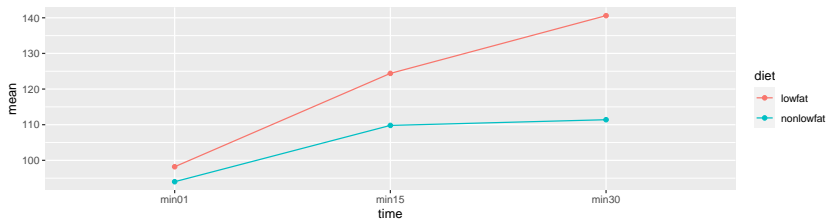
```
# A tibble: 6 x 4
# Groups:   time [3]
  time  diet      mean    sd
  <chr> <chr>   <dbl> <dbl>
1 min01 lowfat    98.2  3.70
2 min01 nonlowfat  94    4.53
3 min15 lowfat   124.   8.62
4 min15 nonlowfat 110.  13.1
5 min30 lowfat   141.   7.20
6 min30 nonlowfat 111.   7.92
```

- Pulse rates at any given time higher for lowfat (diet effect),
- Pulse rates increase over time of exercise (time effect),
- but the *amount by which pulse rate higher* for a diet depends on time: diet by time interaction.

# Interaction plot

- We went to trouble of finding means by group, so making interaction plot is now mainly easy:

```
ggplot(summ, aes(x = time, y = mean, colour = diet,  
                 group = diet)) + geom_point() + geom_line
```





## Comment on interaction plot

- ▶ The lines are not parallel, so there is interaction between diet and time for the runners.
- ▶ The effect of time on pulse rate is different for the two diets, even though all the subjects here were running.