

## Tidying data: extras

# Packages

```
library(tidyverse)
```

## The pig feed data again

```
my_url <- "http://ritsokiguess.site/datafiles/pigs1.txt"
pigs <- read_table(my_url)
pigs
```

```
# A tibble: 5 x 5
  pig feed1 feed2 feed3 feed4
<dbl> <dbl> <dbl> <dbl> <dbl>
1     1  60.8  68.7  92.6  87.9
2     2   57   67.7  92.1  84.2
3     3   65   74   90.2  83.1
4     4  58.6  66.3  96.5  85.7
5     5  61.7  69.8  99.1  90.3
```

## Make longer (as before)

```
pigs %>% pivot_longer(-pig, names_to="feed",  
                      values_to="weight") -> pigs_longer  
  
pigs_longer
```

```
# A tibble: 20 x 3
```

	pig	feed	weight
	<dbl>	<chr>	<dbl>
1	1	feed1	60.8
2	1	feed2	68.7
3	1	feed3	92.6
4	1	feed4	87.9
5	2	feed1	57
6	2	feed2	67.7
7	2	feed3	92.1
8	2	feed4	84.2
9	3	feed1	65
10	3	feed2	74

## Make wider two ways 1/2

`pivot_wider` is inverse of `pivot_longer`:

```
pigs_longer %>%  
  pivot_wider(names_from=feed, values_from=weight)
```

```
# A tibble: 5 x 5  
  pig feed1 feed2 feed3 feed4  
  <dbl> <dbl> <dbl> <dbl> <dbl>  
1     1  60.8  68.7  92.6  87.9  
2     2   57   67.7  92.1  84.2  
3     3   65   74   90.2  83.1  
4     4  58.6  66.3  96.5  85.7  
5     5  61.7  69.8  99.1  90.3
```

we are back where we started.

## Make wider 2/2

Or

```
pigs_longer %>%  
  pivot_wider(names_from=pig, values_from=weight)
```

```
# A tibble: 4 x 6  
  feed    `1`    `2`    `3`    `4`    `5`  
  <chr> <dbl> <dbl> <dbl> <dbl> <dbl>  
1 feed1  60.8   57    65    58.6  61.7  
2 feed2  68.7  67.7   74    66.3  69.8  
3 feed3  92.6  92.1  90.2  96.5  99.1  
4 feed4  87.9  84.2  83.1  85.7  90.3
```

## Disease presence and absence at two locations

Frequencies of plants observed with and without disease at two locations:

Species	Disease present		Disease absent	
	Location X	Location Y	Location X	Location Y
A	44	12	38	10
B	28	22	20	18

This has two rows of headers, so I rewrote the data file:

Species	present_x	present_y	absent_x	absent_y
A	44	12	38	10
B	28	22	20	18

## Read in

... into data frame called prevalence:

```
my_url <- "http://ritsokiguess.site/STAC32/disease.txt"
prevalence <- read_table(my_url)
prevalence
```

# A tibble: 2 x 5

	Species	present_x	present_y	absent_x	absent_y
	<chr>	<dbl>	<dbl>	<dbl>	<dbl>
1	A	44	12	38	10
2	B	28	22	20	18



## Lengthen and separate

```
prevalence %>%  
  pivot_longer(-Species, names_to = "column",  
               values_to = "freq") %>%  
  separate_wider_delim(column, "_",  
                       names = c("disease", "location"))
```

# A tibble: 8 x 4

	Species	disease	location	freq
	<chr>	<chr>	<chr>	<dbl>
1	A	present	x	44
2	A	present	y	12
3	A	absent	x	38
4	A	absent	y	10
5	B	present	x	28
6	B	present	y	22
7	B	absent	x	20
8	B	absent	y	18

## Making longer, the better way

```
prevalence %>%  
  pivot_longer(-Species, names_to=c("disease", "location"),  
               names_sep="_",  
               values_to="frequency") -> prevalence_longer  
prevalence_longer
```

# A tibble: 8 x 4

	Species	disease	location	frequency
	<chr>	<chr>	<chr>	<dbl>
1	A	present	x	44
2	A	present	y	12
3	A	absent	x	38
4	A	absent	y	10
5	B	present	x	28
6	B	present	y	22
7	B	absent	x	20
8	B	absent	y	18

## Making wider, different ways 1/2

```
prevalence_longer %>%  
  pivot_wider(names_from=c(Species, location),  
              values_from=frequency)
```

```
# A tibble: 2 x 5  
  disease    A_x    A_y    B_x    B_y  
  <chr>    <dbl> <dbl> <dbl> <dbl>  
1 present     44     12     28     22  
2 absent     38     10     20     18
```

## Making wider, different ways 2/2

```
prevalence_longer %>%  
  pivot_wider(names_from=location, values_from=frequency)
```

```
# A tibble: 4 x 4
```

	Species	disease	x	y
	<chr>	<chr>	<dbl>	<dbl>
1	A	present	44	12
2	A	absent	38	10
3	B	present	28	22
4	B	absent	20	18

# Interlude

Pigs data again:

```
pigs_longer %>%  
  group_by(feed) %>%  
  summarize(weight_mean=mean(weight))
```

```
# A tibble: 4 x 2  
  feed weight_mean  
  <chr>         <dbl>  
1 feed1         60.6  
2 feed2         69.3  
3 feed3         94.1  
4 feed4         86.2
```

# What if summary is more than one number?

eg. quartiles:

```
pigs_longer %>%  
  group_by(feed) %>%  
  summarize(r=quantile(weight, c(0.25, 0.75)))
```

Warning: Returning more (or less) than 1 row per `summarise()` group was deprecated dplyr 1.1.0.

i Please use `reframe()` instead.

i When switching from `summarise()` to `reframe()`, remember that `reframe()` always returns an ungrouped data frame and adjust accordingly.

`summarise()` has grouped output by 'feed'. You can override using the `.groups` argument.

```
# A tibble: 8 x 2  
# Groups:   feed [4]  
  feed      r  
  <chr> <dbl>  
1 feed1  58.6  
2 feed1  61.7  
3 feed2  67.7  
4 feed2  69.8  
5 feed3  92.1  
6 feed3  96.5
```

## Following the hint (gives no warning)

```
pigs_longer %>%  
  group_by(feed) %>%  
  reframe(r=quantile(weight, c(0.25, 0.75)))
```

```
# A tibble: 8 x 2
```

```
  feed      r
```

```
  <chr> <dbl>
```

```
1 feed1  58.6
```

```
2 feed1  61.7
```

```
3 feed2  67.7
```

```
4 feed2  69.8
```

```
5 feed3  92.1
```

```
6 feed3  96.5
```

```
7 feed4  84.2
```

```
8 feed4  87.9
```

this also works

```
pigs_longer %>%  
  group_by(feed) %>%  
  summarize(r=list(quantile(weight, c(0.25, 0.75)))) %>%  
  unnest(r)
```

```
# A tibble: 8 x 2
```

```
  feed      r  
  <chr> <dbl>
```

```
1 feed1  58.6  
2 feed1  61.7  
3 feed2  67.7  
4 feed2  69.8  
5 feed3  92.1  
6 feed3  96.5  
7 feed4  84.2  
8 feed4  87.9
```



Or, even better, use `enframe`:

```
quantile(pigs_longer$weight, c(0.25, 0.75))
```

```
      25%      75%  
65.975 90.225
```

```
enframe(quantile(pigs_longer$weight, c(0.25, 0.75)))
```

```
# A tibble: 2 x 2  
  name  value  
  <chr> <dbl>  
1 25%    66.0  
2 75%    90.2
```

## A nice look

Run this one line at a time to see how it works:

```
pigs_longer %>%  
  group_by(feed) %>%  
  summarize(r=list(enframe(quantile(weight, c(0.25, 0.75)))))  
  unnest(r) %>%  
  pivot_wider(names_from=name, values_from=value) -> d  
d
```

```
# A tibble: 4 x 3  
  feed `25%` `75%`  
  <chr> <dbl> <dbl>  
1 feed1  58.6  61.7  
2 feed2  67.7  69.8  
3 feed3  92.1  96.5  
4 feed4  84.2  87.9
```

## A hairy one

18 people receive one of three treatments. At 3 different times (pre, post, followup) two variables y and z are measured on each person:

```
my_url <- "http://ritsokiguess.site/STAC32/repmes.txt"
repmes0 <- read_table(my_url)
repmes0
```

# A tibble: 18 x 8

	treatment	rep	pre_y	post_y	fu_y	pre_z	post_z	fu_z
	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
1	A	1	3	13	9	0	0	9
2	A	2	0	14	10	6	6	3
3	A	3	4	6	17	8	2	6
4	A	4	7	7	13	7	6	4
5	A	5	3	12	11	6	12	6
6	A	6	10	14	8	13	3	8
7	B	1	9	11	17	8	11	27
8	B	2	4	16	13	9	3	26

## Create unique ids

```
repmes0 %>% mutate(id=str_c(treatment, ".", rep)) %>%  
  select(-rep) %>%  
  select(id, everything()) -> repmes  
repmes
```

# A tibble: 18 x 8

	id <chr>	treatment <chr>	pre_y <dbl>	post_y <dbl>	fu_y <dbl>	pre_z <dbl>	post_z <dbl>	fu_z <dbl>
1	A.1	A	3	13	9	0	0	9
2	A.2	A	0	14	10	6	6	3
3	A.3	A	4	6	17	8	2	6
4	A.4	A	7	7	13	7	6	4
5	A.5	A	3	12	11	6	12	6
6	A.6	A	10	14	8	13	3	8
7	B.1	B	9	11	17	8	11	27
8	B.2	B	4	16	13	9	3	26
9	B.3	B	8	10	9	12	0	18

## Attempt 1

```
repmes %>% pivot_longer(contains("_"),
                        names_to=c("time", "var"),
                        names_sep="_",
                        values_to = "vvv"
                        )
```

# A tibble: 108 x 5

	id	treatment	time	var	vvv
	<chr>	<chr>	<chr>	<chr>	<dbl>
1	A.1	A	pre	y	3
2	A.1	A	post	y	13
3	A.1	A	fu	y	9
4	A.1	A	pre	z	0
5	A.1	A	post	z	0
6	A.1	A	fu	z	9
7	A.2	A	pre	y	0
8	A.2	A	post	y	14

## Comment

This is *too* long! We wanted a column called *y* and a column called *z*, but they have been pivoted-longer too.

## Attempt 2

```
repmes %>% pivot_longer(contains("_"),  
                        names_to=c("time", ".value"),  
                        names_sep="_"  
                        ) -> repmes3
```

repmes3

# A tibble: 54 x 5

	id	treatment	time	y	z
	<chr>	<chr>	<chr>	<dbl>	<dbl>
1	A.1	A	pre	3	0
2	A.1	A	post	13	0
3	A.1	A	fu	9	9
4	A.2	A	pre	0	6
5	A.2	A	post	14	6
6	A.2	A	fu	10	3
7	A.3	A	pre	4	8
8	A.3	A	post	6	2

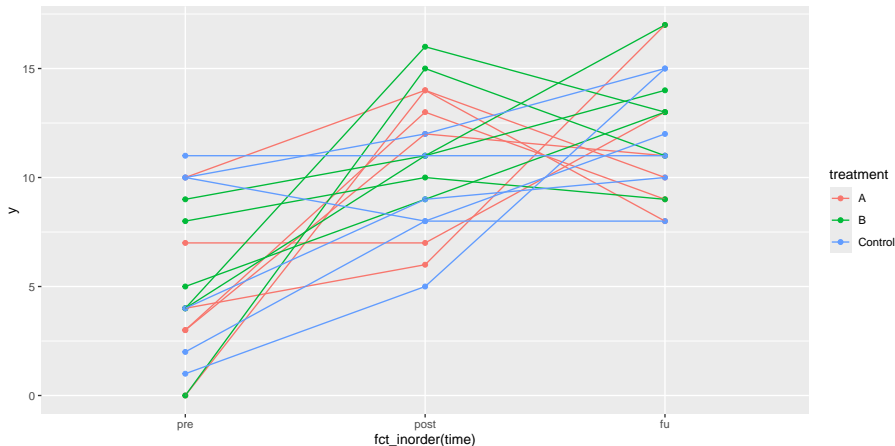
## Comment

This has done what we wanted.



## Make a graph

```
ggplot(repmes3, aes(x=fct_inorder(time), y=y,
                    colour=treatment, group = id)) +
  geom_point() + geom_line()
```

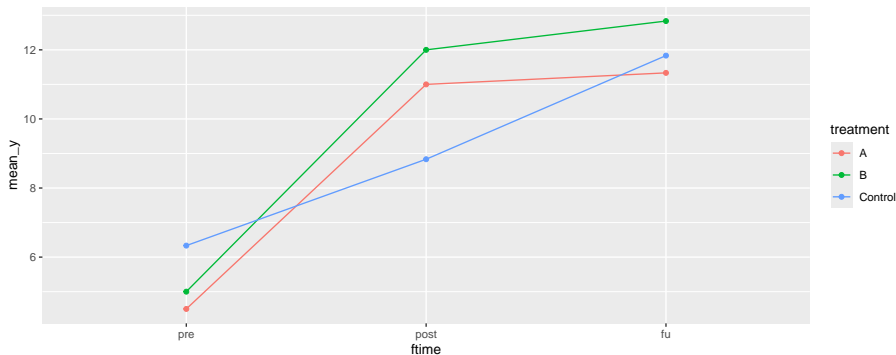


# Comment

- A so-called “spaghetti plot”:
  - ▶ The three measurements for each person are joined by lines
  - ▶ The lines are coloured by treatment.

## Or do the plot with means

```
repmes3 %>% group_by(treatment, ftime=fct_inorder(time)) %>%  
  summarize(mean_y=mean(y)) %>%  
  ggplot(aes(x=ftime, y=mean_y, colour=treatment,  
             group=treatment)) +  
    geom_point() + geom_line()
```



## Comment

- On average, the two real treatments go up and level off
- but the control group is very different.