Joins

PSY 410: Data Science for Psychology

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Setup

Why join data?

Three files, one question

Your participant took a survey on Monday and did a cognitive task on Tuesday. The survey data is in one CSV. The task data is in another. Their demographics are in a third.

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You want to ask: *"Did anxious participants respond more slowly?"*

. . .

You can't answer that from any single file. You need **joins** — the tool that connects separate tables through a shared key.

Two tables, one question

```
# Participant information
participants <- tibble(
  participant_id = 1:4,
  age = c(22, 25, 19, 31),
  condition = c("Control", "Treatment", "Treatment", "Control")
)

# Survey responses (collected separately)
survey <- tibble(
```

```
  participant_id = c(1, 2, 3, 5),  # Note: 4 is missing, 5 is extra
  depression = c(12, 18, 10, 25),
  anxiety = c(15, 20, 12, 30)
)
```

The two tables

Participants:

```
participants
```

```
# A tibble: 4 x 3
  participant_id   age condition
           <int> <dbl> <chr>
1              1    22 Control
2              2    25 Treatment
3              3    19 Treatment
4              4    31 Control
```

Survey:

```
survey
```

```
# A tibble: 4 x 3
  participant_id depression anxiety
           <dbl>      <dbl>   <dbl>
1              1         12      15
2              2         18      20
3              3         10      12
4              5         25      30
```

. . .

How do we combine these based on `participant_id`?

Keys

What are keys?

Keys are variables that uniquely identify observations and connect tables.

. . .

Primary key: Uniquely identifies each observation in a table

- `participant_id` in the participants table
- Each participant appears only once

. . .

Foreign key: References the primary key of another table

- `participant_id` in the survey table
- Links back to the participants table

Checking for unique keys

Before joining, verify that your key truly identifies each row:

```
# Check if participant_id is unique
participants |>
  count(participant_id) |>
  filter(n > 1)
```

```
# A tibble: 0 x 2
# i 2 variables: participant_id <int>, n <int>
```

. . .

Empty result = good! Each participant appears only once.

When keys aren't unique

Sometimes keys aren't unique (e.g., longitudinal data):

```r
longitudinal <- tibble(
  participant_id = c(1, 1, 2, 2, 3, 3),
  timepoint = c(1, 2, 1, 2, 1, 2),
  depression = c(20, 15, 18, 12, 25, 22)
)
```

. . .

Here, the **combination** of `participant_id` + `timepoint` is the key:

```r
longitudinal |>
  count(participant_id, timepoint) |>
  filter(n > 1)
```

```
# A tibble: 0 x 3
# i 3 variables: participant_id <dbl>, timepoint <dbl>, n <int>
```

Mutating joins

The join family

Mutating joins add columns from one table to another:

Function	Keeps rows from...
`left_join()`	Left table (all rows)
`right_join()`	Right table (all rows)
`inner_join()`	Both tables (only matches)
`full_join()`	Both tables (all rows)

left_join(): Most common

Keep **all** rows from the left table, add matching data from the right:

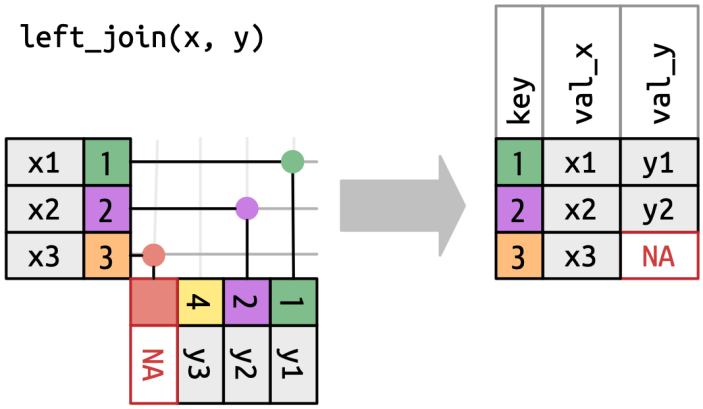
```r
participants |>
  left_join(survey, by = "participant_id")
```

```
# A tibble: 4 x 5
  participant_id   age condition depression anxiety
           <dbl> <dbl> <chr>           <dbl>   <dbl>
1              1    22 Control            12      15
2              2    25 Treatment          18      20
3              3    19 Treatment          10      12
4              4    31 Control            NA      NA
```

. . .

- Participant 4 has no survey data → `NA`
- Participant 5 from survey isn't in participants → excluded

Visualizing left_join()



All rows from the left (blue) table are kept.

right_join(): The mirror

Keep **all** rows from the right table:

```
participants |>
  right_join(survey, by = "participant_id")
```

```
# A tibble: 4 x 5
  participant_id   age condition depression anxiety
           <dbl> <dbl> <chr>           <dbl>   <dbl>
1              1    22 Control            12      15
```

```
2              2    25 Treatment          18       20
3              3    19 Treatment          10       12
4              5    NA <NA>               25       30
```

. . .

Now participant 5 is included (with `NA` for age/condition), but participant 4 is excluded.

inner_join(): Only matches

Keep **only** rows that exist in both tables:

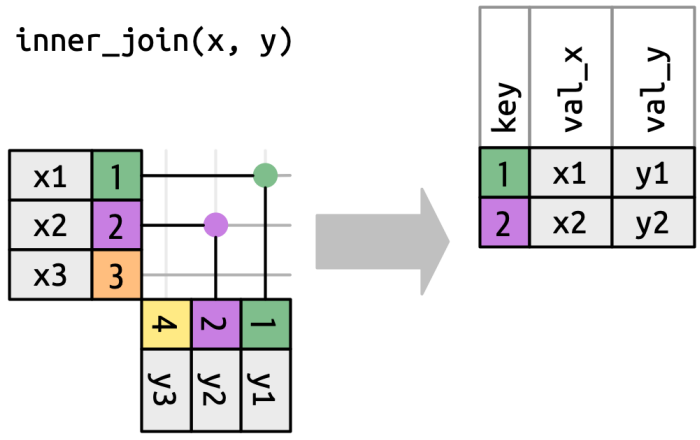
```
participants |>
  inner_join(survey, by = "participant_id")
```

```
# A tibble: 3 x 5
  participant_id   age condition depression anxiety
           <dbl> <dbl> <chr>           <dbl>   <dbl>
1              1    22 Control            12      15
2              2    25 Treatment          18      20
3              3    19 Treatment          10      12
```

. . .

- Participant 4 excluded (no survey data)
- Participant 5 excluded (not in participants)

Visualizing inner_join()



Only matching rows are kept.

full_join(): Everything

Keep **all** rows from both tables:

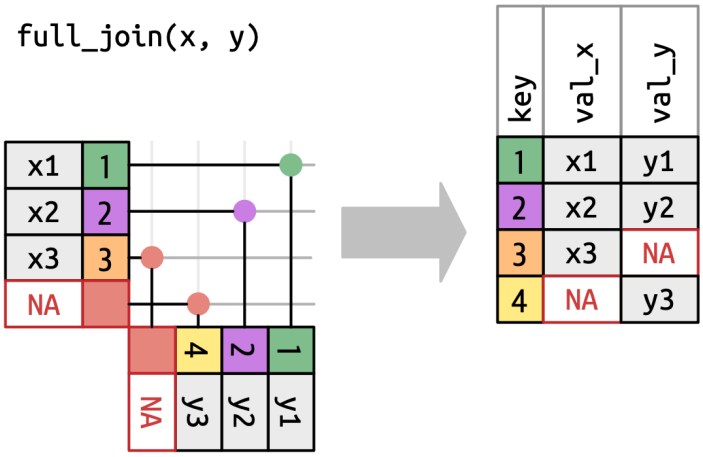
```
participants |>
  full_join(survey, by = "participant_id")
```

```
# A tibble: 5 x 5
  participant_id   age condition depression anxiety
           <dbl> <dbl> <chr>           <dbl>   <dbl>
1              1    22 Control            12      15
2              2    25 Treatment          18      20
3              3    19 Treatment          10      12
4              4    31 Control            NA      NA
5              5    NA <NA>               25      30
```

. . .

Every participant appears, with `NA` where data is missing.

Visualizing full_join()



All rows from both tables are kept.

Which join should I use?

Most common in psychology: `left_join()`

. . .

Use when:

- You have a main participant table
- You want to add additional data (surveys, behavioral tasks)
- You want to keep all participants, even those with missing data

. . .

> **Tip**
>
> Start with `left_join()` unless you have a specific reason to use another type.

Psychology example: Adding demographics

```
# Task data
task_data <- tibble(
  participant_id = c(1, 2, 3, 1, 2, 3),
  trial = c(1, 1, 1, 2, 2, 2),
  reaction_time = c(450, 380, 520, 430, 395, 510)
)

# Add participant info to each trial
task_data |>
  left_join(participants, by = "participant_id")
```

```
# A tibble: 6 x 5
  participant_id trial reaction_time   age condition
           <dbl> <dbl>         <dbl> <dbl> <chr>
1              1     1           450    22 Control
2              2     1           380    25 Treatment
3              3     1           520    19 Treatment
4              1     2           430    22 Control
5              2     2           395    25 Treatment
6              3     2           510    19 Treatment
```

Joining by multiple keys

For longitudinal data, join on multiple columns:

```
# Time 1 scores
time1 <- tibble(
  id = c(1, 2, 3),
  time = 1,
  depression = c(20, 18, 25)
)

# Time 2 scores
time2 <- tibble(
  id = c(1, 2, 3),
  time = 2,
  depression = c(15, 12, 22)
)
```

Combining longitudinal data

```
# Combine into one table
all_times <- bind_rows(time1, time2)

# Add baseline demographics
all_times |>
  left_join(
    participants |> select(participant_id, age, condition),
    by = c("id" = "participant_id")  # Keys have different names
  )
```

```
# A tibble: 6 x 5
     id  time depression   age condition
  <dbl> <dbl>      <dbl> <dbl> <chr>
1     1     1         20    22 Control
2     2     1         18    25 Treatment
3     3     1         25    19 Treatment
4     1     2         15    22 Control
5     2     2         12    25 Treatment
6     3     2         22    19 Treatment
```

Pair coding break

Your turn: Combine study data

You have three tables from a therapy study:

```
baseline <- tibble(
  id = 1:5,
  age = c(25, 30, 22, 35, 28),
  baseline_depression = c(22, 25, 18, 30, 20)
)

treatment <- tibble(
  id = c(1, 2, 3, 4),  # Missing id 5
  condition = c("CBT", "Control", "CBT", "Control")
)

followup <- tibble(
  id = c(1, 2, 3, 5),  # Missing id 4, but has id 5
  followup_depression = c(12, 23, 10, 18)
)
```

1. Create a dataset with baseline info and treatment condition (keep all participants)
2. Add followup data (keep all from step 1)
3. How many participants are missing followup data?

Time: 10 minutes

Filtering joins

A different purpose

Filtering joins don't add columns — they filter rows based on whether matches exist:

- `semi_join()` — Keep rows that **have** a match
- `anti_join()` — Keep rows that **don't have** a match

semi_join(): Has a match

Keep rows from the left table that exist in the right table:

```
# Which participants completed the survey?
participants |>
  semi_join(survey, by = "participant_id")
```

```
# A tibble: 3 x 3
  participant_id   age condition
           <int> <dbl> <chr>
1              1    22 Control
2              2    25 Treatment
3              3    19 Treatment
```

. . .

Only participants 1, 2, and 3 completed the survey.

anti_join(): No match

Keep rows from the left table that **don't** exist in the right table:

```
# Which participants didn't complete the survey?
participants |>
  anti_join(survey, by = "participant_id")
```

```
# A tibble: 1 x 3
  participant_id   age condition
           <int> <dbl> <chr>
1              4    31 Control
```

. . .

Participant 4 didn't complete the survey.

Psychology use case: Attrition analysis

```r
# Who was enrolled
enrolled <- tibble(
  participant_id = 1:10,
  condition = rep(c("Treatment", "Control"), each = 5)
)

# Who completed
completed <- tibble(
  participant_id = c(1, 2, 3, 4, 7, 8, 9, 10)  # Missing 5 and 6
)

# Who dropped out?
enrolled |>
  anti_join(completed, by = "participant_id")
```

```
# A tibble: 2 x 2
  participant_id condition
           <int> <chr>
1              5 Treatment
2              6 Control
```

Attrition by condition

```r
dropout <- enrolled |>
  anti_join(completed, by = "participant_id")

dropout |>
  count(condition)
```

```
# A tibble: 2 x 2
  condition     n
  <chr>     <int>
1 Control       1
2 Treatment     1
```

. . .

> ⚠ Warning
>
> Both dropouts were from the Treatment condition — this could bias results!

Common join problems

Problem 1: Keys with different names

```
demographics <- tibble(
  subj_id = 1:3,
  age = c(25, 30, 22)
)

scores <- tibble(
  participant = c(1, 2, 3),
  depression = c(18, 22, 15)
)
```

. . .

Solution: Use named vector in `by`:

```
demographics |>
  left_join(scores, by = c("subj_id" = "participant"))
```

```
# A tibble: 3 x 3
  subj_id   age depression
    <dbl> <dbl>      <dbl>
1       1    25         18
2       2    30         22
3       3    22         15
```

Problem 2: Duplicate keys

```
# Duplicate in left table
participants_dup <- tibble(
  id = c(1, 1, 2, 3),  # ID 1 appears twice!
```

```
  age = c(25, 25, 30, 22)
)

task_scores <- tibble(
  id = c(1, 2, 3),
  score = c(85, 90, 88)
)
```

What happens with duplicates?

```
participants_dup |>
  left_join(task_scores, by = "id")
```

```
# A tibble: 4 x 3
     id   age score
  <dbl> <dbl> <dbl>
1     1    25    85
2     1    25    85
3     2    30    90
4     3    22    88
```

. . .

Each duplicate gets matched → creates extra rows!

. . .

> **!** Important
>
> Always check for duplicate keys before joining.

Problem 3: Missing keys

```
# Some participants have NA for id
messy_data <- tibble(
  id = c(1, 2, NA, 3),
  response = c("Yes", "No", "Yes", "No")
)
```

```r
demographics <- tibble(
  id = 1:3,
  age = c(25, 30, 22)
)
```

Joining with NAs

```r
messy_data |>
  left_join(demographics, by = "id")
```

```
# A tibble: 4 x 3
     id response   age
  <dbl> <chr>    <dbl>
1     1 Yes         25
2     2 No          30
3    NA Yes         NA
4     3 No          22
```

. . .

Row with `NA` id can't match → gets `NA` for age.

Fix the data before joining!

Problem 4: Many-to-many relationships

```r
# Multiple trials per participant
trials <- tibble(
  id = c(1, 1, 2, 2),
  trial = c(1, 2, 1, 2),
  rt = c(450, 430, 380, 390)
)

# Multiple sessions per participant
sessions <- tibble(
  id = c(1, 1, 2, 2),
  session = c(1, 2, 1, 2),
  mood = c(5, 6, 4, 5)
)
```

Many-to-many result

```
trials |>
  left_join(sessions, by = "id")
```

```
# A tibble: 8 x 5
     id trial    rt session  mood
  <dbl> <dbl> <dbl>   <dbl> <dbl>
1     1     1   450       1     5
2     1     1   450       2     6
3     1     2   430       1     5
4     1     2   430       2     6
5     2     1   380       1     4
6     2     1   380       2     5
7     2     2   390       1     4
8     2     2   390       2     5
```

. . .

Creates all combinations — probably not what you want!

Solution: Be more specific about what you're joining on, or reshape first.

Practical psychology examples

Example 1: Qualtrics + demographics

```
# Survey responses exported from Qualtrics
qualtrics <- tibble(
  ResponseId = c("R_1", "R_2", "R_3"),
  PHQ9_total = c(12, 18, 8),
  GAD7_total = c(10, 15, 6)
)

# Demographics collected separately
demo <- tibble(
  ResponseId = c("R_1", "R_2", "R_3"),
  age = c(25, 30, 22),
  gender = c("Female", "Male", "Female")
```

```
)

# Combine
qualtrics |>
  left_join(demo, by = "ResponseId")
```

```
# A tibble: 3 x 5
  ResponseId PHQ9_total GAD7_total   age gender
  <chr>           <dbl>      <dbl> <dbl> <chr>
1 R_1                12         10    25 Female
2 R_2                18         15    30 Male
3 R_3                 8          6    22 Female
```

Example 2: Pre-post intervention

```
pre_test <- tibble(
  participant = 1:4,
  depression_pre = c(22, 25, 18, 20)
)

post_test <- tibble(
  participant = c(1, 2, 4),  # 3 dropped out
  depression_post = c(12, 23, 15)
)

# Combine and compute change
pre_test |>
  left_join(post_test, by = "participant") |>
  mutate(change = depression_pre - depression_post)
```

```
# A tibble: 4 x 4
  participant depression_pre depression_post change
        <dbl>          <dbl>           <dbl>  <dbl>
1           1             22              12     10
2           2             25              23      2
3           3             18              NA     NA
4           4             20              15      5
```

Example 3: Item-level to scale-level

```r
# Individual items
items <- tibble(
  id = rep(1:3, each = 5),
  item = rep(1:5, times = 3),
  response = c(3,4,3,4,3, 2,3,2,3,2, 4,5,4,5,4)
)

# Participant info
participants_info <- tibble(
  id = 1:3,
  condition = c("Control", "Treatment", "Treatment")
)

# Compute scale scores then join
items |>
  group_by(id) |>
  summarize(scale_mean = mean(response)) |>
  left_join(participants_info, by = "id")
```

```
# A tibble: 3 x 3
     id scale_mean condition
  <int>      <dbl> <chr>
1     1        3.4 Control
2     2        2.4 Treatment
3     3        4.4 Treatment
```

End-of-deck exercise

Practice: Longitudinal study

You have data from a three-wave longitudinal study:

```r
# Baseline demographics
baseline_demo <- tibble(
  pid = 1:6,
  age = c(20, 22, 25, 19, 24, 21),
  condition = rep(c("Intervention", "Control"), each = 3)
```

```r
)

# Time 1 assessment
time1_scores <- tibble(
  pid = 1:6,
  depression_t1 = c(22, 25, 18, 20, 24, 19)
)

# Time 2 assessment (2 dropouts)
time2_scores <- tibble(
  pid = c(1, 2, 3, 4, 6),  # Missing 5
  depression_t2 = c(15, 24, 12, 18, 17)
)

# Time 3 assessment (1 more dropout)
time3_scores <- tibble(
  pid = c(1, 2, 3, 6),  # Missing 4 and 5
  depression_t3 = c(12, 22, 10, 15)
)
```

Your tasks

1. Create a complete dataset with all timepoints
2. Compute change scores (T1 to T3)
3. Identify who dropped out at each wave
4. Check if dropout differs by condition

Wrapping up

Join decision flowchart

Ask yourself:

1. **Do I want to add columns?**
   - Yes → Use a mutating join
   - No → Use a filtering join
2. **Which rows do I want to keep?**
   - All from left → `left_join()`
   - All from right → `right_join()`

- Only matches → `inner_join()`
- Everything → `full_join()`

3. **Am I filtering rows?**
   - Keep matches → `semi_join()`
   - Keep non-matches → `anti_join()`

Key takeaways

1. **Joins combine data** from multiple tables using key variables
2. **Check your keys** for uniqueness before joining
3. **`left_join()` is your workhorse** — keeps all rows from your main table
4. **Filtering joins** help identify completers vs. dropouts
5. **Watch for common problems:** duplicate keys, different key names, NAs
6. **Always inspect** the result to ensure it matches expectations

Before next class

Read:

- R4DS Ch 18: Missing values

Do:

- Submit Assignment 6
- Check if your final project needs joins
- Practice joining your own data files

The one thing to remember

If your data lives in separate files, joins are how you ask a question that spans all of them.

See you Wednesday for handling missing data!