Cognitive process:

- 1. Take the **ydat** dataset, **then**
- 2. **filter()** for genes in the leucine biosynthesis pathway, **then**
- 3. **group_by()** the limiting nutrient, **then**
- 4. **summarize()** to correlate rate and expression, **then**
- 5. **mutate()** to round *r* to two digits, *then*
- 6. **arrange()** by rounded correlation coefficients

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The old way:

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arrange(
    mutate(
        summarize(
            group_by(
                filter(ydat, bp=="leucine biosynthesis"),
                nutrient),
        r=cor(rate, expression)),
    r=round(r, 2)),
r)
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```

The dplyr way:

```
ydat %>%
  filter(bp=="leucine biosynthesis") %>%
  group_by(nutrient) %>%
  summarize(r=cor(rate, expression)) %>%
  mutate(r=round(r,2)) %>%
  arrange(r)
```