Repeated Measures in R

Choose paired tests, ANCOVA or longitudinal models from the estimand

Rverse Analytics

Repeated measurements are not independent groups. The correct method depends on the design and target: within-person change, final value adjusted for baseline, or the full trajectory.

Decision map

Design / question	Preferred starting point	Why
One group, two times	paired *t* / Wilcoxon signed-rank	direct within-person contrast
Two randomized groups, baseline + final	ANCOVA of final adjusted for baseline	efficient final-time estimand
≥3 visits or irregular follow-up	mixed model	models correlation and incomplete trajectories
Complete balanced ≥3 visits	repeated-measures ANOVA	usable if assumptions fit
Population-average longitudinal effect	GEE	marginal estimand

Reshape and verify pairing

```
library(dplyr)
library(tidyr)

long <- wide |>
  pivot_longer(c(baseline, week6, week12),
    names_to = "visit", values_to = "score") |>
  mutate(visit = factor(visit,
    levels = c("baseline", "week6", "week12")))

stopifnot(!anyDuplicated(long[c("id", "visit")]))
with(long, table(group, visit, useNA = "ifany"))
```

Two measurements

```
# Paired t-test: analyse differences, not two independent samples
with(wide, t.test(week12, baseline, paired = TRUE))

# Inspect the distribution of paired differences
diff <- wide$week12 - wide$baseline
qqnorm(diff); qqline(diff)

# Robust rank alternative; zeros and symmetry matter
with(wide, wilcox.test(week12, baseline,
                       paired = TRUE, exact = FALSE, conf.int = TRUE))
```

Baseline + final in a randomized trial

```
wide$group <- relevel(factor(wide$group), ref = "Control")

fit_ancova <- lm(week12 ~ group + baseline, data = wide)
broom::tidy(fit_ancova, conf.int = TRUE)
emmeans::emmeans(fit_ancova, ~ group) |>
  pairs(adjust = "none")

# Check whether baseline slope is plausibly common
fit_slope <- lm(week12 ~ group * baseline, data = wide)
anova(fit_ancova, fit_slope)
```

Avoid comparing “significant change in treatment” with “non-significant change in control.” That is not a test of the between-group treatment effect.

Full longitudinal trajectory

```
library(lme4)
library(emmeans)
```

```r
fit_mm <- lmer(score ~ group * visit + (1 | id),
               data = long, REML = TRUE, na.action = na.exclude)

# Adjusted group differences at each visit
emm <- emmeans(fit_mm, ~ group | visit)
pairs(emm, adjust = "holm")

# Planned difference-in-differences contrast
cell <- emmeans(fit_mm, ~ group * visit)
contrast(cell, interaction = "revpairwise", adjust = "holm")
```

If time is approximately linear and equally interpretable per unit, model numeric time and consider `(time | id)`. If visit-specific changes matter, keep time categorical.

Classical repeated-measures ANOVA

```r
# Complete, balanced data only; subject identifies repeated units
fit_rm <- aov(score ~ group * visit + Error(id / visit), data = long)
summary(fit_rm)

# rstatix supplies Mauchly and corrected tests in a tidy workflow
rstatix::anova_test(data = long, dv = score, wid = id,
                    within = visit, between = group)
```

Assumption	If violated
Normal residuals	inspect residuals; robust/sensitivity model
Sphericity for within factor	Greenhouse-Geisser correction
Complete balanced cases	mixed model usually preferable
Same covariance for all	model residual/random-effects structure

Missing visits

- A mixed model uses all observed outcomes under its likelihood assumptions; it does not create missing values.
- The usual interpretation relies on MAR conditional on variables in the model.
- Include strong predictors of missingness and outcome when scientifically justified.
- Compare with multiple imputation or an MNAR sensitivity analysis when dropout may be informative.

Reporting checklist

- State time points, allowable windows, analysed sample and observations per visit.
- Name the estimand: change, adjusted final difference or trajectory contrast.
- Report adjusted estimates with 95% CIs and multiplicity handling.
- For ANOVA, report sphericity tests/corrections and effect size.
- For mixed models, report fixed/random structure, covariance, convergence and missing-data assumption.
