README — Feedback Function and Performance on Variable Differential Reinforcement of Low Rates: Tempus Urgit vel Abundat? (analysis scripts + outputs)

Project overview

This folder contains the R code used to (a) decode MED-PC event files, (b) compute and model inter-response time (IRT) survival functions (VI and VDRL), and (c) analyze/visualize feedback functions (including a mixed-effects Hill fit) and response-rate summaries/plots.

Directory structure

JEAB_25/
  decoder.R
    - Core decoder for MED-PC outputs. Reads raw session files and returns a
      standardized event-level data frame (subject, session, event, time_stamp, etc.).

  survival.R
    - Survival analysis at the individual level (per rat), including:
      - subject-specific refractory-time correction (minimum positive IRT)
      - Kaplan–Meier curves and piecewise exponential fits
      - figure export for individual survival panels
    - Produces: Figures/Figure9.png

  survival_agg.R
    - Aggregated survival analysis:
      - Aggregates IRTs across selected sessions per subject
      - Applies refractory-time correction (shift by min positive IRT)
      - Estimates global breakpoints via PWEXP (MLE)
      - VDRL inference: compares CoxPH vs CoxME (1|subject) using LR Chi-square
      - Plotting overlay: fits a piecewise-exponential mixed model via survSplit + glmer
        to obtain segment hazards (lambdas) for the black model overlay line
      - Computes segment proportions (prop_1, prop_2, prop_3) from the empirical IRTs
      - Excludes subject JL1 ONLY for the aggregated VDRL analysis (as specified)
    - Produces: Figures/Figure10.png (VDRL survival + overlay + breakpoints)

Figures/Figure8.png (VI survival + overlay + breakpoint)
    - Prints: Cox model comparison (VDRL) + final parameter table (VI + VDRL)

  feedback_function.R
    - Feedback-function analysis and figure production.
    - Includes:
      - computing/plotting feedback functions
      - fitting/visualizing candidate equations
      - Hill function definition and a mixed-effects Hill model (nlme)
      - spaghetti (random-effects) curves and fixed-effect curve + simulated CI band
    - Produces multiple figure files inside Figures/ (see "Figures" section below).

  response_rates.R
    - Response-rate analysis using ResponseRates.xlsx:
      - violin plots by condition
      - Gaussian LMM vs Gamma GLMM comparison
      - post-hoc emmeans contrasts
      - individual time-series panel plot (per rat)
    - Produces: Figures/Figure7.png (panel plot)

  full_dataframe.R
    - Utility script to build a combined "full_data" data frame from decoded files.
    - Helpful for downstream analyses that need a single long-format data set.

  SomeTrials.R
    - Exploratory / scratch script (non-essential). Kept for transparency.

  get_r2_nlme.R
    - Helper function to compute R^2-like metrics for nlme models.
    - Called by feedback_function.R when evaluating the mixed Hill fit.

  MedScript/
    VDRL.txt
      - MED-PC script/program used to run the VDRL procedure.

  data/
    simulation_beak/
      RDRL10_JL_b_hdi.xlsx
        - Spreadsheet used for a simulation / auxiliary analysis (not required for the

main survival pipeline unless explicitly referenced elsewhere).

Figures/
- Output folder for exported PNG figures created by the scripts above.

Software requirements

R (recommended: >= 4.2)

Core packages used across scripts:
survival
PWEXP
lme4
coxme
nlme
MASS
scales
dplyr
tidyr
readxl
vioplot
performance
emmeans
car
multcomp

Note:
- Some scripts call `source("decoder.R")` and assume the working directory is the
project root (JEAB_25/).
- Some scripts write PNGs to "Figures/". Make sure this folder exists.

Data requirements/assumptions
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1) Raw MED-PC event files:
- The survival scripts expect raw session files to exist in paths like:
data/rats/VDRL10s/
data/rats/VI30s/
and they are decoded by decoder.R.
- If these folders are not present in your shared archive, you must add them
locally (or update the paths in the scripts) to reproduce survival results.

2) Response-rate spreadsheet:
- response_rates.R expects:

ResponseRates.xlsx
in the project root (or update the file path).

Reproducing the main results (recommended order)
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1) Aggregated survival analysis (final survival figures + parameter table)
- Run:
source("survival_agg.R")
- Outputs:
Figures/Figure10.png (VDRL aggregated survival + model overlay + breakpoints)
Figures/Figure8.png (VI aggregated survival + model overlay + breakpoint)
and prints the Cox model comparison + parameter table to the console.

Important details implemented in survival_agg.R:
- JL1 is excluded ONLY for the aggregated VDRL analysis.
- Breakpoints are estimated empirically via PWEXP MLE (nbreak = 2 for VDRL, 1 for VI).
- The black model overlay line is computed from the piecewise-exponential mixed model
(survSplit + glmer) using fixed-effect segment hazards (lambdas).

2) Individual survival panels (optional)
- Run:
source("survival.R")
- Output:
Figures/Figure9.png

3) Feedback-function analysis (Hill mixed model + related figures)
- Run:
source("get_r2_nlme.R")
source("feedback_function.R")
- Outputs:
Multiple figures inside Figures/ (see console messages and the png() calls in
feedback_function.R for exact filenames).

4) Response-rate analysis and time-series panels
- Ensure ResponseRates.xlsx is present.
- Run:
source("response_rates.R")
- Output:
Figures/Figure7.png

Notes on key modeling choices

- Refractory-time correction:
  For each subject (within the selected sessions), the smallest strictly positive IRT is
  treated as a refractory bound. In the aggregated survival pipeline, IRTs are shifted by
  subtracting this refractory time and then filtered to remain strictly positive.

- Breakpoints:
  Breakpoints are estimated from aggregated IRTs using PWEXP maximum-likelihood fitting:
    - VDRL: two breakpoints (three segments)
    - VI: one breakpoint (two segments)

- VDRL inference vs visualization:
  In survival_agg.R, VDRL inference for clustering is based on a CoxPH vs. CoxME comparison.
  The black overlay line, however, is drawn from a piecewise-exponential mixed model
  (survSplit + glmer) to obtain segment hazards (lambdas) for a clean parametric survival
  curve overlay on the Kaplan–Meier estimate.

Agreement analysis

Agreement analysis, used in Figures 3 and 4, was done using eirasagree (R package), available at: https://doi.org/10.7910/DVN/AGJPZH

Contact/citation

If you use or adapt these scripts, please cite the associated manuscript (JEAB submission)
and acknowledge the code archive (this folder) as the computational supplement.

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