

Data Preprocessing & Analysis

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Anticipating the Beat: Rhythm and Meter in Developmental Dyslexia

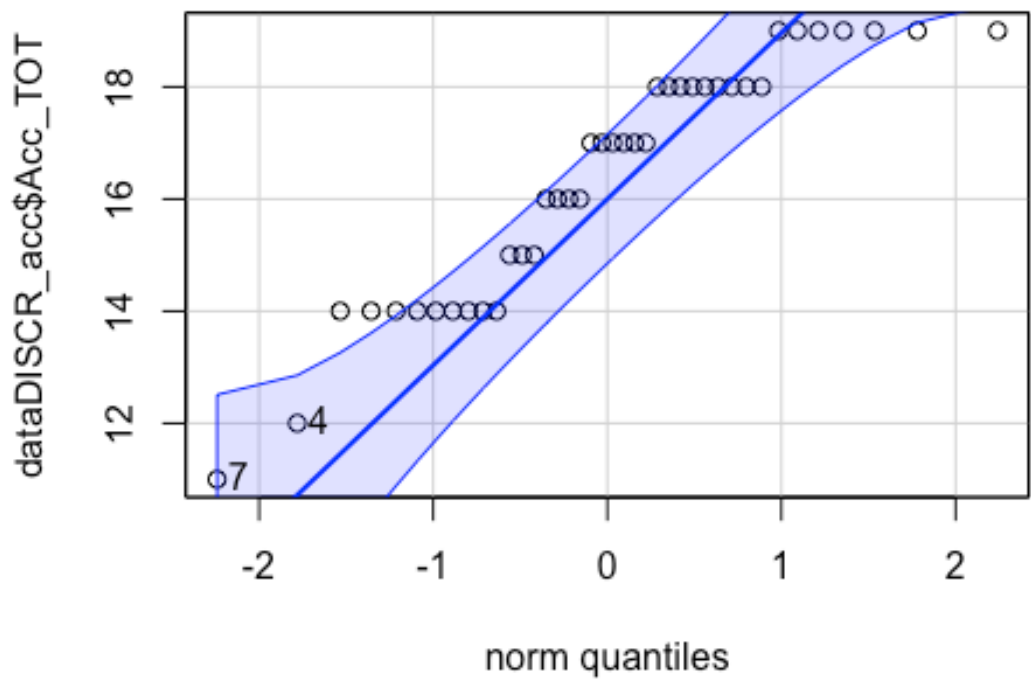
This is the analysis pipeline for the paper “Anticipating the beat: Rhythm and Meter in Developmental Dyslexia” by Carioti et al.

DISCRIMINATION

Descriptive analysis:

	item	group1	vars	n	mean	sd	median	trimmed	mad	min	max	range
X11	1	DYS	1	20	15.95	2.459675	16.5	16.125	3.7065	11	19	8
X12	2	TDC	1	20	16.80	1.735087	17.0	16.875	1.4826	14	19	5
			skew		kurtosis		se					
X11			-0.3284550		-1.249130		0.5500000					
X12			-0.2825678		-1.297391		0.3879772					

Group comparison through the Wilcoxon Mann-Whitney Test:



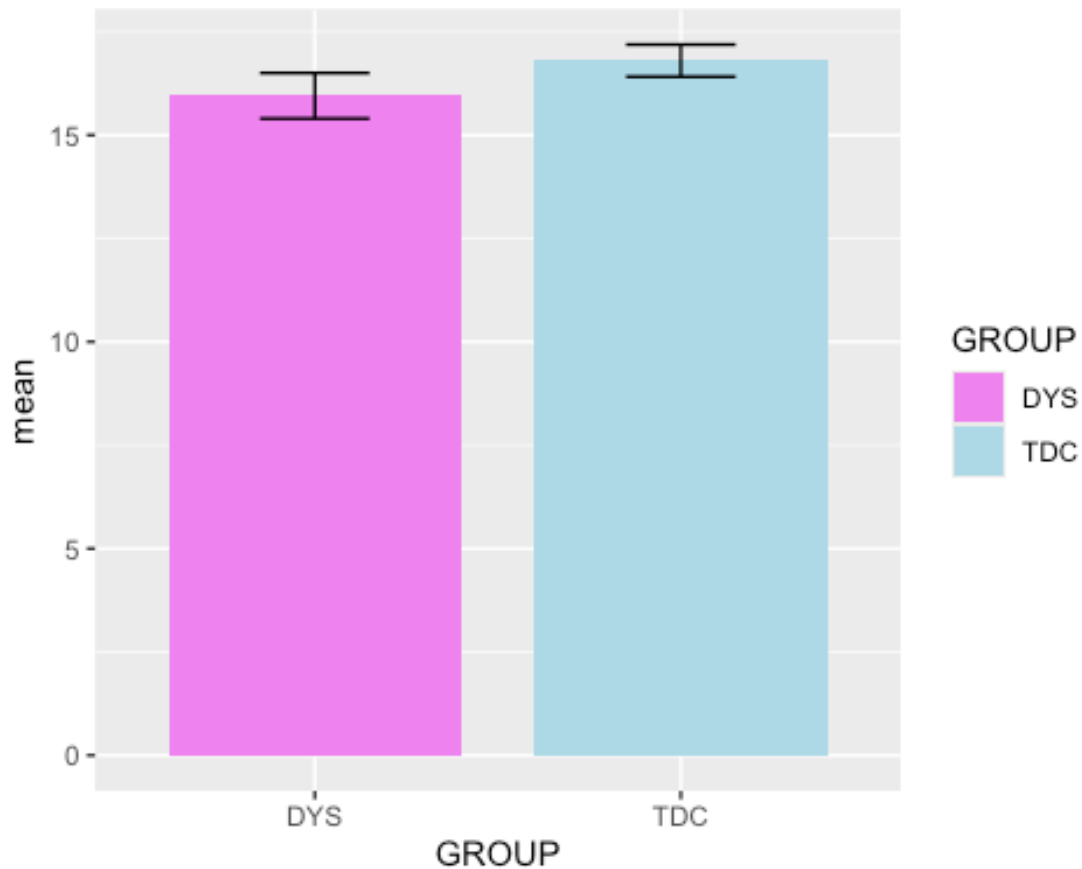
Wilcoxon rank sum test with continuity correction

data: dataDISCR_acc\$Acc_TOT by dataDISCR_acc\$Group

W = 163.5, p-value = 0.3222

alternative hypothesis: true location shift is not equal to 0

Supplementary Image 1

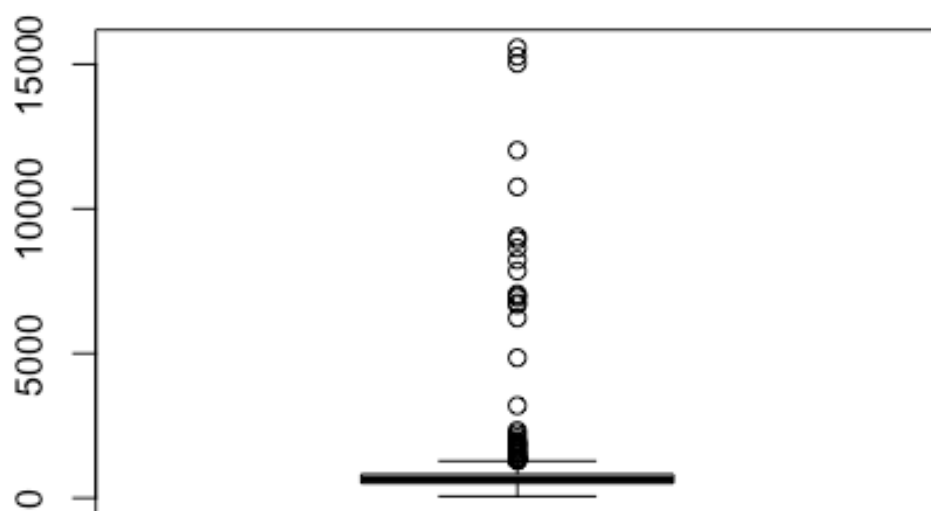


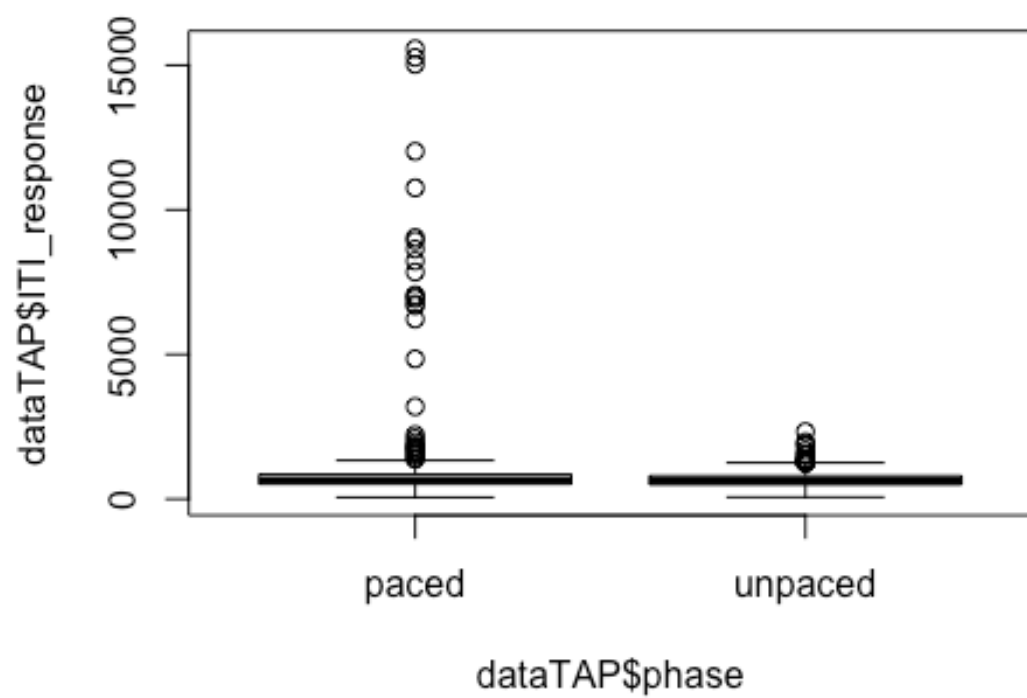
TAPPING

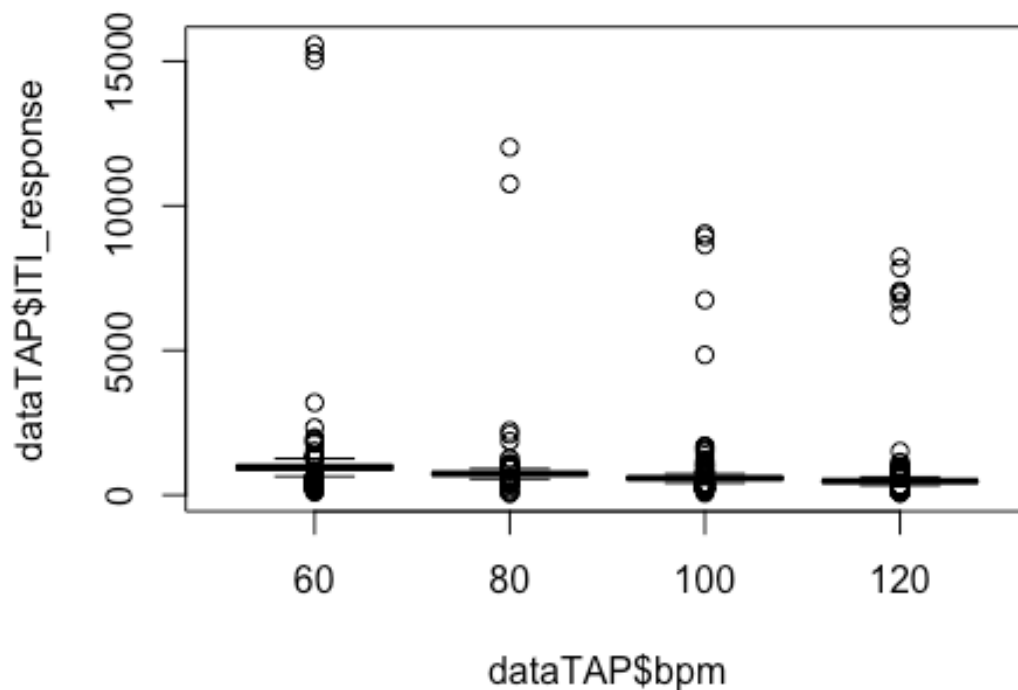
1. Raw data

For each participant, trial, condition, and tempo, retain beat timestamps, tap timestamps, paced/unpaced condition, trial order, group, and BPM. Original timestamps should never be modified.

2. Data Exploration







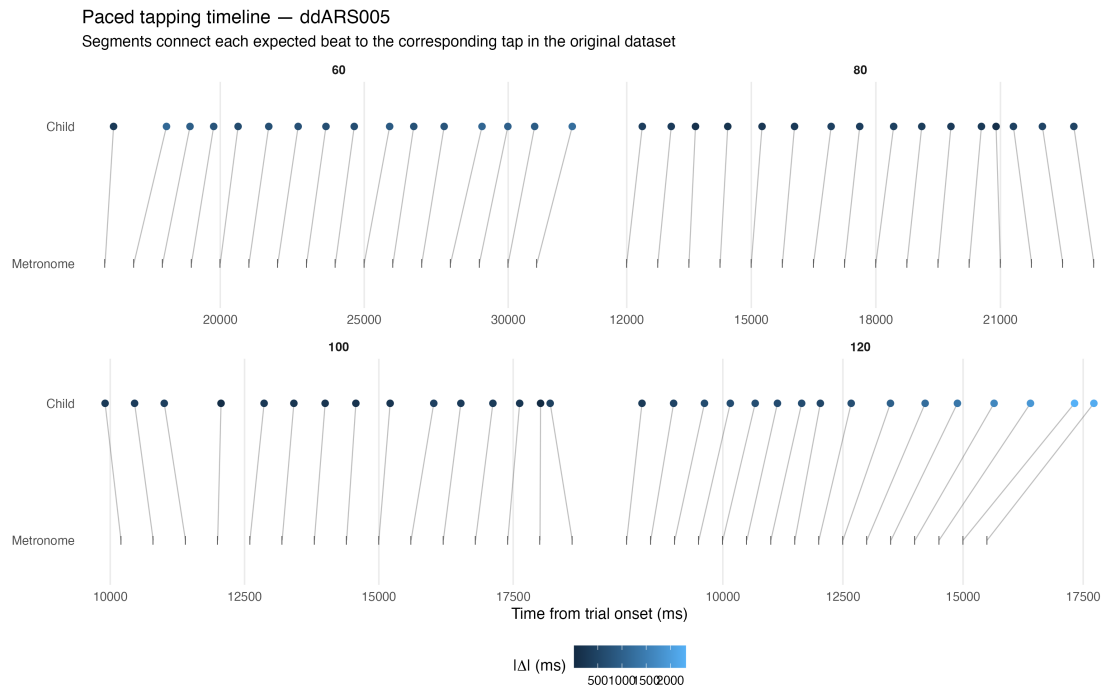
Individual exploration:

Possible double or missed clicks could shift the time series in the Excel file, thereby biasing the calculation of asynchrony. In the paced phase, these events can be identified solely on the basis of the reference timestamps.

For example, we could explore the situation of a DYS participant:

```
# A tibble: 16 × 5
  out_iresp out_tref out_tresp out_tdelta ITI_response
1         1    16000    16294         294          NA
2         2    17000    18132        1132        1838
3         3    18000    18949         949         817
4         4    19000    19771         771         822
5         5    20000    20619         619         848
6         6    21000    21684         684        1065
7         7    22000    22705         705        1021
8         8    23000    23671         671         966
9         9    24000    24653         653         982
10        10    25000    25883         883        1230
11        11    26000    26720         720         837
12        12    27000    27776         776        1056
13        13    28000    29091        1091        1315
14        14    29000    29988         988         897
```

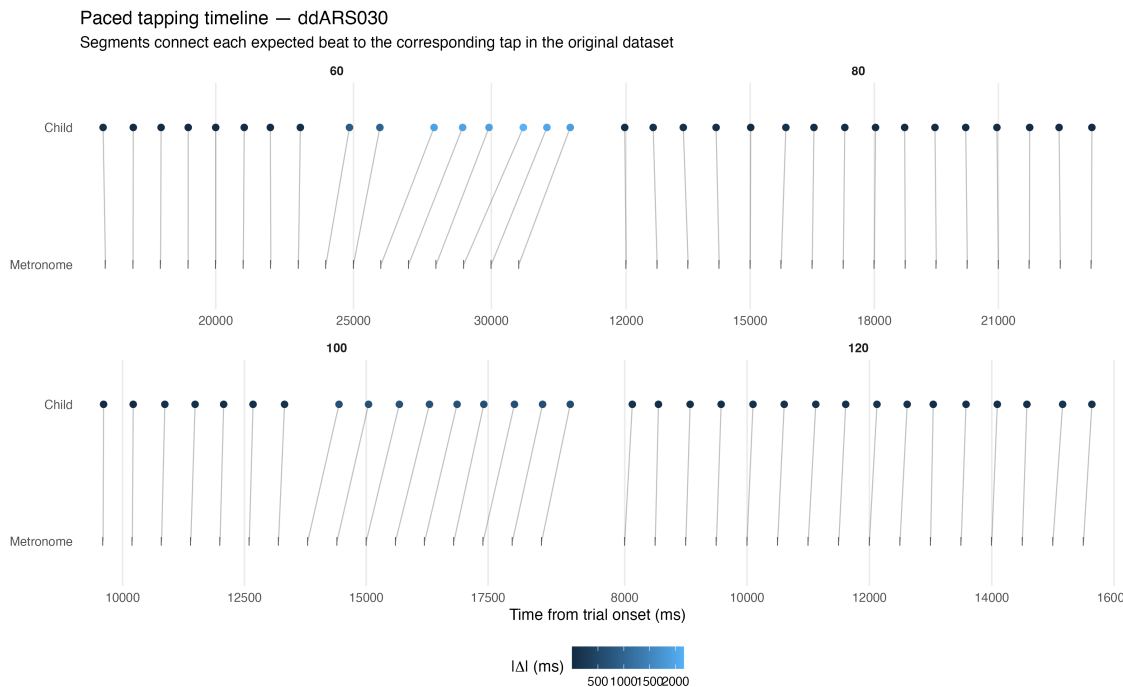
15	15	30000	30919	919	931
16	16	31000	32225	1225	1306



As shown in the data and illustrated in the figure, at 60 BPM, for example, the second click should actually be assigned to the third beat. Consequently, the second beat should be considered a missed click.

Let us now consider another example from the TDC group.

```
# A tibble: 16 × 5
  out_iresp out_tref out_tresp out_tdelta ITI_response
1         1    16000    15914        -86          NA
2         2    17000    17009         9        1095
3         3    18000    18018        18        1009
4         4    19000    19002         2         984
5         5    20000    19999        -1         997
6         6    21000    21034        34        1035
7         7    22000    21981       -19         947
8         8    23000    23070        70        1089
9         9    24000    24852       852        1782
10        10    25000    25955       955        1103
11        11    26000    27921      1921        1966
12        12    27000    28957      1957        1036
13        13    28000    29915      1915         958
14        14    29000    31159      2159        1244
15        15    30000    32015      2015         856
16        16    31000    32862      1862         847
```



If we examine this example, the issue occurs at the ninth beat, which was most likely missed by the participant. As a consequence, the response that appears to correspond to the ninth beat should instead be assigned to the tenth beat.

Similarly, double clicks, like missed clicks, may shift the time series, leading to an incorrect alignment between responses and reference beats.

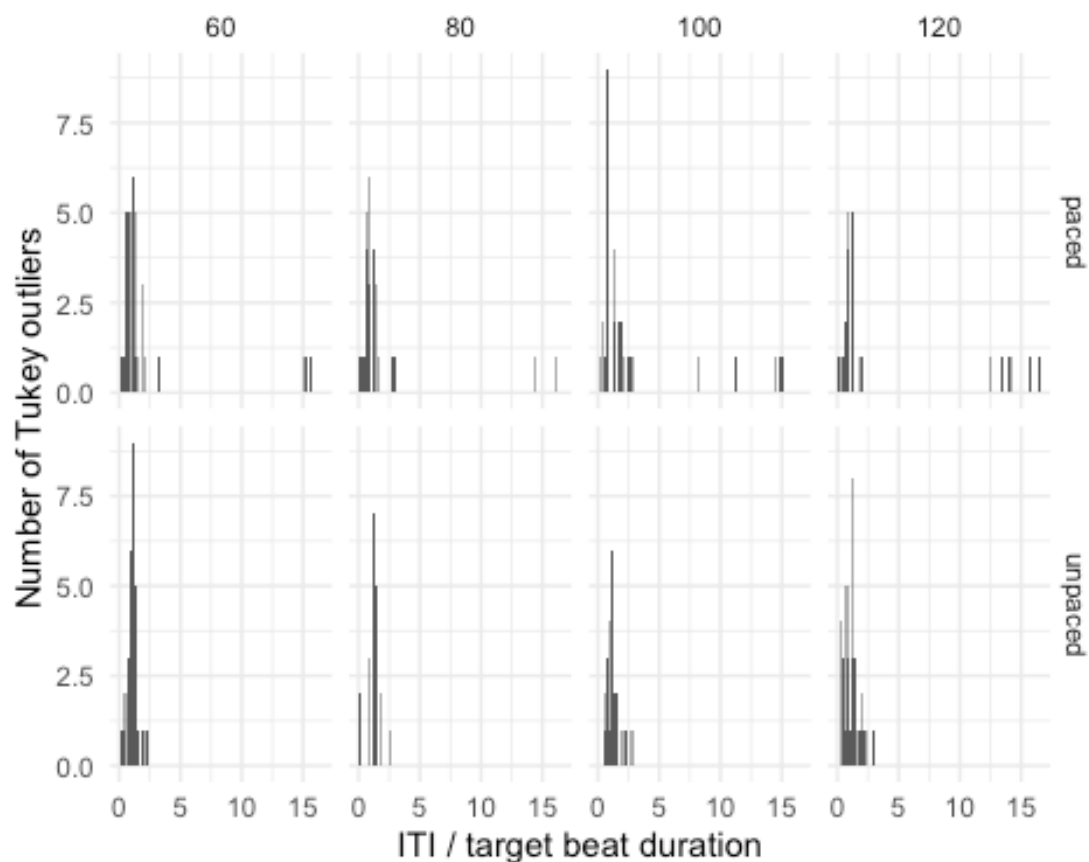
- 1) To identify these events and exclude them from the calculation of inter-tap intervals (ITIs), we can inspect the ITI ratio and detect intervals that are either excessively long or excessively short to be considered valid.
- 2) To correct the resulting time-series misalignment and obtain an accurate estimate of mean asynchrony, a time-series realignment algorithm can then be applied.

2.1. Outliers Classification based on ITI ratio

First, outliers are identified using the Tukey rule based on boxplots (Tukey, 1977). The ITI ratio is then examined. The ITI ratio quantifies the duration of each produced inter-tap interval (ITI) relative to the expected interval for the corresponding tempo. Therefore, it should be interpreted as a measure of interval duration rather than of temporal asynchrony with respect to the external pacing signal.

```
# A tibble: 20 × 4
  phase bpm  tukey_outlier    n
1 paced  60    FALSE        602
2 paced  60     TRUE         42
3 paced  60     NA          37
4 paced  80    FALSE       567
5 paced  80     TRUE         35
6 paced  80     NA          38
```

7	paced	100	FALSE	583
8	paced	100	TRUE	39
9	paced	100	NA	35
10	paced	120	FALSE	581
11	paced	120	TRUE	33
12	paced	120	NA	33
13	unpaced	60	FALSE	486
14	unpaced	60	TRUE	39
15	unpaced	80	FALSE	455
16	unpaced	80	TRUE	24
17	unpaced	100	FALSE	457
18	unpaced	100	TRUE	32
19	unpaced	120	FALSE	458
20	unpaced	120	TRUE	48



```
# A tibble: 1 × 5
  min    q1 median    q3    max
1 0.08 0.76  1.08  1.31 16.5
```

```
# A tibble: 5 × 2
  `cut(iti_ratio, breaks = c(0, 0.5, 1.5, 2.5, 3.5, Inf))` n
1 (0,0.5] 27
2 (0.5,1.5] 208
3 (1.5,2.5] 31
```

4 (2.5,3.5]	9
5 (3.5,Inf]	17

Let's explore lower outliers:

```
tukey_outliers %>%
  arrange(iti_ratio) %>%
  dplyr::select(
    participant_ID,
    bpm,
    phase,
    out_iresp,
    ITI_response,
    ITI_target,
    iti_ratio
  ) %>%
  head(30)
```

A tibble: 30 × 7

	participant_ID	bpm	phase	out_iresp	ITI_response	ITI_target	iti_ratio
1	ddARS035	80	paced	15	60	750	0.08
2	ddARS035	80	unpaced	25	66	750	0.088
3	ddARS020	60	paced	12	95	1000	0.095
4	ddARS035	100	paced	10	64	600	0.107
5	ddARS020	80	unpaced	21	87	750	0.116
6	ddARS020	60	unpaced	28	134	1000	0.134
7	ddARS035	120	paced	11	73	500	0.146
8	ddARS035	120	unpaced	25	78	500	0.156
9	ddARS009	120	paced	5	90	500	0.18
10	ddARS035	120	unpaced	19	90	500	0.18

ⓘ 20 more rows

Classification of outliers as:

Category.	ITI_ratio	CV?	Reason
Normal	about 1	✓	Good tapping rate
Little deviation	0.5–1.5	✓	Valid tapping
Double click	< 0.5	✗	motor artifact
Beat lost	1.5–2.5	✗	missing
different beat lost	2.5–3.5	✗	missing
Breack	>3.5	✗	task interrupted.

possible_double_click	single_interval	one_missing
162	4257	36
two_missing	pause	
9	17	

2.2 Needleman–Wunsch temporal sequence alignment

We will use the Needleman–Wunsch algorithm, only to establish the correspondence between expected beats and observed taps. Classify each event as matched tap, missing tap, extra tap, or double click (if distinguished separately). Do not alter the timestamps of valid taps.

A global dynamic-programming alignment, conceptually derived from Needleman–Wunsch, was adapted to match expected metronome events and observed tapping responses while allowing omissions and additional responses.

References (in order of relevance):

Needleman, S. B., & Wunsch, C. D. (1970). A general method applicable to the search for similarities in the amino acid sequence of two proteins. *Journal of molecular biology*, 48(3), 443-453.

de Moura, G. R. (2019). Time series data imputation-Comparison of Dynamic Time Warping with Needleman-Wunsch algorithm.

Syed, H., Das, A. (2015). Temporal Needleman-Wunsch. *IEEE International Conference on Data Science and Advanced Analytics (DSAA)*. AliClu – Temporal sequence alignment for clustering longitudinal clinical data Kwan MP, Xiao N, Ding G. Assessing Activity Pattern Similarity with Multidimensional Sequence Alignment based on a Multiobjective Optimization Evolutionary Algorithm. *Geogr Anal*. 2015 Jul;46(3):297-320. doi: 10.1111/gean.12040. PMID: 26190858; PMCID: PMC4501399.

Huang M, Shah ND, Yao L. Evaluating global and local sequence alignment methods for comparing patient medical records. *BMC Med Inform Decis Mak*. 2019 Dec 19;19(Suppl 6):263. doi: 10.1186/s12911-019-0965-y. PMID: 31856819; PMCID: PMC6921442.

To reconstruct the correspondence between metronome beats and participants' taps, we implemented a modified version of the Needleman–Wunsch dynamic programming algorithm. Our procedure is inspired by the Needleman–Wunsch framework for global sequence alignment but extends it to temporal event alignment by replacing symbolic substitution scores with a metric cost based on the temporal distance between expected and observed events. The algorithm searches for the alignment that minimizes the overall cost of the entire sequence rather than minimizing the temporal error of individual beat–tap pairs.

Prior to alignment, consecutive taps occurring within a predefined temporal window were considered double clicks and collapsed into a single response, retaining the first tap. This preprocessing step prevents rapid repeated responses from artificially inflating the number of taps while preserving the original temporal structure of the performance.

The alignment was then performed using three parameters.

First, a *maximum matching distance* (`max_match_frac`) defined the largest temporal discrepancy that could still be considered a plausible beat–tap correspondence. Candidate matches exceeding this threshold were forbidden and therefore could not be selected by the algorithm.

Second, a *gap penalty* (`gap_penalty`) determined the cost of introducing an unmatched beat (omission) or an unmatched tap (extra response). Rather than representing a temporal threshold, this parameter controls the algorithm’s preference for preserving sequence continuity. Higher values make omissions and extra taps increasingly costly, encouraging the algorithm to maintain continuous alignments whenever plausible correspondences exist.

Finally, a double-click threshold (`double_click_frac`) determined the temporal interval below which consecutive taps were merged before alignment.

For the final analyses, the gap penalty was fixed to 0.50 of the metronome period. This choice reflects the assumption that omissions and extra taps should only be introduced when no plausible beat–tap correspondence exists, favouring the reconstruction of continuous tapping sequences while avoiding unnecessary fragmentation of the alignment.

```
### We will work only on the paced data:
dataEntr<- subset(dataTAP_classified, dataTAP_classified$phase=="paced")

#####
# Entrainment: temporal realignment
# Central parameter configuration
#
# Outputs:
# - per_beat
# - extras
# - double_clicks_removed
# - diagnostics
# - dataEntr_aligned
# - one timeline PNG for each participant
#####

# LOAD PACKAGES
library(dplyr)
library(ggplot2)
library(stringr)

# 1) PARAMETERS
# All parameters are expressed as fractions of the metronome period.

params <- list(
  double_click_frac = 0.15,
  gap_penalty_frac  = 0.50,
  max_match_frac    = 0.50
)
```

```

# 2) DATA PREPARATION

if (!"rowid" %in% names(dataEntr)) {
  dataEntr <- dataEntr %>%
    mutate(
      rowid = dplyr::row_number()
    )
}

# 3) COLLAPSE DOUBLE CLICKS
# Consecutive responses separated by no more than:
# double_click_frac × period_ms
# are considered part of the same double-click cluster.
# The first response is retained.
# Subsequent responses are stored in double_clicks_removed.

collapse_double_clicks <- function(
  t_resp,
  period_ms,
  double_click_frac
) {
  # Remove missing values.
  t_resp <- t_resp[!is.na(t_resp)]

  empty_removed <- tibble(
    retained_tap = numeric(0),
    removed_tap = numeric(0),
    interval_ms = numeric(0)
  )

  # No preprocessing is needed with zero or one response.
  if (length(t_resp) <= 1) {
    return(
      list(
        times = t_resp,
        removed = empty_removed
      )
    )
  }

  double_click_threshold_ms <-
    double_click_frac * period_ms

  kept <- numeric(0)
  removed <- empty_removed

  i <- 1

```

```

while (i <= length(t_resp)) {

  j <- i

  # Extend the cluster while consecutive responses remain within threshold.
  while (
    j + 1 <= length(t_resp) &&
    (t_resp[j + 1] - t_resp[j]) <= double_click_threshold_ms
  ) {
    j <- j + 1
  }

  cluster_indices <- i:j
  retained_tap <- t_resp[i]

  # Keep the first response in the cluster.
  kept <- c(
    kept,
    retained_tap
  )

  # Save subsequent responses as removed double clicks.
  if (length(cluster_indices) > 1) {

    removed_taps <- t_resp[cluster_indices[-1]]

    removed <- bind_rows(
      removed,
      tibble(
        retained_tap = rep(
          retained_tap,
          length(removed_taps)
        ),
        removed_tap = removed_taps,
        interval_ms = removed_taps - retained_tap
      )
    )
  }

  i <- j + 1
}

list(
  times = kept,
  removed = removed
)
}

```

```
# 4) NEEDLEMAN-WUNSCH DYNAMIC-PROGRAMMING ALIGNMENT
# A match is forbidden when its temporal distance exceeds max_match_ms.
```

```
align_times_dp <- function(
  t_ref,
  t_resp,
  miss_penalty_ms,
  extra_penalty_ms,
  max_match_ms = Inf
) {

  n <- length(t_ref)
  m <- length(t_resp)

  # Matrix of cumulative costs.
  C <- matrix(
    Inf,
    nrow = n + 1,
    ncol = m + 1
  )

  # Matrix of optimal moves:
  #
  # 1 = diagonal: match
  # 2 = down: missed beat
  # 3 = right: extra response

  B <- matrix(
    NA_integer_,
    nrow = n + 1,
    ncol = m + 1
  )

  C[1, 1] <- 0

  # First column: all expected beats are missed.
  if (n > 0) {

    for (i in seq_len(n)) {

      C[i + 1, 1] <-
        C[i, 1] +
        miss_penalty_ms

      B[i + 1, 1] <- 2L
    }
  }
}
```

```

# First row: all responses are extra.
if (m > 0) {

  for (j in seq_len(m)) {

    C[1, j + 1] <-
      C[1, j] +
      extra_penalty_ms

    B[1, j + 1] <- 3L
  }
}

# Fill the dynamic-programming matrices.
if (n > 0 && m > 0) {

  for (i in seq_len(n)) {

    for (j in seq_len(m)) {

      match_distance_ms <-
        abs(t_ref[i] - t_resp[j])

      # Prevent matches beyond the maximum allowed distance.
      if (match_distance_ms > max_match_ms) {
        match_distance_ms <- Inf
      }

      candidate_costs <- c(

        # Match.
        C[i, j] +
          match_distance_ms,

        # Missed expected beat.
        C[i, j + 1] +
          miss_penalty_ms,

        # Extra response.
        C[i + 1, j] +
          extra_penalty_ms
      )

      best_move <- which.min(candidate_costs)

      C[i + 1, j + 1] <-
        candidate_costs[best_move]

      B[i + 1, j + 1] <-

```

```

        best_move
    }
}
}

# Backtracking.
i <- n + 1
j <- m + 1

matches <- list()
missed_refs <- integer(0)
extra_resps <- integer(0)

while (i > 1 || j > 1) {

  move <- B[i, j]

  if (is.na(move)) {

    stop(
      paste0(
        "Undefined backtracking move at matrix position i = ",
        i,
        ", j = ",
        j,
        "."
      )
    )
  }

  if (move == 1L) {

    matches[[length(matches) + 1]] <-
      c(i - 1, j - 1)

    i <- i - 1
    j <- j - 1

  } else if (move == 2L) {

    missed_refs <- c(
      missed_refs,
      i - 1
    )

    i <- i - 1

  } else {

```

```

    extra_resps <- c(
      extra_resps,
      j - 1
    )

    j <- j - 1
  }
}

matches <- if (length(matches) > 0) {

  do.call(
    rbind,
    rev(matches)
  )

} else {

  NULL
}

list(
  matches = matches,
  missed_refs = sort(missed_refs),
  extra_resps = sort(extra_resps),
  total_cost = C[n + 1, m + 1]
)
}

# 5) REALIGN ONE PARTICIPANT-BY-BPM SUBSET

realign_subject_bpm <- function(
  df_sb,
  p = params
) {

  # Sort rows according to expected metronome time.
  df_sb <- df_sb %>%
    arrange(out_tref)

  if (!"ITI_target" %in% names(df_sb)) {
    stop("Column 'ITI_target' is missing.")
  }

  period_values <- unique(
    df_sb$ITI_target[
      !is.na(df_sb$ITI_target)
    ]
  )

```

```

)

if (length(period_values) == 0) {
  stop(
    "No valid value of 'ITI_target' was found in this subset."
  )
}

if (length(period_values) > 1) {
  warning(
    "Multiple values of 'ITI_target' were found in this subset; ",
    "the first value will be used."
  )
}

period_ms <- period_values[1]

if (!is.finite(period_ms) || period_ms <= 0) {
  stop(
    "'ITI_target' must contain a positive finite value."
  )
}

# Convert fractional parameters to milliseconds.
miss_penalty_ms <-
  p$gap_penalty_frac *
  period_ms

extra_penalty_ms <-
  p$gap_penalty_frac *
  period_ms

max_match_ms <-
  p$max_match_frac *
  period_ms

# Expected beat sequence.
ref_ok <- which(
  !is.na(df_sb$out_tref)
)

t_ref <- df_sb$out_tref[ref_ok]
ref_rowid <- df_sb$rowid[ref_ok]

# Raw response sequence.
resp_ok <- which(
  !is.na(df_sb$out_tresp)
)

```

```

t_resp_raw <- df_sb$out_tresp[resp_ok]

# Collapse double clicks.
collapsed <- collapse_double_clicks(
  t_resp = t_resp_raw,
  period_ms = period_ms,
  double_click_frac = p$double_click_frac
)

t_resp_clean <- collapsed$times

double_clicks_removed <- if (
  nrow(collapsed$removed) > 0
) {

  collapsed$removed %>%
    mutate(
      status = "double_click_removed"
    )

} else {

  NULL
}

# Align expected beats and cleaned responses.
alignment <- align_times_dp(
  t_ref = t_ref,
  t_resp = t_resp_clean,
  miss_penalty_ms = miss_penalty_ms,
  extra_penalty_ms = extra_penalty_ms,
  max_match_ms = max_match_ms
)

# One output row for every expected beat.
per_beat <- tibble(
  ref_rowid = ref_rowid,
  t_ref = t_ref,
  status = "matched",
  resp_idx_clean = NA_integer_,
  t_resp = NA_real_,
  delta_ms = NA_real_
)

if (
  !is.null(alignment$matches) &&
  nrow(alignment$matches) > 0
) {

```

```

matched_ref_indices <-
  alignment$matches[, 1]

matched_resp_indices <-
  alignment$matches[, 2]

per_beat$resp_idx_clean[
  matched_ref_indices
] <- matched_resp_indices

per_beat$t_resp[
  matched_ref_indices
] <- t_resp_clean[
  matched_resp_indices
]

per_beat$delta_ms[
  matched_ref_indices
] <-
  per_beat$t_resp[
    matched_ref_indices
  ] -
  per_beat$t_ref[
    matched_ref_indices
  ]
}

# Label missed expected beats.
if (length(alignment$missed_refs) > 0) {

  per_beat$status[
    alignment$missed_refs
  ] <- "missed_ref"
}

# Store extra responses.
extras <- if (
  length(alignment$extra_resps) > 0
) {

  tibble(
    t_resp_extra =
      t_resp_clean[
        alignment$extra_resps
      ],
    status = "extra_resp"
  )

} else {

```

```

    NULL
  }

  # Assign corrected trial numbers only to matched beats.
  matched_rows <- which(
    per_beat$status == "matched"
  )

  per_beat$trial_corrected <- NA_integer_

  per_beat$trial_corrected[
    matched_rows
  ] <- seq_along(matched_rows)

  list(
    per_beat = per_beat,
    extras = extras,
    double_clicks_removed = double_clicks_removed,
    period_ms = period_ms,
    total_alignment_cost =
      alignment$total_cost,
    thresholds = list(
      double_click_ms =
        p$double_click_frac *
        period_ms,
      miss_penalty_ms =
        miss_penalty_ms,
      extra_penalty_ms =
        extra_penalty_ms,
      max_match_ms =
        max_match_ms
    )
  )
}

# 6) REALIGN THE COMPLETE DATASET
# The alignment is performed separately for every:
# participant_ID x bpm

realign_all <- function(
  dataEntr,
  subject_var = "participant_ID",
  p = params
) {

  keys <- dataEntr %>%
    distinct(
      .data[[subject_var]],
      bpm
    ) %>%

```

```

    arrange(
      .data[[subject_var]],
      bpm
    )

per_beat_all <- list()
extras_all <- list()
double_clicks_all <- list()
diagnostics_all <- list()

for (i in seq_len(nrow(keys))) {

  subject_id <-
    keys[[i, subject_var]]

  bpm_value <-
    keys[[i, "bpm"]]

  df_sb <- dataEntr %>%
    filter(
      .data[[subject_var]] == subject_id,
      bpm == bpm_value
    )

  if (nrow(df_sb) == 0) {
    next
  }

  result <- realign_subject_bpm(
    df_sb = df_sb,
    p = p
  )

  # Expected beats.
  per_beat_all[[length(per_beat_all) + 1]] <-
    result$per_beat %>%
    mutate(
      !!subject_var := subject_id,
      bpm = bpm_value
    )

  # Extra responses.
  if (!is.null(result$extras)) {

    extras_all[[length(extras_all) + 1]] <-
      result$extras %>%
      mutate(
        !!subject_var := subject_id,
        bpm = bpm_value
      )
  }
}

```

```

}

# Double clicks removed during preprocessing.
if (!is.null(result$double_clicks_removed)) {

  double_clicks_all[[length(double_clicks_all) + 1]] <-
    result$double_clicks_removed %>%
    mutate(
      !!subject_var := subject_id,
      bpm = bpm_value
    )
}

# Participant-by-BPM diagnostics.
diagnostics_all[[length(diagnostics_all) + 1]] <- tibble(
  !!subject_var := subject_id,
  bpm = bpm_value,
  period_ms = result$period_ms,
  double_click_ms =
    result$thresholds$double_click_ms,
  miss_penalty_ms =
    result$thresholds$miss_penalty_ms,
  extra_penalty_ms =
    result$thresholds$extra_penalty_ms,
  max_match_ms =
    result$thresholds$max_match_ms,
  total_alignment_cost =
    result$total_alignment_cost,
  n_expected_beats =
    nrow(result$per_beat),
  n_matches =
    sum(
      result$per_beat$status ==
        "matched"
    ),
  n_missed_beats =
    sum(
      result$per_beat$status ==
        "missed_ref"
    ),
  n_extra_responses =
    if (is.null(result$extras)) {
      0L
    } else {
      nrow(result$extras)
    },
  n_double_clicks_removed =
    if (
      is.null(
        result$double_clicks_removed
      )

```

```

    ) {
      0L
    } else {
      nrow(
        result$double_clicks_removed
      )
    }
  )
}

list(
  per_beat =
    if (length(per_beat_all) > 0) {
      bind_rows(per_beat_all)
    } else {
      tibble()
    },

  extras =
    if (length(extras_all) > 0) {
      bind_rows(extras_all)
    } else {
      tibble()
    },

  double_clicks_removed =
    if (length(double_clicks_all) > 0) {
      bind_rows(double_clicks_all)
    } else {
      tibble()
    },

  diagnostics =
    if (length(diagnostics_all) > 0) {
      bind_rows(diagnostics_all)
    } else {
      tibble()
    }
)
}

```

7) PLOT THE POST-ALIGNMENT TIMELINE

For each participant, one panel is shown for each BPM condition.

Grey vertical marks: expected metronome beats

Red vertical marks: missed beats

Filled points: matched responses

Open circles: extra responses

plot_timeline_aligned <- function(

```

    per_beat_tbl,
    extras_tbl,
    subject_id,
    subject_var = "participant_ID"
  ) {

    per_beat_subject <- per_beat_tbl %>%
      filter(
        .data[[subject_var]] ==
          subject_id
      )

    extras_subject <- if (
      !is.null(extras_tbl) &&
      nrow(extras_tbl) > 0
    ) {

      extras_tbl %>%
        filter(
          .data[[subject_var]] ==
            subject_id
        )

    } else {

      NULL
    }

    metronome <- per_beat_subject %>%
      mutate(
        y = 0
      )

    matched <- per_beat_subject %>%
      filter(
        status == "matched"
      ) %>%
      mutate(
        y_ref = 0,
        y_resp = 1
      )

    missed <- per_beat_subject %>%
      filter(
        status == "missed_ref"
      ) %>%
      mutate(
        y = 0
      )
  }

```

```

extra <- if (
  !is.null(extras_subject) &&
  nrow(extras_subject) > 0
) {

  extras_subject %>%
    mutate(
      y = 1.1
    )

} else {

  NULL
}

ggplot() +

  # Lines connecting expected beats and matched responses.
  geom_segment(
    data = matched,
    aes(
      x = t_ref,
      xend = t_resp,
      y = y_ref,
      yend = y_resp,
      group = interaction(
        bpm,
        trial_corrected
      )
    ),
    linewidth = 0.35,
    alpha = 0.6
  ) +

  # Expected metronome beats.
  geom_point(
    data = metronome,
    aes(
      x = t_ref,
      y = y
    ),
    shape = 124,
    size = 3,
    alpha = 0.9,
    color = "grey30"
  ) +

  # Missed expected beats.
  geom_point(
    data = missed,

```

```

    aes(
      x = t_ref,
      y = y
    ),
    shape = 124,
    size = 3,
    alpha = 1,
    color = "#cc3d3d"
  ) +

  # Matched child responses.
  geom_point(
    data = matched,
    aes(
      x = t_resp,
      y = 1,
      color = abs(delta_ms)
    ),
    size = 2
  ) +

  # Extra responses.
  {
    if (!is.null(extra)) {

      geom_point(
        data = extra,
        aes(
          x = t_resp_extra,
          y = y
        ),
        shape = 21,
        size = 2,
        stroke = 0.3,
        fill = NA,
        color = "#6a3d9a"
      )
    }
  } +

  facet_wrap(
    ~ bpm,
    ncol = 2,
    scales = "free_x"
  ) +

  scale_y_continuous(
    breaks = c(0, 1),
    labels = c(
      "Metronome",

```

```

    "Child"
  ),
  limits = c(
    -0.25,
    1.35
  )
) +

labs(
  title = paste0(
    "Realigned timeline - ",
    subject_id
  ),
  subtitle = paste0(
    "Matched responses, missed beats, and extra responses ",
    "after BPM-adaptive realignment"
  ),
  x = "Time (ms)",
  y = NULL,
  color = "|Delta| (ms)"
) +

theme_minimal(
  base_size = 12
) +

theme(
  panel.grid.major.y =
    element_blank(),
  panel.grid.minor =
    element_blank(),
  legend.position =
    "bottom",
  strip.text =
    element_text(face = "bold")
)
}

# 8) RUN THE COMPLETE REALIGNMENT

RA <- realign_all(
  dataEntr = dataEntr,
  subject_var = "participant_ID",
  p = params
)

# 9) CREATE THE SEPARATE OUTPUT OBJECTS

per_beat <- RA$per_beat %>%

```

```

mutate(
  alignment_version = "central",
  double_click_frac =
    params$double_click_frac,
  gap_penalty_frac =
    params$gap_penalty_frac,
  max_match_frac =
    params$max_match_frac
)

extras <- RA$extras %>%
  mutate(
    alignment_version = "central",
    double_click_frac =
      params$double_click_frac,
    gap_penalty_frac =
      params$gap_penalty_frac,
    max_match_frac =
      params$max_match_frac
  )

double_clicks_removed <-
  RA$double_clicks_removed %>%
  mutate(
    alignment_version = "central",
    double_click_frac =
      params$double_click_frac,
    gap_penalty_frac =
      params$gap_penalty_frac,
    max_match_frac =
      params$max_match_frac
  )

diagnostics <- RA$diagnostics %>%
  mutate(
    alignment_version = "central",
    double_click_frac =
      params$double_click_frac,
    gap_penalty_frac =
      params$gap_penalty_frac,
    max_match_frac =
      params$max_match_frac
  )

# 10) SAVE ONE TIMELINE PLOT PER PARTICIPANT

output_directory <-

```

```

"entrainment_timeline_aligned"

if (!dir.exists(output_directory)) {

  dir.create(
    output_directory,
    recursive = TRUE
  )
}

subjects <- unique(
  dataEntr$participant_ID
)

for (subject_id in subjects) {

  plot_object <- plot_timeline_aligned(
    per_beat_tbl = per_beat,
    extras_tbl = extras,
    subject_id = subject_id,
    subject_var = "participant_ID"
  )

  output_filename <- file.path(
    output_directory,
    paste0(
      str_replace_all(
        subject_id,
        "[^[:alnum:]]_+",
        "_"
      ),
      "_timelineAligned_byBPM.png"
    )
  )

  ggsave(
    filename = output_filename,
    plot = plot_object,
    width = 12,
    height = 7.5,
    dpi = 300
  )
}

# 11) JOIN ALIGNED VALUES BACK TO THE ORIGINAL DATASET

dataEntr_aligned <- dataEntr %>%
  left_join(
    per_beat %>%

```

```

    dplyr::select(
      ref_rowid,
      delta_ms,
      status,
      trial_corrected
    ),
    by = c(
      "rowid" = "ref_rowid"
    )
  ) %>%
  mutate(
    alignment_version = "central",
    double_click_frac =
      params$double_click_frac,
    gap_penalty_frac =
      params$gap_penalty_frac,
    max_match_frac =
      params$max_match_frac
  )

```

12) CHECK THE OUTPUT OBJECTS

```
View(per_beat)
```

```
View(extras)
```

```
View(double_clicks_removed)
```

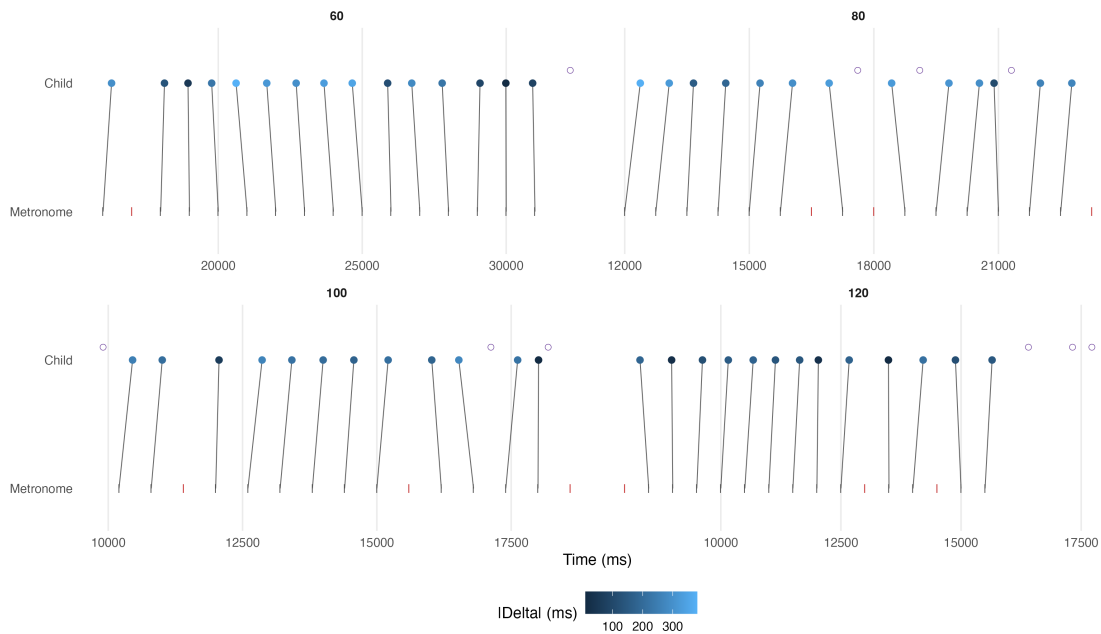
```
View(diagnostics)
```

```
View(dataEntr_aligned)
```

Result of the realignment for the two esemplificative cases considered above:

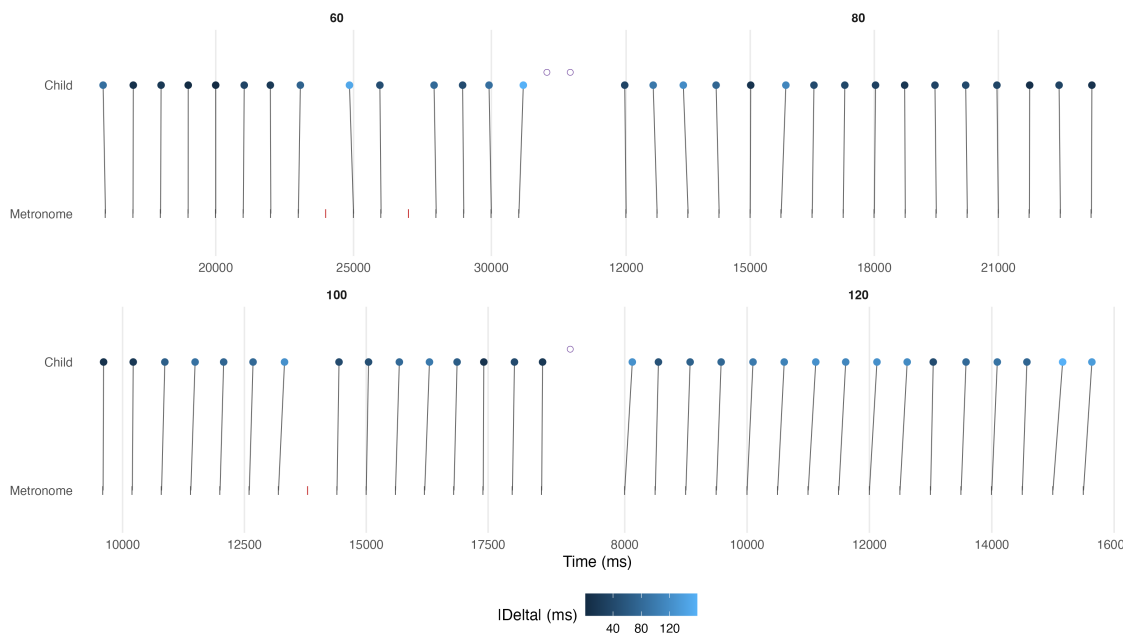
Realigned timeline — ddARS005

Matched responses, missed beats, and extra responses after BPM-adaptive realignment



Realigned timeline — ddARS030

Matched responses, missed beats, and extra responses after BPM-adaptive realignment



2.3 Comparisons between NW and outliers' classification:

	60	80	100	120
possible_double_click	43	4	26	25
single_interval	593	594	580	576
one_missing	4	0	8	6
two_missing	1	2	3	0
pause	3	2	5	7

	60	80	100	120
matched	607	607	583	583
missed_ref	74	33	74	64

bpm	single_interval	totale	percentuale	
60	60	593	644	92.08
80	80	594	602	98.67
100	100	580	622	93.25
120	120	576	614	93.81

bpm	matched	totale	percentuale	
60	60	607	681	89.13
80	80	607	640	94.84
100	100	583	657	88.74
120	120	583	647	90.11

Check whether possible double click were matched based on NW:

	possible_double_click	single_interval	one_missing	two_missing
matched	43	2210	10	3
missed_ref	55	133	8	3

	pause
matched	17
missed_ref	0

Analyses based on circular statistics require the identification of the corresponding reference beat and can therefore only be performed in the paced condition using the Needleman–Wunsch alignment procedure. In contrast, analyses based on inter-tap intervals (ITI) and the coefficient of variation (CV), which will be performed in both paced and unpaced conditions, rely on consecutive tap intervals and can therefore be based on the interval-based boxplot procedure. Although the latter does not explicitly reconstruct the beat sequence, comparison with the Needleman–Wunsch alignment showed that the proportion of information discarded was limited to only a few percentage points, supporting its use for ITI- and CV-based analyses.

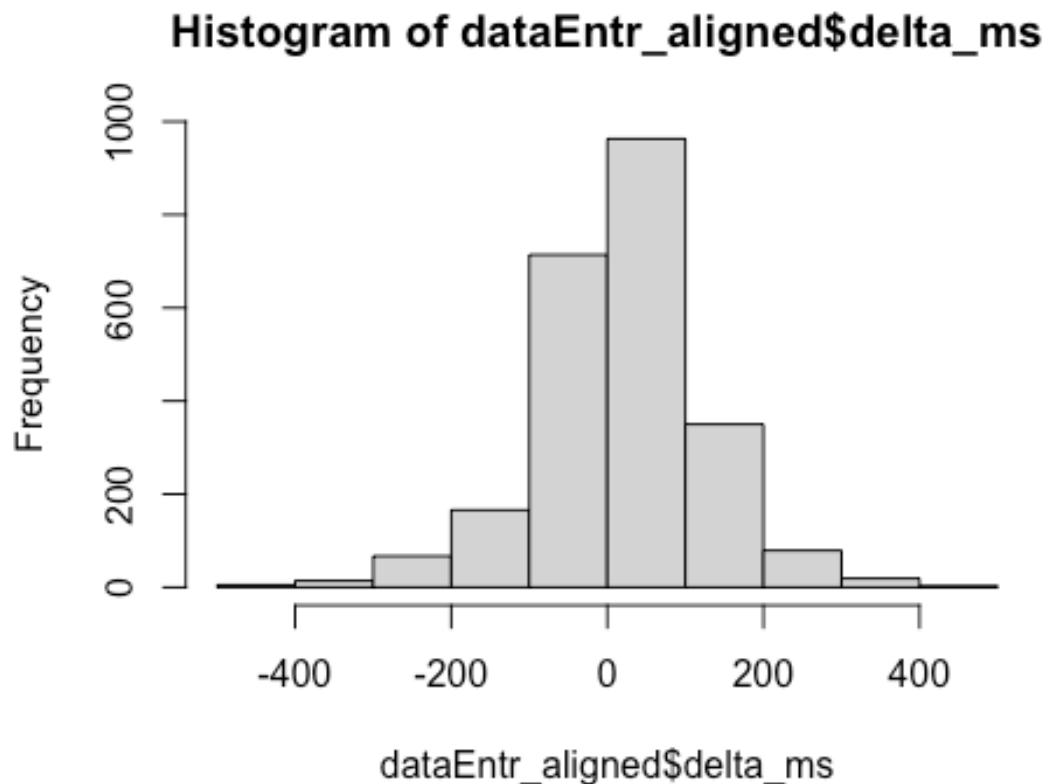
bpm	single_interval	matched_NW	perc_information_retained
1 60	593	607	97.69
2 80	594	607	97.86
3 100	580	583	99.49
4 120	576	583	98.80

Indeed, for analyses based on ITIs, the interval-based procedure retained between 97.7% and 99.5% of the observations classified as valid by the Needleman–Wunsch alignment, indicating only a minimal loss of usable information.

3. Group-Comparisons-Paced phase

3.1. Temporal Asynchrony

In this analysis we will perform the group comparison on the dependent variable “delta_ms”, i.e., the temporal distance between the target beat and the participant click. The *delta_ms* is calculated on the participants’ realigned time-series.



Analysis of Deviance Table (Type III Wald chisquare tests)

Response: delta_ms

	Chisq	Df	Pr(>Chisq)
(Intercept)	2.2102	1	0.1370997
Group	3.4496	1	0.0632679 .
bpm	51.9735	3	3.034e-11 ***
Group:bpm	19.0160	3	0.0002713 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Linear mixed model fit by REML ['lmerMod']

Formula: delta_ms ~ Group * bpm + (1 | participant_ID)

Data: dataEntr_aligned

REML criterion at convergence: 28670.9

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.3127	-0.5282	0.0094	0.5248	4.8907

Random effects:

Groups	Name	Variance	Std.Dev.
participant_ID	(Intercept)	1867	43.21
Residual		9798	98.99

Number of obs: 2380, groups: participant_ID, 40

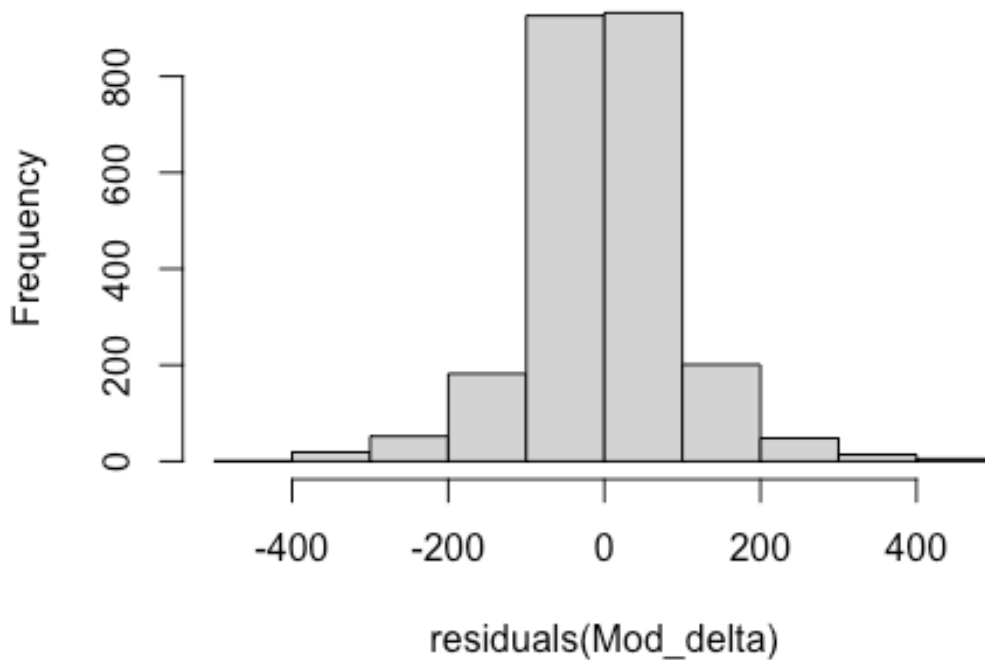
Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	-16.706	11.237	-1.487
GroupTDC	29.454	15.858	1.857
bpm80	50.368	8.126	6.199
bpm100	49.993	8.197	6.099
bpm120	25.226	8.252	3.057
GroupTDC:bpm80	-30.790	11.385	-2.704
GroupTDC:bpm100	-46.440	11.500	-4.038
GroupTDC:bpm120	-11.924	11.506	-1.036

Correlation of Fixed Effects:

	(Intr)	GrpTDC	bpm80	bpm100	bpm120	GTDC:8	GTDC:10
GroupTDC	-0.709						
bpm80	-0.361	0.256					
bpm100	-0.357	0.253	0.495				
bpm120	-0.355	0.252	0.491	0.487			
GrpTDC:bp80	0.257	-0.359	-0.714	-0.353	-0.350		
GrpTDC:b100	0.255	-0.355	-0.353	-0.713	-0.347	0.495	
GrpTDC:b120	0.255	-0.355	-0.352	-0.349	-0.717	0.495	0.490

Histogram of residuals(Mod_delta)



```
bpm = 60:
contrast estimate SE df t.ratio p.value
DYS - TDC -29.45 15.9 58.1 -1.857 0.0683
```

```
bpm = 80:
contrast estimate SE df t.ratio p.value
DYS - TDC 1.34 15.9 58.1 0.084 0.9332
```

```
bpm = 100:
contrast estimate SE df t.ratio p.value
DYS - TDC 16.99 15.9 59.4 1.065 0.2910
```

```
bpm = 120:
contrast estimate SE df t.ratio p.value
DYS - TDC -17.53 15.9 59.4 -1.099 0.2761
```

Degrees-of-freedom method: kenward-roger

```
Group = DYS:
contrast estimate SE df t.ratio p.value
bpm60 - bpm80 -50.368 8.13 2337 -6.198 <.0001
bpm60 - bpm100 -49.993 8.20 2336 -6.099 <.0001
bpm60 - bpm120 -25.226 8.25 2336 -3.057 0.0121
bpm80 - bpm100 0.375 8.21 2336 0.046 1.0000
```

bpm80 - bpm120	25.142	8.26	2337	3.042	0.0127
bpm100 - bpm120	24.767	8.33	2336	2.973	0.0158

Group = TDC:

contrast	estimate	SE	df	t.ratio	p.value
bpm60 - bpm80	-19.578	7.97	2334	-2.455	0.0674
bpm60 - bpm100	-3.553	8.07	2335	-0.440	0.9714
bpm60 - bpm120	-13.302	8.02	2335	-1.659	0.3458
bpm80 - bpm100	16.025	8.06	2335	1.989	0.1924
bpm80 - bpm120	6.277	8.01	2335	0.784	0.8618
bpm100 - bpm120	-9.749	8.10	2335	-1.204	0.6246

Degrees-of-freedom method: kenward-roger

P value adjustment: tukey method for comparing a family of 4 estimates

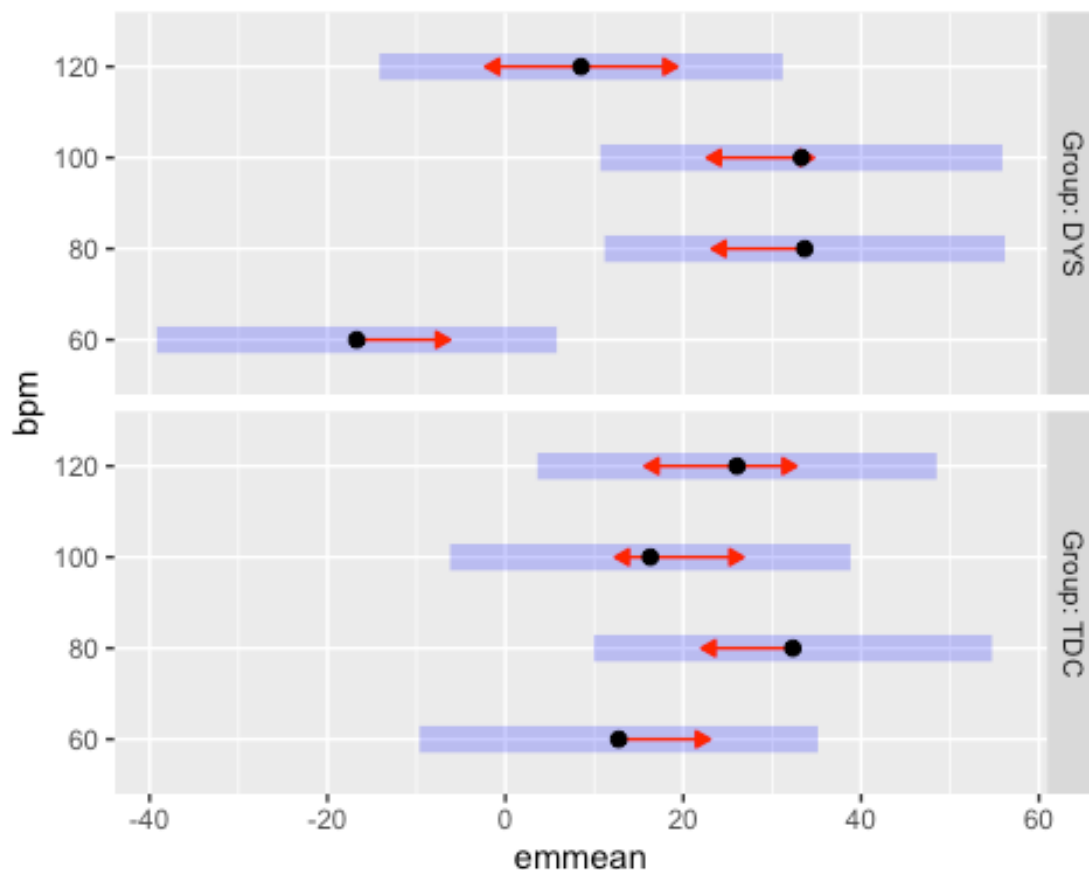
contrast	estimate	SE	df	t.ratio	p.value
DYS bpm60 - TDC bpm60	-29.454	15.90	58.1	-1.857	0.5848
DYS bpm60 - DYS bpm80	-50.368	8.13	2336.6	-6.198	<.0001
DYS bpm60 - TDC bpm80	-49.032	15.90	58.1	-3.092	0.0570
DYS bpm60 - DYS bpm100	-49.993	8.20	2335.9	-6.099	<.0001
DYS bpm60 - TDC bpm100	-33.007	15.90	58.7	-2.076	0.4422
DYS bpm60 - DYS bpm120	-25.226	8.25	2336.2	-3.057	0.0467
DYS bpm60 - TDC bpm120	-42.756	15.90	58.4	-2.693	0.1455
TDC bpm60 - DYS bpm80	-20.914	15.90	58.2	-1.318	0.8882
TDC bpm60 - TDC bpm80	-19.578	7.97	2334.4	-2.455	0.2155
TDC bpm60 - DYS bpm100	-20.539	15.90	58.7	-1.292	0.8984
TDC bpm60 - TDC bpm100	-3.553	8.07	2334.9	-0.440	0.9999
TDC bpm60 - DYS bpm120	4.228	15.90	59.1	0.265	1.0000
TDC bpm60 - TDC bpm120	-13.302	8.02	2334.9	-1.659	0.7138
DYS bpm80 - TDC bpm80	1.336	15.90	58.1	0.084	1.0000
DYS bpm80 - DYS bpm100	0.375	8.21	2336.1	0.046	1.0000
DYS bpm80 - TDC bpm100	17.361	15.90	58.8	1.091	0.9561
DYS bpm80 - DYS bpm120	25.142	8.26	2336.8	3.042	0.0487
DYS bpm80 - TDC bpm120	7.612	15.90	58.4	0.479	0.9997
TDC bpm80 - DYS bpm100	-0.961	15.90	58.7	-0.060	1.0000
TDC bpm80 - TDC bpm100	16.025	8.06	2334.7	1.989	0.4896
TDC bpm80 - DYS bpm120	23.807	15.90	59.1	1.495	0.8071
TDC bpm80 - TDC bpm120	6.277	8.01	2334.6	0.784	0.9940
DYS bpm100 - TDC bpm100	16.986	15.90	59.4	1.065	0.9615
DYS bpm100 - DYS bpm120	24.767	8.33	2335.8	2.973	0.0596
DYS bpm100 - TDC bpm120	7.238	15.90	59.0	0.455	0.9998
TDC bpm100 - DYS bpm120	7.781	16.00	59.8	0.487	0.9997
TDC bpm100 - TDC bpm120	-9.749	8.10	2335.0	-1.204	0.9311
DYS bpm120 - TDC bpm120	-17.530	15.90	59.4	-1.099	0.9545

Degrees-of-freedom method: kenward-roger

P value adjustment: tukey method for comparing a family of 8 estimates

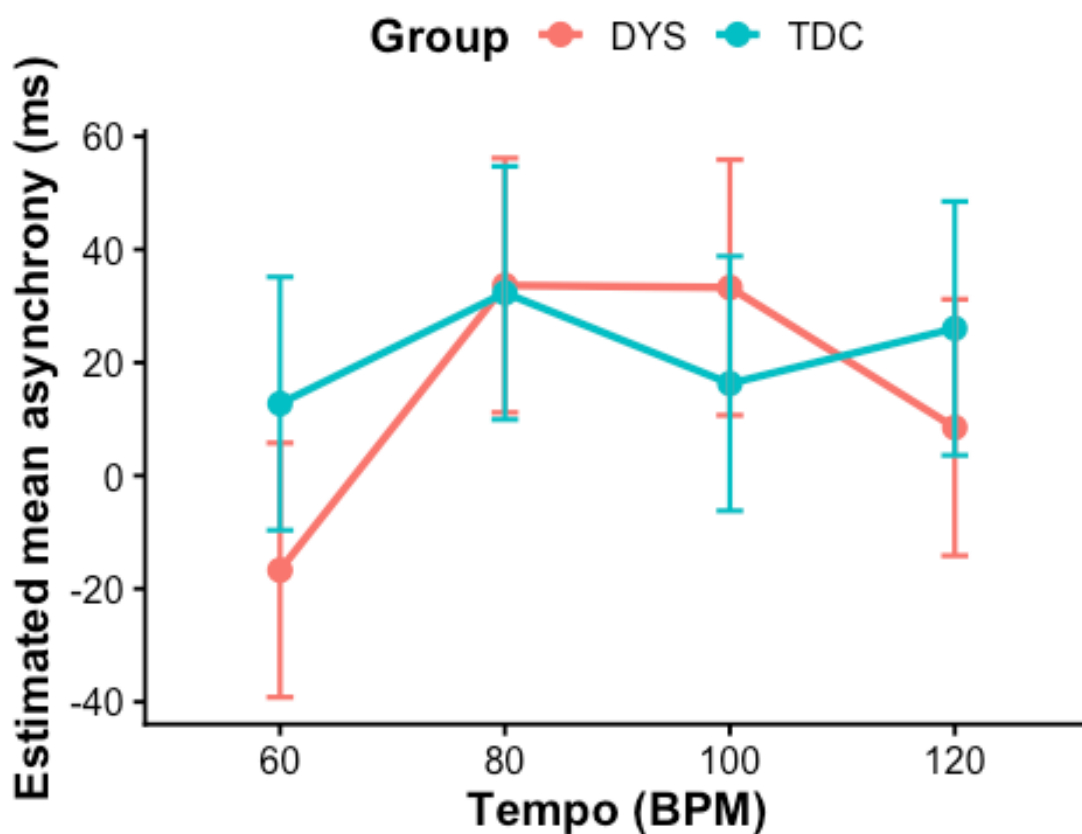
Supplementary Figure 2

Estimated marginal means (black dots) and 95% confidence intervals (blue bars) of tapping onset across tempi (60, 80, 100, and 120 bpm) in the dyslexia (DYS) and typically developing control (TDC) groups. Red arrows indicate the direction and magnitude of temporal anticipation relative to the metronome beat, with positive values indicating anticipatory responses and negative values indicating delayed responses.



Supplementary Figure 3

Estimated marginal means ($\pm 95\%$ confidence intervals) of sensorimotor asynchrony (ms) across tempi (60, 80, 100, and 120 BPM) for children with developmental dyslexia (DYS) and typically developing controls (TDC). Negative values reflect anticipatory responses (taps occurring before the metronome beat), whereas positive values reflect delayed responses (taps occurring after the beat).



3.2 Quadratic Effect of Tempo

Test of the “optimal temporal window” hypothesis (McAuley et al., 2006).

Analysis of Deviance Table (Type III Wald chisquare tests)

Response: delta_ms

	Chisq	Df	Pr(>Chisq)
(Intercept)	12.7520	1	0.0003556 ***
Group	0.7494	1	0.3866658
bpm_c	8.2982	1	0.0039685 **
I(bpm_c^2)	41.8393	1	9.909e-11 ***
Group:bpm_c	1.9723	1	0.1602002
Group:I(bpm_c^2)	15.9639	1	6.456e-05 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Linear mixed model fit by REML ['lmerMod']

Formula: delta_ms ~ Group * (bpm_c + I(bpm_c^2)) + (1 | participant_ID)

Data: dataEntr_aligned

REML criterion at convergence: 28733.2

Scaled residuals:

	Min	1Q	Median	3Q	Max
	-4.3193	-0.5150	0.0015	0.5257	4.8744

Random effects:

Groups	Name	Variance	Std.Dev.
participant_ID	(Intercept)	1863	43.16
Residual		9819	99.09

Number of obs: 2380, groups: participant_ID, 40

Fixed effects:

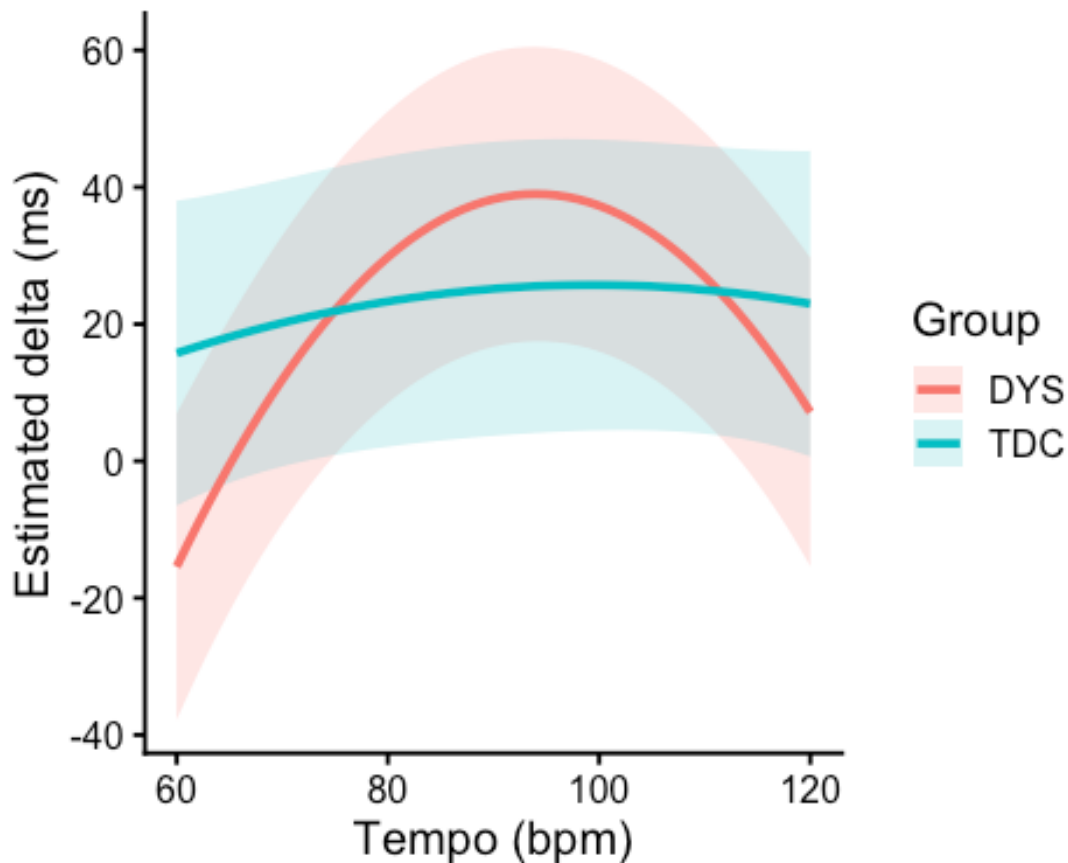
	Estimate	Std. Error	t value
(Intercept)	38.255258	10.712759	3.571
GroupTDC	-13.093019	15.124554	-0.866
bpm_c	0.376090	0.130557	2.881
I(bpm_c^2)	-0.047099	0.007281	-6.468
GroupTDC:bpm_c	-0.255756	0.182111	-1.404
GroupTDC:I(bpm_c^2)	0.040662	0.010177	3.995

Correlation of Fixed Effects:

	(Intr)	GrpTDC	bpm_c	I(_^2)	GTDC:_
GroupTDC	-0.708				
bpm_c	0.001	-0.001			
I(bpm_c^2)	-0.338	0.240	0.018		
GrpTDC:bpm_c	-0.001	0.002	-0.717	-0.013	
GTDC:I(_^2)	0.242	-0.336	-0.013	-0.715	0.010

Figure 1

Nonlinear pattern of temporal asynchrony across tempi in the DYS and TDC groups.



3.4 Circular Statistic on non-aligned data:

Relative phase angles were summarized using circular statistics. Synchronization consistency was quantified using the mean resultant vector length (R), ranging from 0, indicating dispersed phases, to 1, indicating perfect phase consistency. Circular variance was calculated as $1-R$, whereas circular standard deviation was computed as $-2\ln(R)$ (Fisher, 1993; Jammalamadaka & SenGupta, 2001). Rayleigh tests were additionally used to assess whether taps showed significant phase concentration.

For each tap compute the asynchrony (tap time – beat time) and convert it into relative phase (degrees or radians), allowing comparisons across tempi.

```
dataEntr$delta_ms<- dataEntr$out_tresp-dataEntr$out_tref

dataEntr$theta<- 360*(dataEntr$delta_ms/dataEntr$ITI_target)

dataEntr$theta <- ((dataEntr$theta + 180) %% 360) - 180

summary(dataEntr$theta)

  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
-180.00 -22.20   11.16   10.38  46.80  179.64

range(dataEntr$theta, na.rm = TRUE)
```

```
[1] -180.00 179.64
```

```
#circular mean phase
```

```
library(dplyr)
```

```
library(circular)
```

Attaching package: 'circular'

The following objects are masked from 'package:stats':

```
sd, var
```

```
sync_trial <- dataEntr %>%  
  filter(!is.na(theta)) %>%  
  mutate(  
    theta_rad = theta * pi / 180  
  ) %>%  
  group_by(participant_ID, bpm) %>%  
  summarise(  
    n_taps = n(),  
  
    mean_cos = mean(cos(theta_rad)),  
    mean_sin = mean(sin(theta_rad)),  
  
    mean_phase_rad = atan2(mean_sin, mean_cos),  
    mean_phase_deg = mean_phase_rad * 180 / pi,  
  
    ITI_target = first(ITI_target),  
  
    mean_asynchrony_ms =  
      mean_phase_deg / 360 * ITI_target,  
  
    .groups = "drop"  
  )
```

Synchronization precision

Compute the mean resultant vector length (R). R close to 1 indicates highly consistent phase locking, whereas R close to 0 indicates poor synchronization consistency. Circular variance, circular SD, or Shannon entropy-based indices may also be explored.

```
sync_trial <- sync_trial %>%  
  mutate(  
    R = sqrt(mean_cos^2 + mean_sin^2),  
  
    circular_variance = 1 - R,  
  
    circular_sd_rad = if_else(  
      R > 0,  
      sqrt(-2 * log(R)),
```

```

    NA_real_
  ),

  circular_sd_deg = circular_sd_rad * 180 / pi
)

```

Rayleigh test

Optionally perform a Rayleigh test for each trial to verify whether taps show a preferred phase (phase locking). Use primarily as a quality or descriptive measure rather than an automatic exclusion criterion.

```

#compute the score from the theta value in the dataEntr dataset
rayleigh_trial <- dataEntr %>%
  filter(!is.na(theta)) %>%
  group_by(participant_ID, bpm) %>%
  summarise(
    rayleigh_p = {
      ang <- circular(
        theta,
        units = "degrees",
        template = "none",
        modulo = "2pi",
        zero = 0,
        rotation = "counter"
      )

      rayleigh.test(ang)$p.value
    },

    .groups = "drop"
  )

#merge these data with sync_trial
sync_trial <- sync_trial %>%
  left_join(
    rayleigh_trial,
    by = c("participant_ID", "bpm")
  )

summary(sync_trial$mean_asynchrony_ms)

  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
-258.14 -28.42   24.41   21.12  65.61  374.99

summary(sync_trial$R)

  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.05834 0.68575 0.83903 0.75211 0.91423 0.98420

summary(sync_trial$rayleigh_p)

```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
0.0000003	0.0000006	0.0000011	0.0526223	0.0001947	0.9199134

Check for phase-locking

```
summary(sync_trial$R)

  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.05834 0.68575 0.83903 0.75211 0.91423 0.98420

sync_trial <- sync_trial %>%
  mutate(
    rayleigh_significant = rayleigh_p < .05
  )

table(sync_trial$rayleigh_significant, useNA = "ifany")

FALSE  TRUE
   18   142

prop.table(table(sync_trial$rayleigh_significant))

FALSE  TRUE
0.1125 0.8875
```

The Rayleigh test indicated significant phase locking in 88.7% of participant × tempo sequences, confirming that participants were generally synchronized with the pacing stimulus.

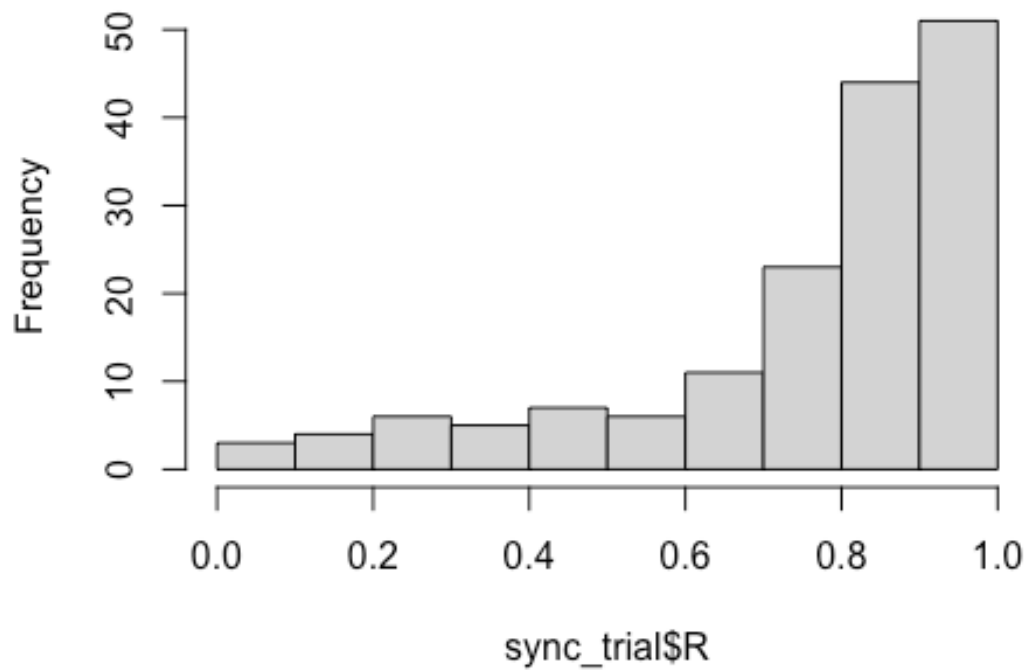
```
# A tibble: 4 × 4
  bpm  n_trials n_phase_locked proportion_phase_locked
1 60      40          37             0.925
2 80      40          40             1
3 100     40          34             0.85
4 120     40          31             0.775
```

As a quality check, the Rayleigh test was used to assess whether tapping responses exhibited significant phase locking to the pacing stimulus. Overall, 92.5% of participant × tempo sequences showed significant phase locking (60 bpm: 95%; 80 bpm: 100%; 100 bpm: 95%; 120 bpm: 80%), indicating that the vast majority of sequences reflected successful synchronization.

DYS	TDC
80	80

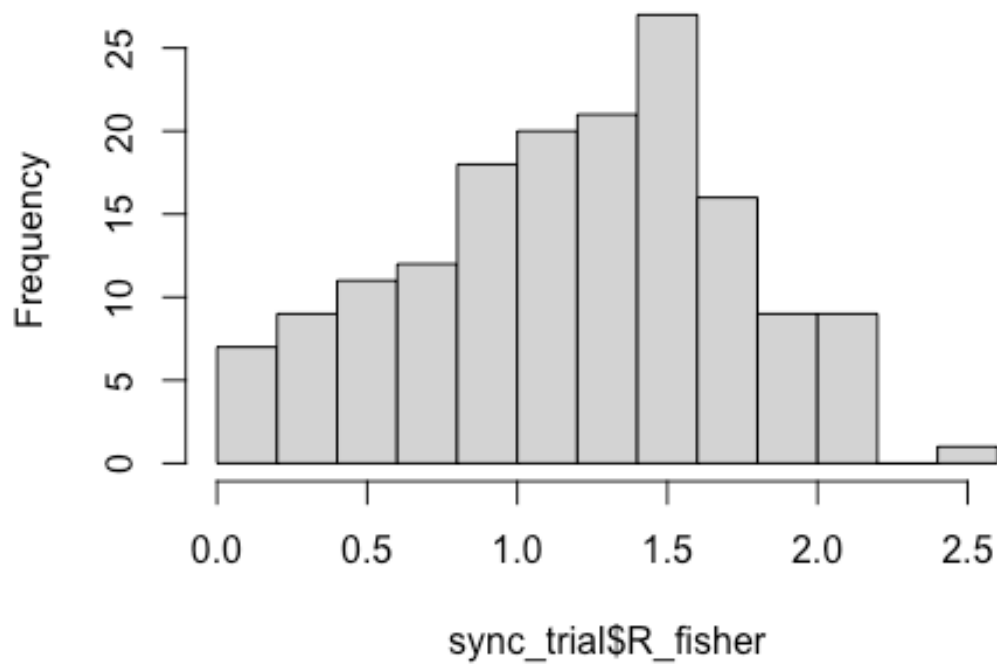
PHASE LOCKING

Histogram of sync_trial\$R

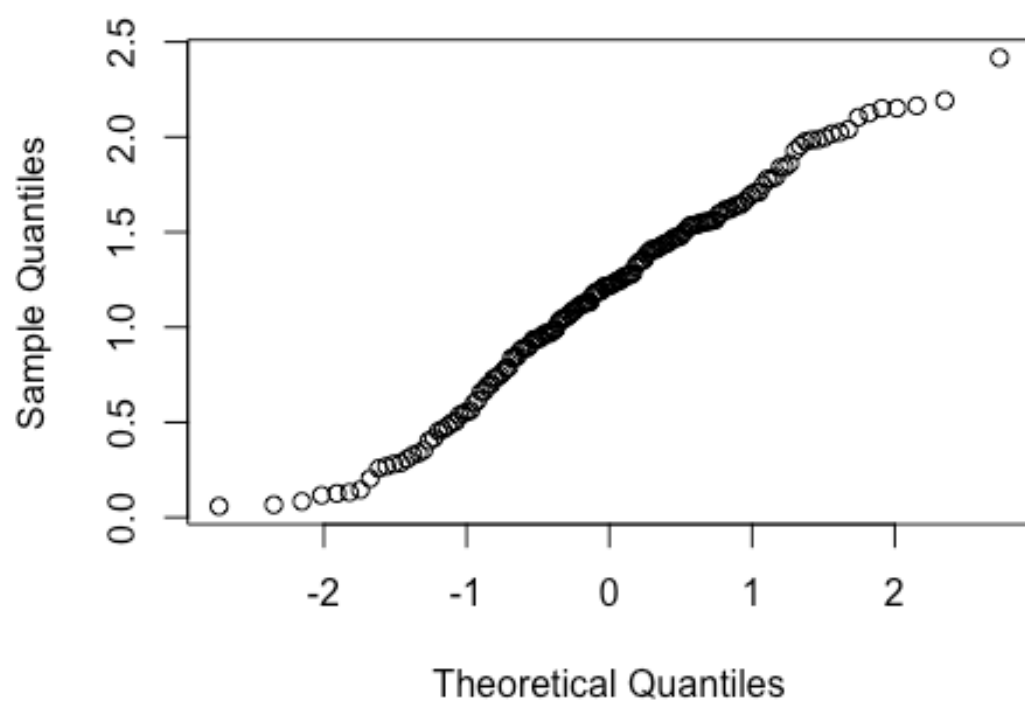


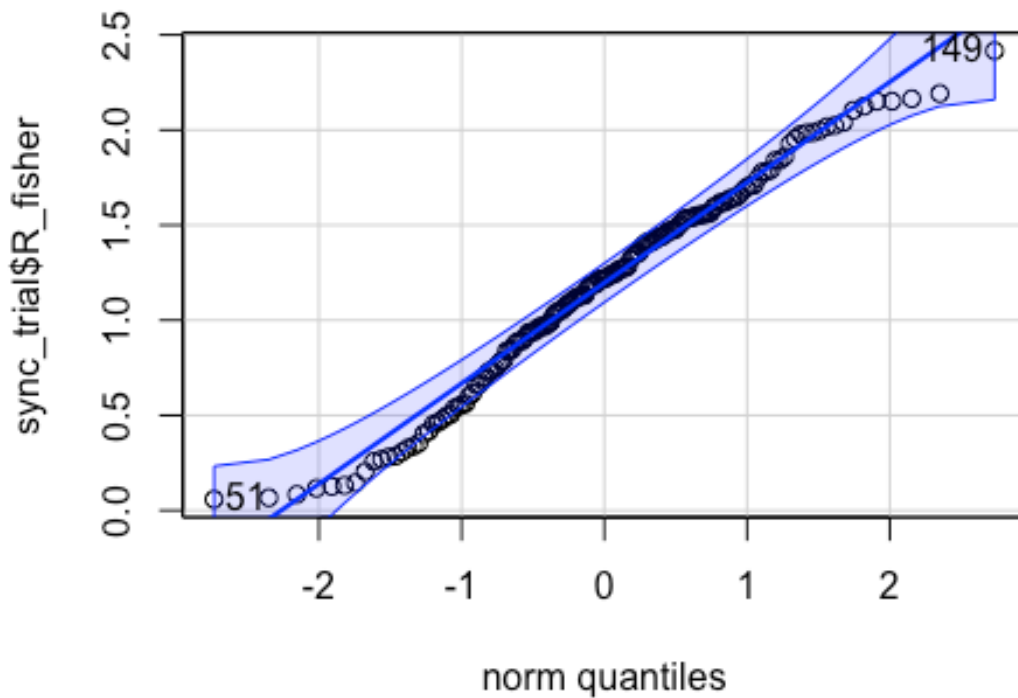
The variable must be transformed due to the nature of the distribution:

Histogram of sync_trial\$R_fisher



Normal Q-Q Plot





```
[1] 149 51
```

Analysis of Deviance Table (Type III Wald chisquare tests)

Response: R_fisher

	Chisq	Df	Pr(>Chisq)
(Intercept)	97.2521	1	< 2.2e-16 ***
Group	9.2996	1	0.002292 **
factor(bpm)	10.9033	3	0.012260 *
Group:factor(bpm)	4.8001	3	0.187031

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Linear mixed model fit by REML ['lmerMod']

Formula: R_fisher ~ Group * factor(bpm) + (1 | participant_ID)

Data: sync_trial

REML criterion at convergence: 213.4

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.31571	-0.62288	-0.01171	0.62847	2.19221

Random effects:

Groups	Name	Variance	Std.Dev.
participant_ID	(Intercept)	0.07419	0.2724
Residual		0.15597	0.3949

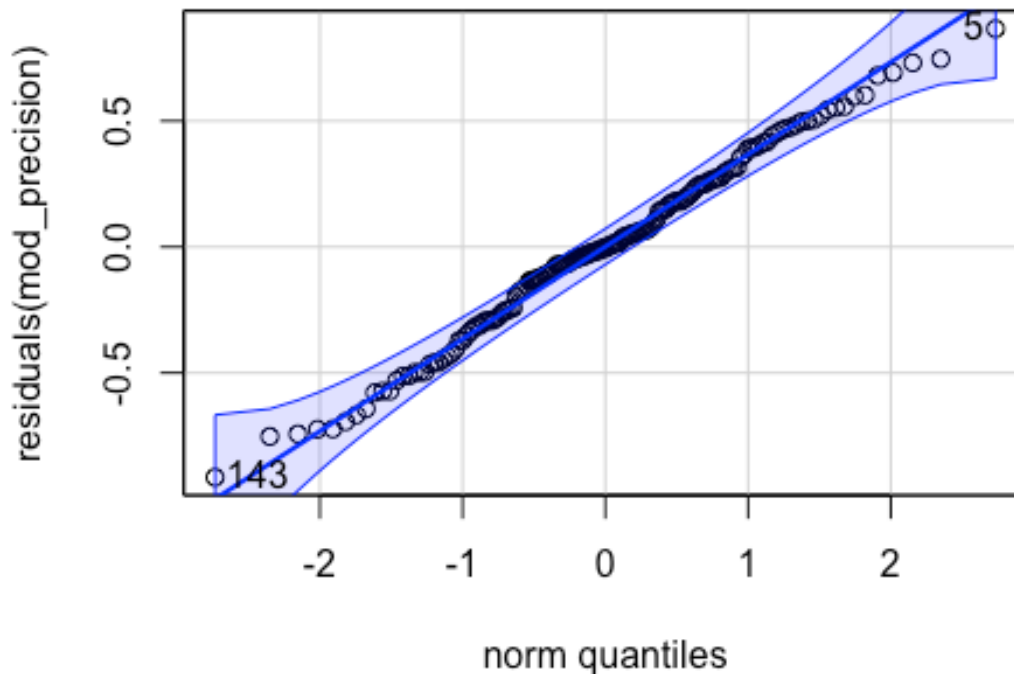
Number of obs: 160, groups: participant_ID, 40

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	1.05790	0.10727	9.862
GroupTDC	0.46264	0.15171	3.050
factor(bpm)80	0.02354	0.12489	0.188
factor(bpm)100	-0.12381	0.12489	-0.991
factor(bpm)120	-0.34433	0.12489	-2.757
GroupTDC:factor(bpm)80	-0.07977	0.17662	-0.452
GroupTDC:factor(bpm)100	-0.12588	0.17662	-0.713
GroupTDC:factor(bpm)120	0.22979	0.17662	1.301

Correlation of Fixed Effects:

	(Intr)	GrpTDC	fc()80	f()100	f()120	GTDC:()8	GTDC:()10
GroupTDC	-0.707						
fctr(bpm)80	-0.582	0.412					
fctr(bp)100	-0.582	0.412	0.500				
fctr(bp)120	-0.582	0.412	0.500	0.500			
GrpTDC:()80	0.412	-0.582	-0.707	-0.354	-0.354		
GrTDC:()100	0.412	-0.582	-0.354	-0.707	-0.354	0.500	
GrTDC:()120	0.412	-0.582	-0.354	-0.354	-0.707	0.500	0.500



item	group1	vars	n	mean	sd	median	trimmed	mad
X11	1	DYS	1 80	0.6619666	0.2569535	0.7478659	0.6934277	0.21057736
X12	2	TDC	1 80	0.8422497	0.1598154	0.8953113	0.8762700	0.07939407
	min	max	range	skew	kurtosis	se		
X11	0.0583430	0.9656805	0.9073375	-0.9039339	-0.371664	0.02872828		
X12	0.1441403	0.9841969	0.8400566	-2.2291437	5.247770	0.01786790		

Post-hoc for groups:

contrast	estimate	SE	df	t.ratio	p.value
DYS - TDC	-0.469	0.106	38	-4.405	0.0001

Results are averaged over the levels of: bpm
Degrees-of-freedom method: kenward-roger

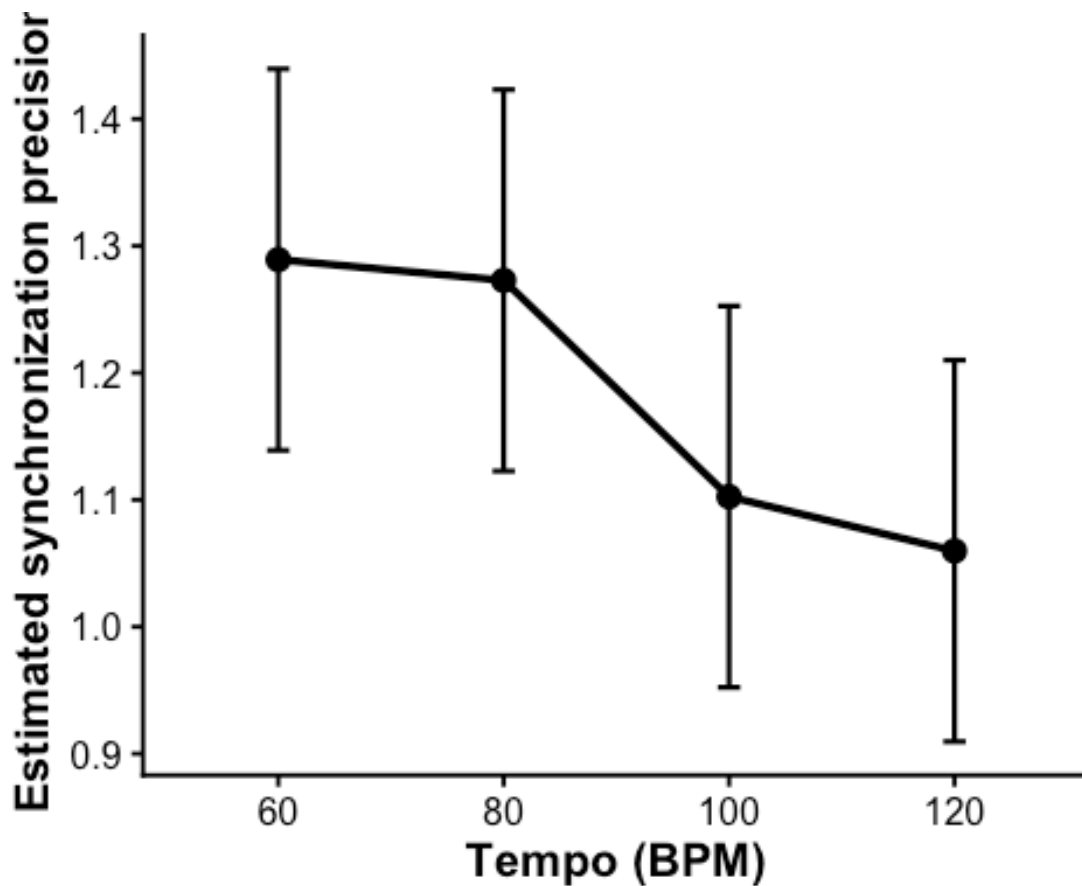
Post-hoc for bpm:

contrast	estimate	SE	df	t.ratio	p.value
bpm60 - bpm80	0.0163	0.0883	114	0.185	0.9977
bpm60 - bpm100	0.1868	0.0883	114	2.115	0.1546
bpm60 - bpm120	0.2294	0.0883	114	2.598	0.0512
bpm80 - bpm100	0.1704	0.0883	114	1.930	0.2215
bpm80 - bpm120	0.2131	0.0883	114	2.413	0.0803
bpm100 - bpm120	0.0427	0.0883	114	0.483	0.9626

Results are averaged over the levels of: Group
Degrees-of-freedom method: kenward-roger
P value adjustment: tukey method for comparing a family of 4 estimates

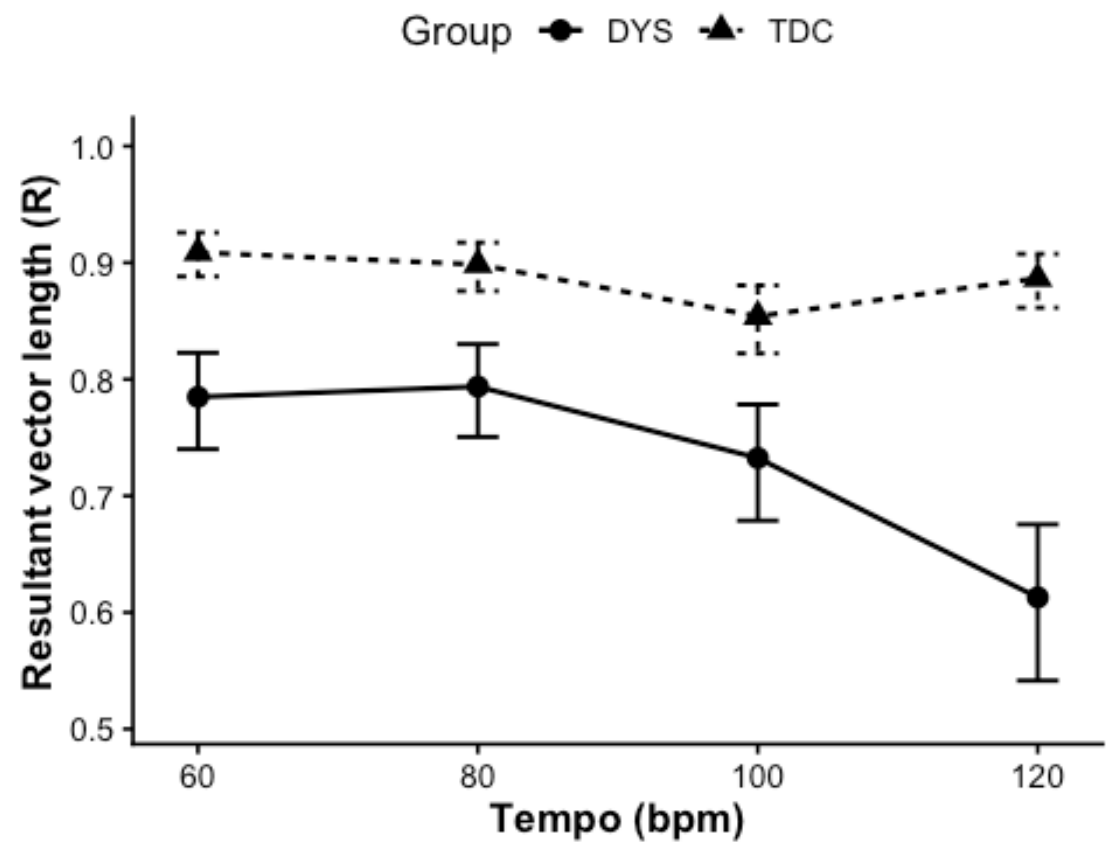
Supplementary Figure 4

Estimated marginal means ($\pm 95\%$ confidence intervals) of the mean resultant length (R), indexing synchronization precision, across the four tempi (60, 80, 100, and 120 BPM) in all participants. Higher R values indicate greater temporal consistency of tapping relative to the metronome beat.



Supplementary Figure 5

Estimated marginal means ($\pm 95\%$ confidence intervals) of the mean resultant length (R) across the four tempi (60, 80, 100, and 120 BPM) for children with developmental dyslexia (DYS) and typically developing controls (TDC). The mean resultant length (R) indexes synchronization precision, with higher values indicating greater temporal consistency of tapping relative to the metronome beat.



Across tempi, healthy controls showed greater phase consistency than children with dyslexia. Phase consistency varied as a function of tempo, but the effect of tempo did not differ significantly between groups.

4. Paced & Unpaced phase

For continuation tapping compute inter-tap intervals (ITIs). Treat intervals crossing missing or extra taps separately from valid ITIs.

We will now work on the whole dataset and cleaning the data based on ITIs

possible_double_click	single_interval	one_missing
162	4257	36
two_missing	pause	
9	17	

Check how many trials per participants remain:

```
# A tibble: 3 × 4
  participant_ID phase    bpm  n_taps
  <fct>          <chr>  <fct> <int>
1 ddARS006      unpaced 80      2
2 ddARS009      unpaced 100     1
3 ddARS010      unpaced 60      3
```

Let's explore the reason why these participants reported a so low number of clicks:

```
, , = 60
```

	possible_double_click	single_interval	one_missing	two_missing	pause
ddARS001	8	7	1	0	0
ddARS002	0	12	0	0	0
ddARS003	6	10	0	0	0
ddARS004	0	10	0	0	0
ddARS005	1	13	0	0	0
ddARS006	0	13	0	0	0
ddARS007	0	13	1	0	0
ddARS008	0	14	0	0	0
ddARS009	0	13	0	0	0
ddARS010	13	3	0	0	0
ddARS011	0	14	0	0	0
ddARS012	0	13	0	0	0
ddARS013	2	14	0	0	0
ddARS014	0	16	0	0	0
ddARS015	0	13	0	0	0
ddARS016	0	10	0	0	0
ddARS017	0	14	0	0	0
ddARS018	0	12	0	0	0
ddARS019	0	14	0	0	0
ddARS020	1	13	0	0	0
ddARS021	0	10	1	0	0
ddARS022	0	14	0	0	0
ddARS023	0	10	0	0	0
ddARS024	0	14	0	0	0
ddARS025	1	11	0	0	0
ddARS026	0	13	0	0	0
ddARS027	0	13	0	0	0
ddARS028	0	15	0	0	0
ddARS029	1	14	0	0	0
ddARS030	0	11	0	0	0
ddARS031	0	12	0	0	0
ddARS032	0	12	0	0	0
ddARS033	0	12	0	0	0
ddARS034	0	13	0	0	0
ddARS035	0	12	0	0	0
ddARS036	0	10	0	0	0

ddARS037	0	13	0	0	0
ddARS038	0	13	0	0	0
ddARS039	1	11	1	0	0
ddARS040	0	13	0	0	0

, , = 80

	possible_double_click	single_interval	one_missing	two_missing	pause
ddARS001	0	11	0	0	0
ddARS002	0	12	0	0	0
ddARS003	0	13	0	0	0
ddARS004	0	10	0	0	0
ddARS005	0	13	0	0	0
ddARS006	0	2	0	0	0
ddARS007	0	16	0	0	0
ddARS008	0	12	0	0	0
ddARS009	0	12	0	0	0
ddARS010	0	14	0	0	0
ddARS011	0	10	0	0	0
ddARS012	0	13	0	0	0
ddARS013	1	12	1	0	0
ddARS014	0	9	1	0	0
ddARS015	0	10	1	0	0
ddARS016	0	13	0	0	0
ddARS017	0	12	0	0	0
ddARS018	0	14	0	0	0
ddARS019	0	13	0	0	0
ddARS020	1	11	0	0	0
ddARS021	0	11	0	0	0
ddARS022	0	13	0	0	0
ddARS023	0	12	0	0	0
ddARS024	0	13	0	0	0
ddARS025	0	11	0	0	0
ddARS026	0	12	0	0	0
ddARS027	0	13	0	0	0
ddARS028	0	14	0	0	0
ddARS029	0	13	0	0	0
ddARS030	0	13	0	0	0
ddARS031	0	10	0	0	0
ddARS032	0	11	0	0	0
ddARS033	0	12	0	0	0
ddARS034	0	12	0	0	0
ddARS035	1	14	0	0	0
ddARS036	0	12	0	0	0
ddARS037	0	12	0	0	0
ddARS038	0	12	0	0	0
ddARS039	0	11	0	0	0
ddARS040	0	10	0	0	0

, , = 100

	possible_double_click	single_interval	one_missing	two_missing	pause
ddARS001	0	11	0	0	0
ddARS002	0	16	0	0	0
ddARS003	0	13	1	0	0
ddARS004	0	11	1	0	0
ddARS005	0	15	0	0	0
ddARS006	0	11	0	0	0
ddARS007	5	11	0	0	0
ddARS008	0	14	0	0	0
ddARS009	14	1	1	0	0
ddARS010	0	14	0	0	0
ddARS011	0	13	0	0	0
ddARS012	0	11	0	0	0
ddARS013	0	16	0	0	0
ddARS014	0	9	0	0	0
ddARS015	0	13	0	0	0
ddARS016	0	11	0	0	0
ddARS017	0	10	0	0	0
ddARS018	0	12	1	0	0
ddARS019	0	11	1	0	0
ddARS020	0	12	0	0	0
ddARS021	0	11	0	0	0
ddARS022	0	13	0	0	0
ddARS023	0	12	0	0	0
ddARS024	0	12	0	0	0
ddARS025	0	12	0	0	0
ddARS026	0	13	0	0	0
ddARS027	0	11	0	0	0
ddARS028	0	13	0	0	0
ddARS029	0	15	0	0	0
ddARS030	0	12	0	0	0
ddARS031	0	11	0	0	0
ddARS032	0	12	0	0	0
ddARS033	0	11	0	0	0
ddARS034	0	13	0	0	0
ddARS035	0	11	0	1	0
ddARS036	0	10	0	1	0
ddARS037	0	6	0	0	0
ddARS038	0	12	0	0	0
ddARS039	0	12	0	0	0
ddARS040	0	6	0	0	0

, , = 120

	possible_double_click	single_interval	one_missing	two_missing	pause
ddARS001	0	11	0	0	0
ddARS002	0	15	0	0	0

ddARS003	0	14	0	0	0
ddARS004	0	15	1	0	0
ddARS005	0	7	0	0	0
ddARS006	0	12	0	0	0
ddARS007	2	10	1	0	0
ddARS008	0	13	0	0	0
ddARS009	1	14	0	0	0
ddARS010	0	13	0	0	0
ddARS011	0	16	0	0	0
ddARS012	0	14	0	0	0
ddARS013	2	14	0	0	0
ddARS014	0	7	1	0	0
ddARS015	0	8	1	0	0
ddARS016	0	13	0	0	0
ddARS017	0	16	0	0	0
ddARS018	0	12	0	0	0
ddARS019	0	12	0	0	0
ddARS020	0	12	0	0	0
ddARS021	0	13	0	0	0
ddARS022	1	11	0	0	0
ddARS023	0	11	0	0	0
ddARS024	0	11	0	0	0
ddARS025	0	12	0	0	0
ddARS026	0	12	0	0	0
ddARS027	0	13	0	0	0
ddARS028	0	12	1	0	0
ddARS029	0	16	0	0	0
ddARS030	0	13	0	0	0
ddARS031	0	12	1	0	0
ddARS032	0	9	0	1	0
ddARS033	0	13	0	0	0
ddARS034	0	11	0	0	0
ddARS035	2	12	0	0	0
ddARS036	0	13	0	0	0
ddARS037	0	11	0	0	0
ddARS038	0	12	0	0	0
ddARS039	0	13	0	0	0
ddARS040	0	13	0	0	0

009 and 010 clicked one time every two beat, while 006 stopped after 1 click.

Is there a group difference for the frequency of outliers?

	DYS	TDC
possible_double_click	57	7
single_interval	956	958
one_missing	14	4
two_missing	0	3
pause	0	0

Pearson's Chi-squared test

```
data: dataTAP_classified_unpaced$iti_class and dataTAP_classified_unpaced$Group  
X-squared = 46.142, df = 3, p-value = 5.291e-10
```

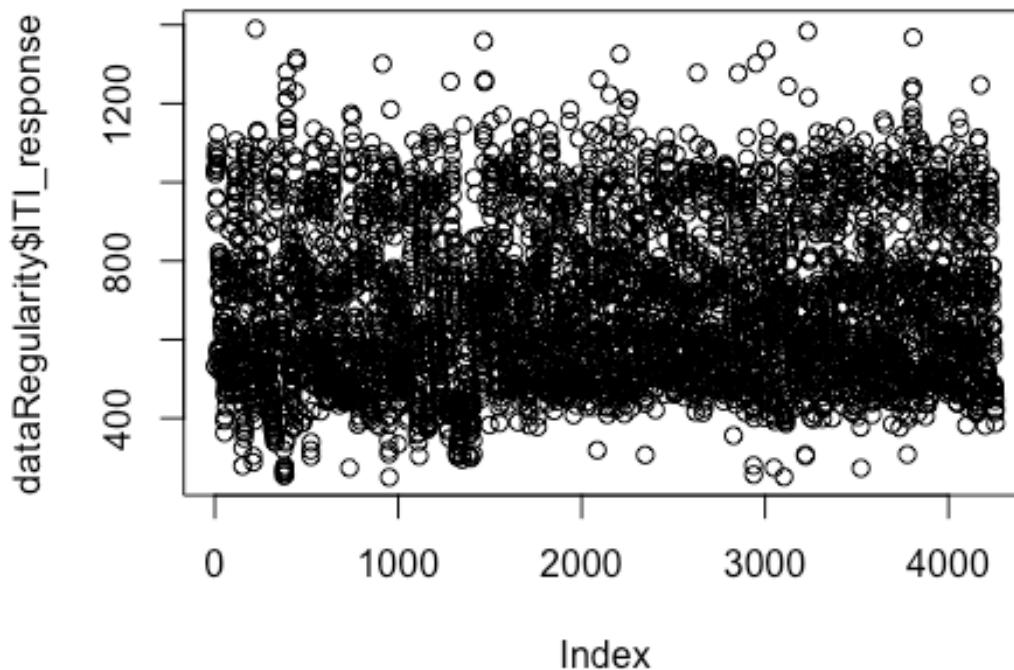
Fisher's Exact Test for Count Data

```
data: tab  
p-value = 0.004824  
alternative hypothesis: two.sided
```

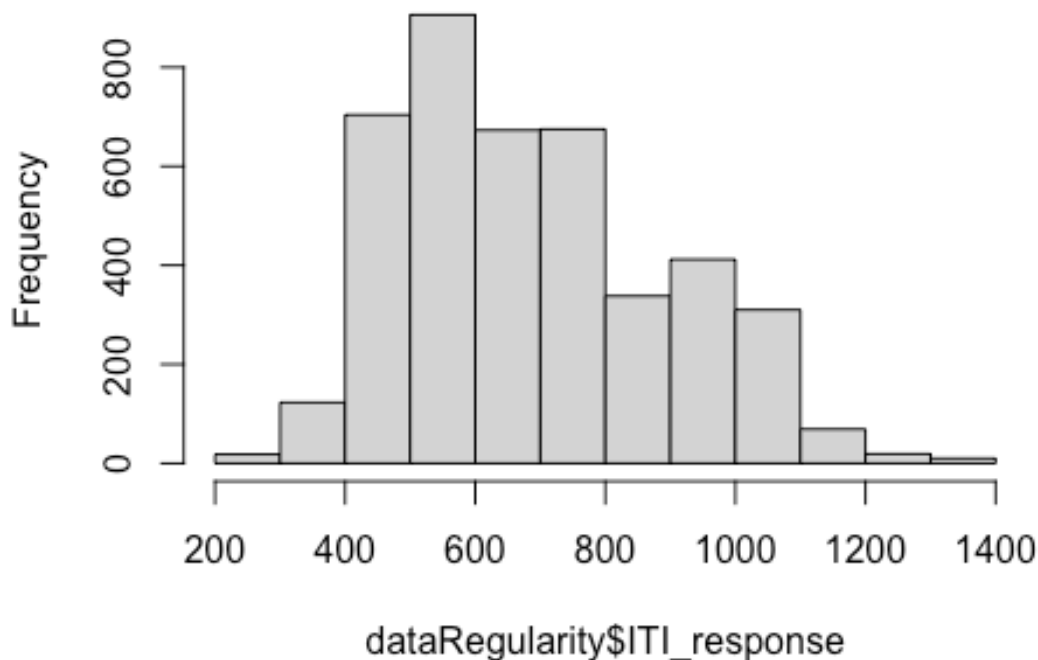
4.1 Timing regularity

The coefficient of variation (CV) was computed only for conditions with at least six recorded taps (five inter-tap intervals), ensuring a sufficiently stable estimate of tapping variability. Conditions with fewer observations were treated as missing for the CV analysis.

Model based on ITIs (trial-level)



Histogram of dataRegularity\$ITI_response



Analysis of Deviance Table (Type III Wald chisquare tests)

Response: ITI_response

	Chisq	Df	Pr(>Chisq)
(Intercept)	17094.1696	1	< 2.2e-16 ***
Group	7.2866	1	0.006947 **
phase	111.4178	1	< 2.2e-16 ***
bpm	5343.9991	3	< 2.2e-16 ***
Group:phase	9.3068	1	0.002283 **
Group:bpm	4.3861	3	0.222675
phase:bpm	44.6898	3	1.077e-09 ***
Group:phase:bpm	4.9381	3	0.176386

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Linear mixed model fit by REML ['lmerMod']

Formula: ITI_response ~ Group * phase * bpm + (1 | participant_ID)

Data: dataRegularity

REML criterion at convergence: 50135

Scaled residuals:

Min	1Q	Median	3Q	Max
-5.0961	-0.4676	0.0058	0.4721	5.2122

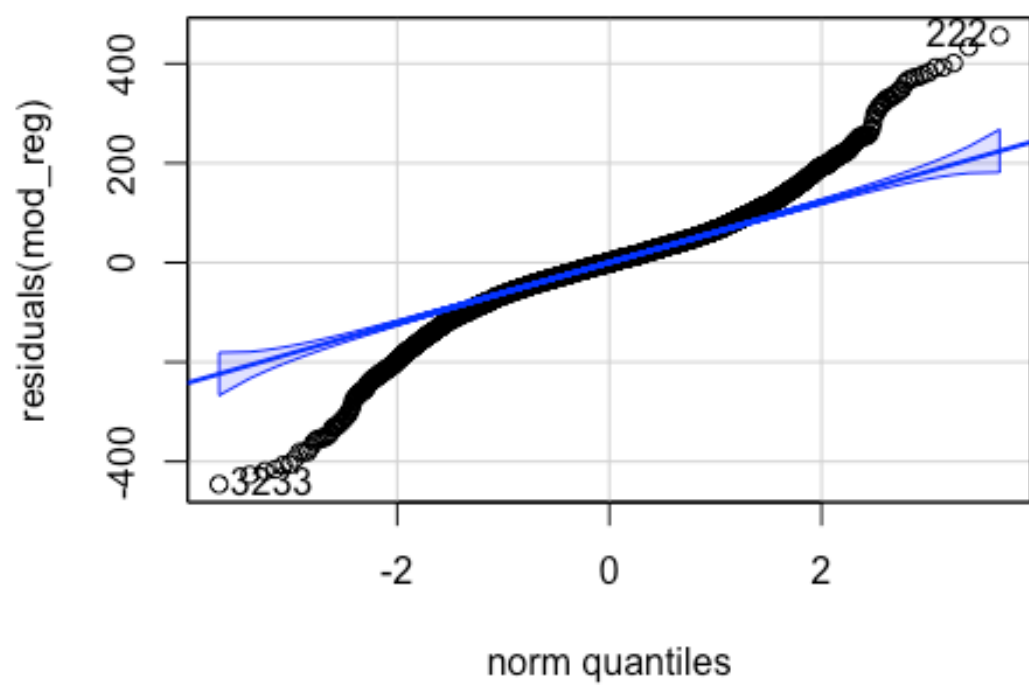
Random effects:

Groups	Name	Variance	Std.Dev.
participant_ID	(Intercept)	591.1	24.31
	Residual	7651.8	87.47

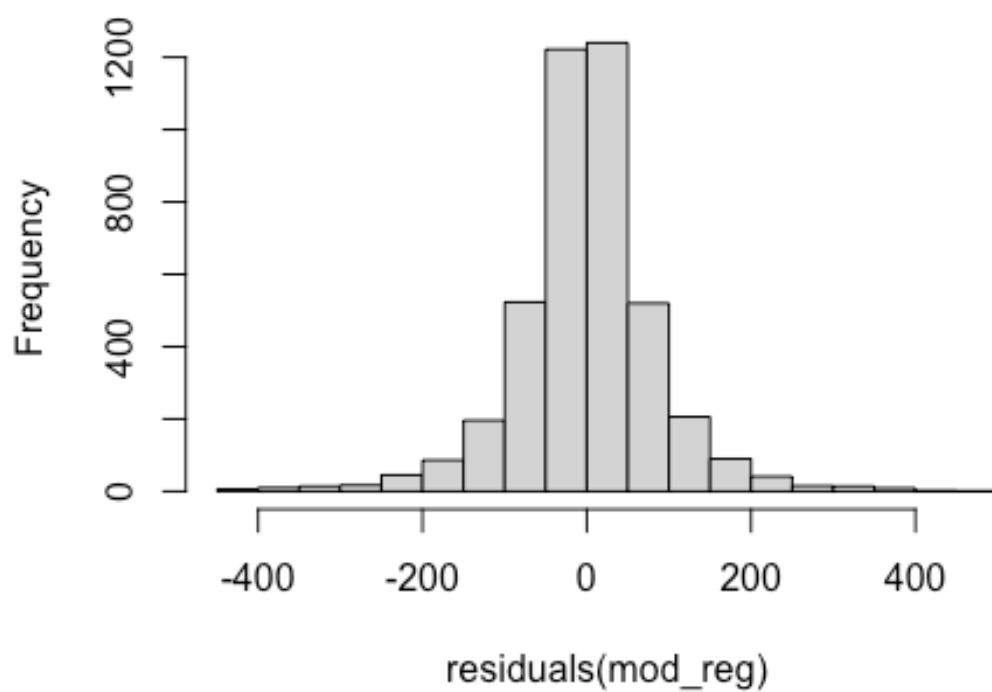
Number of obs: 4257, groups: participant_ID, 40

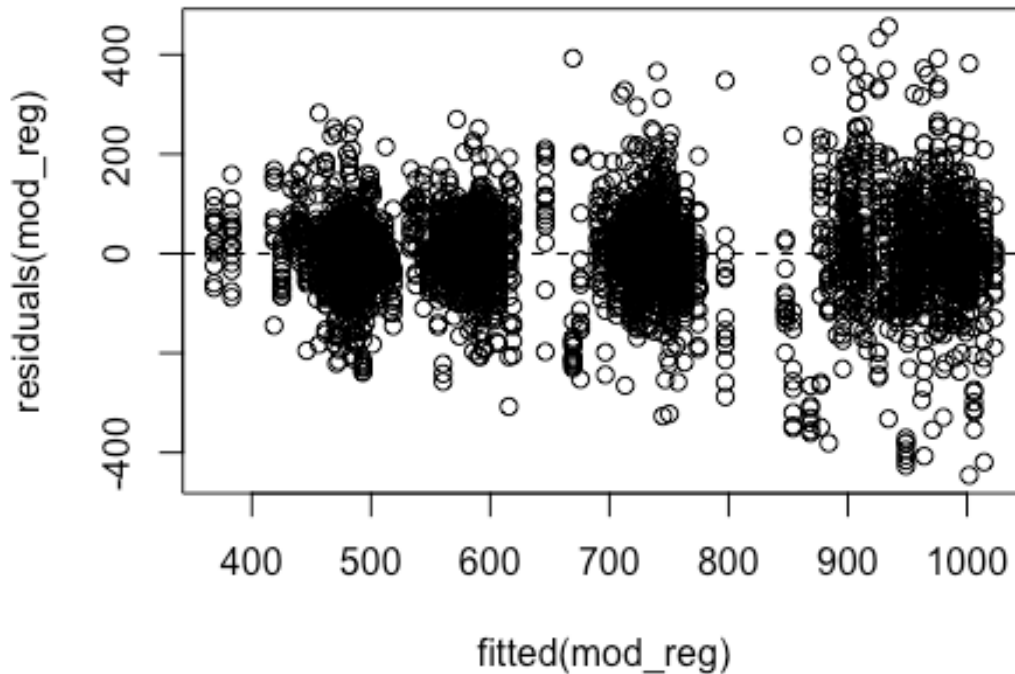
Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	970.718	7.425	130.745
GroupTDC	28.414	10.526	2.699
phaseunpaced	-80.125	7.591	-10.555
bpm80	-231.081	7.153	-32.306
bpm100	-390.020	7.154	-54.521
bpm120	-494.227	7.235	-68.309
GroupTDC:phaseunpaced	32.698	10.718	3.051
GroupTDC:bpm80	-19.313	10.160	-1.901
GroupTDC:bpm100	-17.427	10.227	-1.704
GroupTDC:bpm120	-12.985	10.241	-1.268
phaseunpaced:bpm80	52.861	10.793	4.898
phaseunpaced:bpm100	54.724	10.776	5.078
phaseunpaced:bpm120	65.358	10.748	6.081
GroupTDC:phaseunpaced:bpm80	-25.552	15.213	-1.680
GroupTDC:phaseunpaced:bpm100	-7.258	15.306	-0.474
GroupTDC:phaseunpaced:bpm120	-28.288	15.190	-1.862



Histogram of residuals(mod_reg)





[1] 50171

Visual inspection of model residuals indicated heterogeneity of residual variance across tempo conditions. Therefore, linear mixed-effects models were fitted using the nlme package, specifying a varldent variance structure to allow residual variance to differ across BPM conditions.

To account for heteroscedasticity across tempo conditions, residual variances were allowed to differ across BPM levels using a varldent variance structure.

Analysis of Deviance Table (Type II tests)

Response: ITI_response

	Chisq	Df	Pr(>Chisq)	
Group	6.3827	1	0.011524	*
phase	69.6475	1	< 2.2e-16	***
bpm	15506.4659	3	< 2.2e-16	***
Group:phase	9.3637	1	0.002213	**
Group:bpm	12.3105	3	0.006392	**
phase:bpm	41.2020	3	5.925e-09	***
Group:phase:bpm	5.7965	3	0.121943	

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Linear mixed-effects model fit by REML

Data: dataRegularity

AIC	BIC	logLik
49528.54	49661.94	-24743.27

Random effects:

Formula: ~1 | participant_ID
(Intercept) Residual

StdDev: 24.00917 124.443

Variance function:

Structure: Different standard deviations per stratum

Formula: ~1 | bpm

Parameter estimates:

	60	80	100	120
	1.0000000	0.6801332	0.5184972	0.5025073

Fixed effects: ITI_response ~ Group * phase * bpm

	Value	Std.Error	DF	t-value	p-value
(Intercept)	970.6441	8.971687	4203	108.18970	0.0000
GroupTDC	28.5370	12.734658	38	2.24089	0.0310
phaseunpaced	-79.7748	10.777491	4203	-7.40198	0.0000
bpm80	-231.0587	8.696566	4203	-26.56896	0.0000
bpm100	-389.8203	8.099574	4203	-48.12849	0.0000
bpm120	-493.9772	8.084590	4203	-61.10109	0.0000
GroupTDC:phaseunpaced	32.0393	15.231218	4203	2.10353	0.0355
GroupTDC:bpm80	-19.4100	12.360362	4203	-1.57034	0.1164
GroupTDC:bpm100	-17.9958	11.546448	4203	-1.55856	0.1192
GroupTDC:bpm120	-13.3174	11.476997	4203	-1.16036	0.2460
phaseunpaced:bpm80	52.2063	13.084599	4203	3.98990	0.0001
phaseunpaced:bpm100	54.3409	12.168339	4203	4.46576	0.0000
phaseunpaced:bpm120	66.2917	12.075270	4203	5.48988	0.0000
GroupTDC:phaseunpaced:bpm80	-24.6532	18.467421	4203	-1.33496	0.1820
GroupTDC:phaseunpaced:bpm100	-6.4801	17.235112	4203	-0.37598	0.7069
GroupTDC:phaseunpaced:bpm120	-28.7602	17.067444	4203	-1.68509	0.0920

Correlation:

	(Intr)	GrpTDC	phsnpc	bpm80	bpm100	bpm120	GrTDC:
GroupTDC	-0.705						
phaseunpaced	-0.535	0.377					
bpm80	-0.662	0.467	0.552				
bpm100	-0.711	0.501	0.592	0.733			
bpm120	-0.712	0.502	0.593	0.735	0.789		
GroupTDC:phaseunpaced	0.378	-0.539	-0.708	-0.390	-0.419	-0.420	
GroupTDC:bpm80	0.466	-0.664	-0.388	-0.704	-0.516	-0.517	0.555
GroupTDC:bpm100	0.499	-0.711	-0.416	-0.514	-0.701	-0.553	0.595
GroupTDC:bpm120	0.502	-0.715	-0.418	-0.518	-0.556	-0.704	0.598
phaseunpaced:bpm80	0.441	-0.310	-0.824	-0.665	-0.488	-0.489	0.583
phaseunpaced:bpm100	0.474	-0.334	-0.886	-0.489	-0.666	-0.526	0.627
phaseunpaced:bpm120	0.477	-0.336	-0.893	-0.493	-0.529	-0.670	0.632
GroupTDC:phaseunpaced:bpm80	-0.312	0.445	0.584	0.471	0.346	0.346	-0.825
GroupTDC:phaseunpaced:bpm100	-0.334	0.476	0.626	0.345	0.470	0.371	-0.884
GroupTDC:phaseunpaced:bpm120	-0.338	0.481	0.632	0.348	0.374	0.474	-0.893

GTDC:8 GTDC:10 GTDC:12 phs:80 ph:100 ph:120

GroupTDC

phaseunpaced

bpm80

bpm100

bpm120

GroupTDC:phaseunpaced

GroupTDC:bpm80

GroupTDC:bpm100 0.732

GroupTDC:bpm120 0.737 0.789

phaseunpaced:bpm80 0.468 0.342 0.344

phaseunpaced:bpm100 0.344 0.467 0.370 0.730

phaseunpaced:bpm120 0.347 0.371 0.472 0.736 0.791

GroupTDC:phaseunpaced:bpm80 -0.669 -0.490 -0.493 -0.709 -0.517 -0.521

GroupTDC:phaseunpaced:bpm100 -0.491 -0.670 -0.529 -0.515 -0.706 -0.558

GroupTDC:phaseunpaced:bpm120 -0.496 -0.531 -0.673 -0.521 -0.560 -0.708

GTDC::8 GTDC::10

GroupTDC

phaseunpaced

bpm80

bpm100

bpm120

GroupTDC:phaseunpaced

GroupTDC:bpm80

GroupTDC:bpm100

GroupTDC:bpm120

phaseunpaced:bpm80

phaseunpaced:bpm100

phaseunpaced:bpm120

GroupTDC:phaseunpaced:bpm80

GroupTDC:phaseunpaced:bpm100 0.729

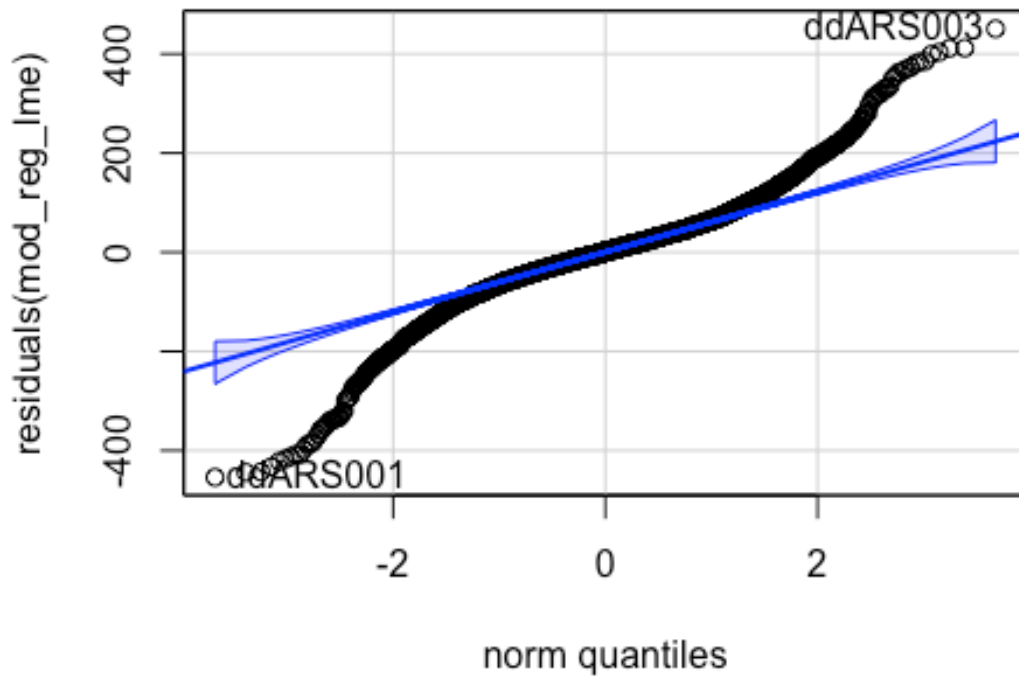
GroupTDC:phaseunpaced:bpm120 0.736 0.789

Standardized Within-Group Residuals:

Min	Q1	Med	Q3	Max
-4.59591717	-0.50630596	0.01454235	0.52362358	4.58381792

Number of Observations: 4257

Number of Groups: 40



phase = paced:

contrast	estimate	SE	df	t.ratio	p.value
DYS - TDC	-15.9	8.41	38	-1.886	0.0670

phase = unpaced:

contrast	estimate	SE	df	t.ratio	p.value
DYS - TDC	-32.9	8.58	38	-3.836	0.0005

Results are averaged over the levels of: bpm
Degrees-of-freedom method: containment

bpm = 60:

contrast	estimate	SE	df	t.ratio	p.value
DYS - TDC	-44.6	10.80	38	-4.144	0.0002

bpm = 80:

contrast	estimate	SE	df	t.ratio	p.value
DYS - TDC	-12.8	9.21	38	-1.391	0.1722

bpm = 100:

contrast	estimate	SE	df	t.ratio	p.value
DYS - TDC	-23.3	8.60	38	-2.712	0.0100

bpm = 120:

contrast	estimate	SE	df	t.ratio	p.value
DYS - TDC	-16.9	8.51	38	-1.981	0.0549

Results are averaged over the levels of: phase
Degrees-of-freedom method: containment

bpm = 60:

contrast	estimate	SE	df	t.ratio	p.value
paced - unpaced	63.8	7.62	4203	8.372	<.0001

bpm = 80:

contrast	estimate	SE	df	t.ratio	p.value
paced - unpaced	23.9	5.22	4203	4.574	<.0001

bpm = 100:

contrast	estimate	SE	df	t.ratio	p.value
paced - unpaced	12.7	4.03	4203	3.139	0.0017

bpm = 120:

contrast	estimate	SE	df	t.ratio	p.value
paced - unpaced	11.8	3.85	4203	3.078	0.0021

Results are averaged over the levels of: Group
Degrees-of-freedom method: containment

phase = paced:

contrast	effect.size	SE	df	lower.CL	upper.CL
DYS - TDC	-0.127	0.0676	38	-0.264	0.00939

phase = unpaced:

contrast	effect.size	SE	df	lower.CL	upper.CL
DYS - TDC	-0.265	0.0690	38	-0.404	-0.12481

Results are averaged over the levels of: bpm
sigma used for effect sizes: 124.4
Degrees-of-freedom method: inherited from containment when re-gridding
Confidence level used: 0.95

bpm = 60:

contrast	effect.size	SE	df	lower.CL	upper.CL
DYS - TDC	-0.358	0.0865	38	-0.533	-0.18297

bpm = 80:

contrast	effect.size	SE	df	lower.CL	upper.CL
DYS - TDC	-0.103	0.0741	38	-0.253	0.04689

bpm = 100:

contrast	effect.size	SE	df	lower.CL	upper.CL
DYS - TDC	-0.187	0.0691	38	-0.327	-0.04747

```
bpm = 120:
contrast  effect.size      SE df lower.CL upper.CL
DYS - TDC      -0.135 0.0684 38   -0.274  0.00301
```

Results are averaged over the levels of: phase

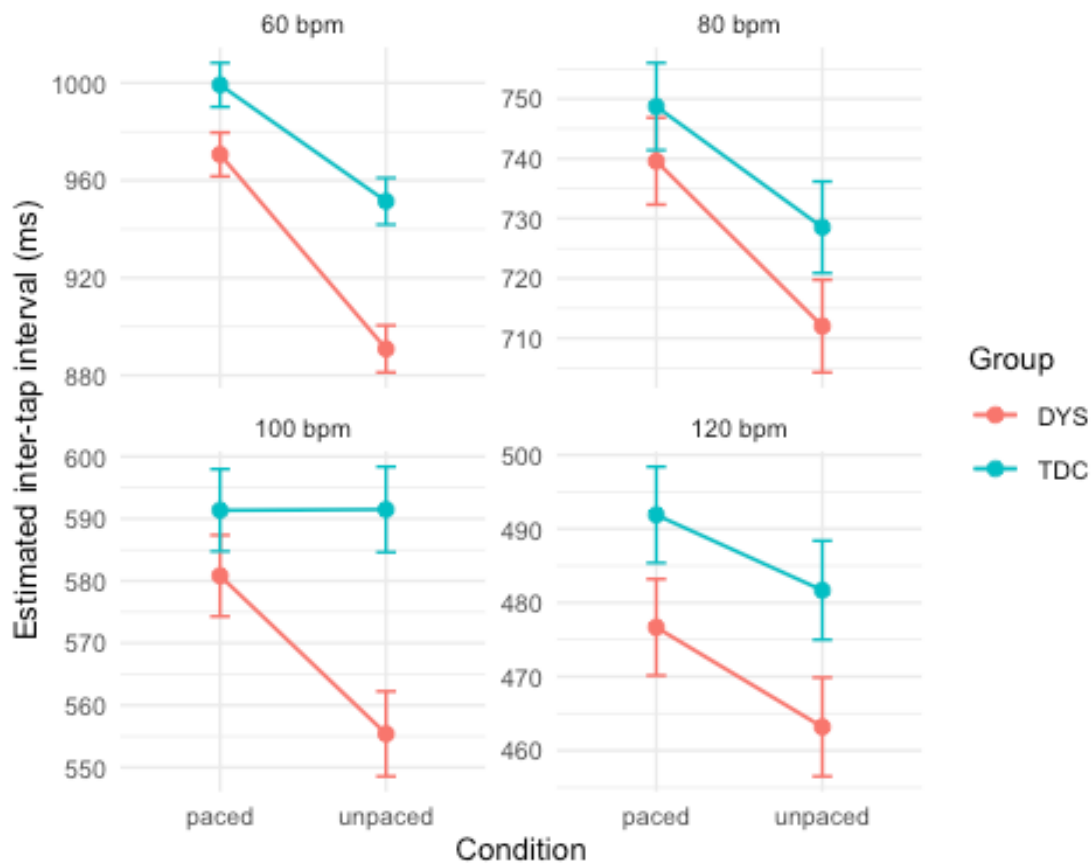
sigma used for effect sizes: 124.4

Degrees-of-freedom method: inherited from containment when re-gridding

Confidence level used: 0.95

Figure 2

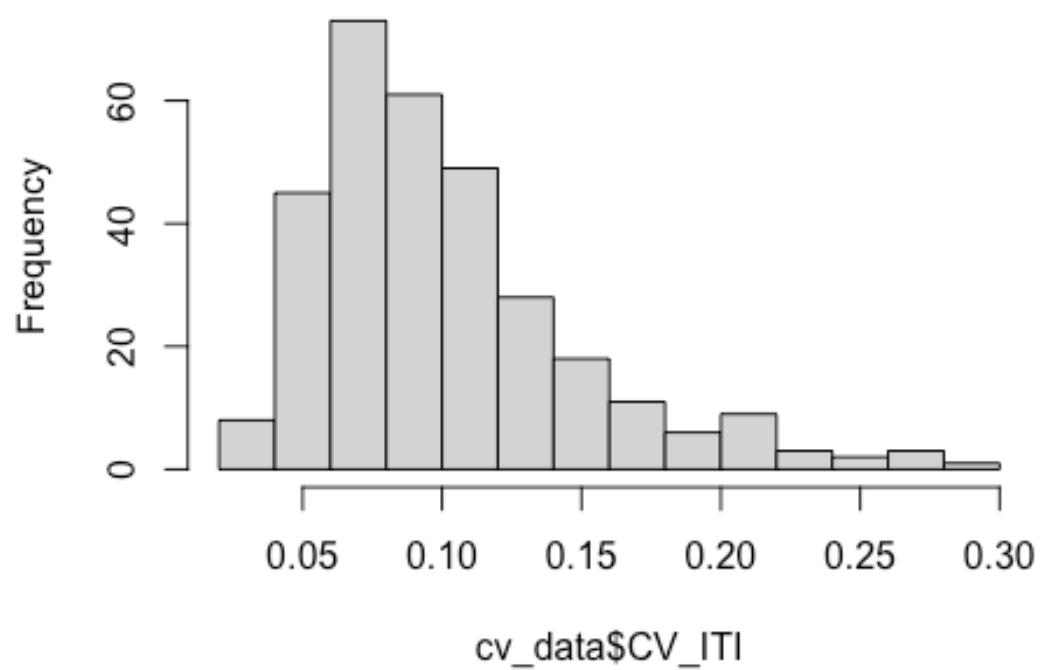
ITIs of TDC and DYS in the paced and unpaced condition of the tapping tasks.

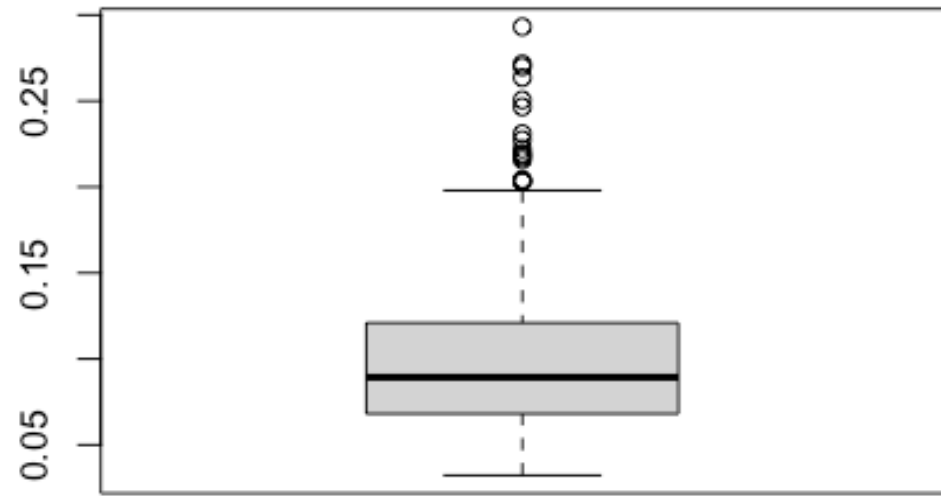


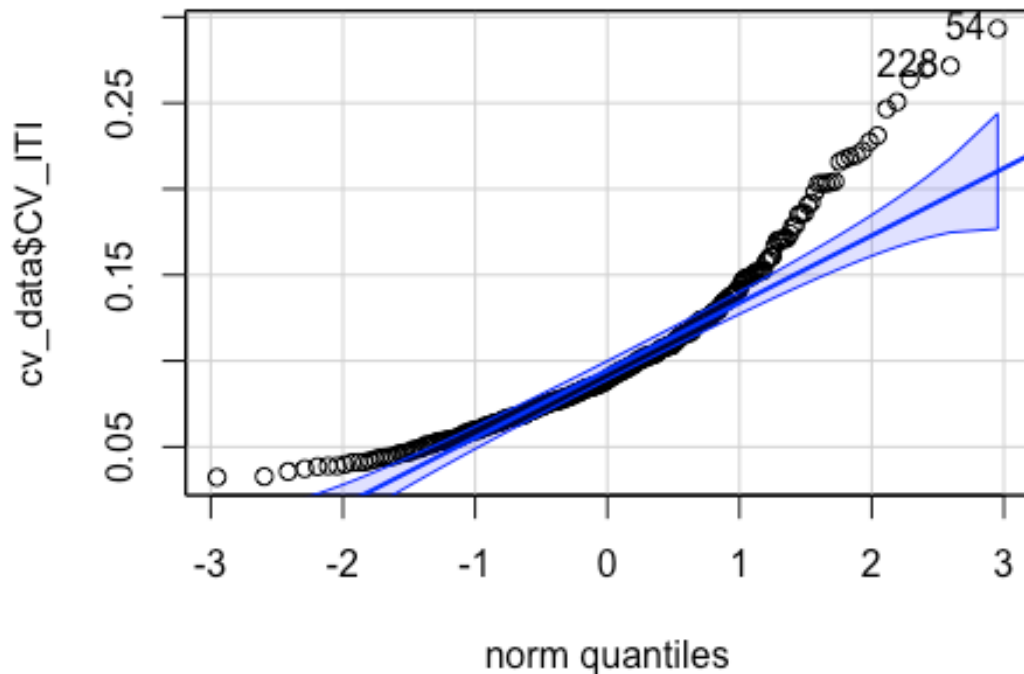
4.2 Response consistency

Model on CVs, based on a gamma distribution:

Histogram of cv_data\$CV_ITI







```
[1] 54 228
```

```
Family: Gamma ( log )
Formula: CV_ITI ~ Group * phase * bpm + (1 | participant_ID)
Data: cv_data
```

AIC	BIC	logLik	-2*log(L)	df.resid
-1170.6	-1102.9	603.3	-1206.6	299

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
participant_ID	(Intercept)	0.04387	0.2095

Number of obs: 317, groups: participant_ID, 40

Dispersion estimate for Gamma family (sigma^2): 0.126

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-2.22733	0.09294	-23.965	<2e-16 ***
GroupTDC	-0.24160	0.13116	-1.842	0.0655 .
phaseunpaced	0.05714	0.11496	0.497	0.6191
bpm80	0.04311	0.11343	0.380	0.7039

bpm100	-0.01059	0.11305	-0.094	0.9253
bpm120	0.10870	0.11342	0.958	0.3379
GroupTDC:phaseunpaced	-0.03801	0.16119	-0.236	0.8136
GroupTDC:bpm80	-0.05534	0.15991	-0.346	0.7293
GroupTDC:bpm100	0.06886	0.15992	0.431	0.6668
GroupTDC:bpm120	-0.04947	0.16003	-0.309	0.7572
phaseunpaced:bpm80	-0.04803	0.16242	-0.296	0.7675
phaseunpaced:bpm100	-0.13728	0.16221	-0.846	0.3974
phaseunpaced:bpm120	-0.11370	0.16113	-0.706	0.4804
GroupTDC:phaseunpaced:bpm80	-0.05568	0.22784	-0.244	0.8069
GroupTDC:phaseunpaced:bpm100	-0.05703	0.22753	-0.251	0.8021
GroupTDC:phaseunpaced:bpm120	0.26191	0.22724	1.153	0.2491

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Analysis of Deviance Table (Type III Wald chisquare tests)

Response: CV_ITI

	Chisq	Df	Pr(>Chisq)
(Intercept)	574.3146	1	< 2e-16 ***
Group	3.3932	1	0.06547 .
phase	0.2471	1	0.61914
bpm	1.3764	3	0.71108
Group:phase	0.0556	1	0.81357
Group:bpm	0.7777	3	0.85480
phase:bpm	0.8972	3	0.82610
Group:phase:bpm	2.6990	3	0.44040

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Group	response	SE	df	asympt.LCL	asympt.UCL
DYS	0.1107	0.00607	Inf	0.0994	0.1233
TDC	0.0861	0.00471	Inf	0.0774	0.0959

Results are averaged over the levels of: phase, bpm

Confidence level used: 0.95

Intervals are back-transformed from the log scale

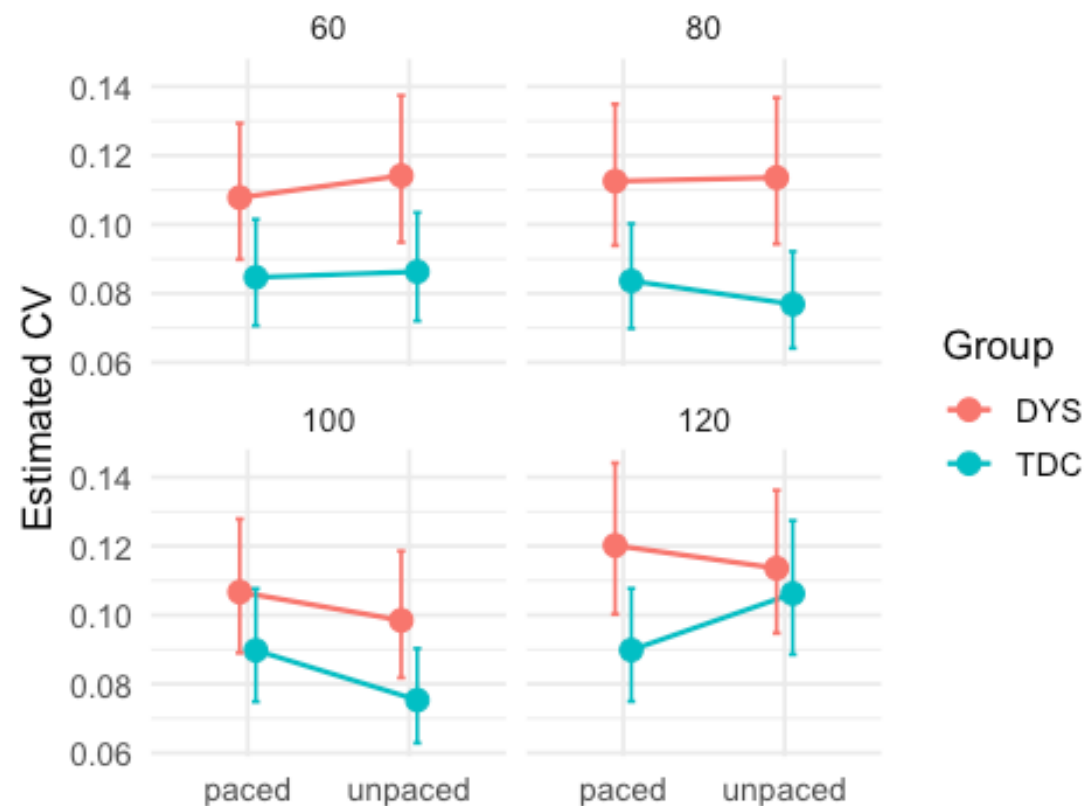
contrast	ratio	SE	df	null	z.ratio	p.value
DYS / TDC	1.29	0.0995	Inf	1	3.241	0.0012

Results are averaged over the levels of: phase, bpm

Tests are performed on the log scale

A trend towards greater temporal variability was observed in the DSA group, irrespective of phase and tempo. Estimated marginal means indicated that children with dyslexia showed a 29% higher coefficient of variation than controls.

Supplementary Figure 6



Supplementary analysis: test of the “optimal temporal window” hypothesis (McAuley et al., 2006). Tempo is modelled as a continuous predictor with linear and quadratic terms to evaluate a potential U-shaped relationship between tapping variability and tempo.

```
Family: Gamma ( log )
Formula:
CV_ITI ~ Group * phase * (bpm_c + I(bpm_c^2)) + (1 | participant_ID)
Data: cv_data
```

AIC	BIC	logLik	-2*log(L)	df.resid
-1175.9	-1123.3	602.0	-1203.9	303

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
participant_ID	(Intercept)	0.04372	0.2091

Number of obs: 317, groups: participant_ID, 40

Dispersion estimate for Gamma family (sigma^2): 0.127

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-2.215303	0.079368	-27.912	<2e-16 ***
GroupTDC	-0.231136	0.112320	-2.058	0.0396 *
phaseunpaced	-0.038176	0.092399	-0.413	0.6795
bpm_c	0.013626	0.017998	0.757	0.4490
I(bpm_c^2)	0.004765	0.010042	0.475	0.6351
GroupTDC:phaseunpaced	-0.119059	0.129576	-0.919	0.3582
GroupTDC:bpm_c	-0.001199	0.025402	-0.047	0.9623
GroupTDC:I(bpm_c^2)	-0.003955	0.014203	-0.278	0.7807
phaseunpaced:bpm_c	-0.021449	0.025594	-0.838	0.4020
phaseunpaced:I(bpm_c^2)	0.004296	0.014375	0.299	0.7651
GroupTDC:phaseunpaced:bpm_c	0.039086	0.036083	1.083	0.2787
GroupTDC:phaseunpaced:I(bpm_c^2)	0.023540	0.020195	1.166	0.2438

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Analysis of Deviance Table (Type III Wald chisquare tests)

Response: CV_ITI

	Chisq	Df	Pr(>Chisq)
(Intercept)	779.0596	1	< 2e-16 ***
Group	4.2346	1	0.03961 *
phase	0.1707	1	0.67948
bpm_c	0.5732	1	0.44900
I(bpm_c^2)	0.2252	1	0.63512
Group:phase	0.8443	1	0.35818
Group:bpm_c	0.0022	1	0.96235
Group:I(bpm_c^2)	0.0775	1	0.78065
phase:bpm_c	0.7023	1	0.40200
phase:I(bpm_c^2)	0.0893	1	0.76506
Group:phase:bpm_c	1.1734	1	0.27870
Group:phase:I(bpm_c^2)	1.3587	1	0.24376

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Further check on outliers

	DYS	TDC
matched	1164	1216
missed_ref	186	59

	DYS	TDC
matched	44.342857	46.323810
missed_ref	7.085714	2.247619

Pearson's Chi-squared test with Yates' continuity correction

```
data: dataEntr_aligned$status and dataEntr_aligned$Group
X-squared = 63.802, df = 1, p-value = 1.376e-15
```

```
[1] 13.77778
```

```
[1] 4.627451
```

	DYS	TDC
possible_double_click	78	20
single_interval	1184	1159
one_missing	8	10
two_missing	0	6
pause	8	9

	DYS	TDC
possible_double_click	3.1426269	0.8058018
single_interval	47.7034649	46.6962127
one_missing	0.3223207	0.4029009
two_missing	0.0000000	0.2417405
pause	0.3223207	0.3626108

Pearson's Chi-squared test

```
data: dataEntr_aligned$iti_class and dataEntr_aligned$Group
X-squared = 38.702, df = 4, p-value = 8.025e-08
```

TIMING ANTICIPATION TASK

The timing anticipation task's data analysis has been reported on a dedicated document titled Anticipation - Preprocessing & Analysis.