

User Curve Functions

We saw in the general overview when first generating our model fits with `bfit` that we could specify the curve with the argument `curveType`. Presently, the `bdots` package contains three options for this: `doubleGauss`, `logistic`, and `polynomial`. Documentation is included for each of these curves.

```
library(bdots)

fit <- bfit(data = cohort_unrelated,
            subject = "Subject",
            time = "Time",
            y = "Fixations",
            group = c("DB_cond", "LookType"),
            curveType = doubleGauss(concave = TRUE),
            cores = 2)
```

Note that each of these is a function in their own right and must be passed in as a call object. Curve functions that include arguments further specifying the type of curve, i.e., `doubleGauss(concave = TRUE)` and `polynomial(degree = n)`, should include these when the call is passed into `bdotsFit` as seen in the example above.

Because each of the functions exists independently of `bfit`, users can specify their own curve functions for the fitting and bootstrapping process. The purpose of this vignette is to demonstrate how to do so. If you find that you have a curve function that is especially useful, please create a request to have it added to the `bdots` package [here](#).

We will examine the `doubleGauss` function in more detail to see how we might go about creating our own. First, let's identify the components of this function

```
doubleGauss
#> function (dat, y, time, params = NULL, concave = TRUE, ...)
#> {
#>   if (is.null(params)) {
#>     params <- dgaussPars(dat, y, time, concave)
#>   }
#>   else {
#>     if (length(params) != 6)
#>       stop("doubleGauss requires 6 parameters be specified for refitting")
#>     if (!all(names(params) %in% c("mu", "ht", "sig1", "sig2",
#>                                   "base1", "base2"))) {
#>       stop("doubleGauss parameters for refitting must be correctly labeled")
#>     }
#>   }
#>   if (is.null(params)) {
#>     return(NULL)
#>   }
#>   y <- str2lang(y)
#>   time <- str2lang(time)
#>   ff <- bquote(. (y) ~ (. (time) < mu) * (exp(-1 * (. (time) -
#>     mu)^2/(2 * sig1^2)) * (ht - base1) + base1) + (mu <=
#>     . (time)) * (exp(-1 * (. (time) - mu)^2/(2 * sig2^2)) *
```

```
#>      (ht - base2) + base2))
#>      attr(,"parnames") <- names(params)
#>      return(list(formula = ff, params = params))
#> }
#> <bytecode: 0x561fb8224c28>
#> <environment: namespace:bdots>
```

There are four things to note:

1. **Arguments** In addition to the argument `concave = TRUE`, which specifies the curve, we also have `dat`, `y`, `time`, `params = NULL`, and `...`. These are the names that must be used for the function to be called correctly. The first represents a `data.frame` or `data.table` subset from the `data` argument to `bdotsFit`, while `y` and `time` correspond to their respective arguments in `bdotsFit` and should assume that the arguments are passed in as `character`. It's important to remember to set `params = NULL`, as this is only used during the refitting step.
2. **Body** As can be seen here, when `params = NULL`, the body of the function computes the necessary starting parameters to be used with the `gnls` fitting function. In this case, the function `dgaussPars` handles the initial parameter estimation and returns a named `numeric`. When `params` is not `NULL`, it's usually a good idea to verify that it is the correct length and has the correct parameter names.
3. **Formula** Care must be exercised when creating the `formula` object, as it must be quoted. One may use `bquote` and `str2lang` to substitute in the `character` values for `y` and `time`. Alternatively, if this is to only be used for a particular data set, one can simply use `quote` with the appropriate values used for `y` and `time`, as we will demonstrate below. Finally, the quoted `formula` should contain a single attribute `parnames` which has the names of the parameters used.
4. **Return Value** All of the curve functions should return a named list with two elements: a quoted `formula` and `params`, a named `numeric` with the parameters.

Briefly, we can see how this function is used by subsetting the data to a single subject and calling it directly.

```
## Return a unique subject/group permutation
dat <- cohort_unrelated[Subject == 1 & DB_cond == 50 & LookType == "Cohort", ]
dat
#>      Subject Time DB_cond Fixations LookType Group
#> 1:         1    0        50  0.011364 Cohort    50
#> 2:         1    4        50  0.011364 Cohort    50
#> 3:         1    8        50  0.011364 Cohort    50
#> 4:         1   12        50  0.011364 Cohort    50
#> 5:         1   16        50  0.022727 Cohort    50
#> ---
#> 497:        1 1984        50  0.022727 Cohort    50
#> 498:        1 1988        50  0.022727 Cohort    50
#> 499:        1 1992        50  0.022727 Cohort    50
#> 500:        1 1996        50  0.022727 Cohort    50
#> 501:        1 2000        50  0.022727 Cohort    50

## See return value
doubleGauss(dat = dat, y = "Fixations", time = "Time", concave = TRUE)
#> $formula
#> Fixations ~ (Time < mu) * (exp(-1 * (Time - mu)^2/(2 * sig1^2)) *
#>      (ht - base1) + base1) + (mu <= Time) * (exp(-1 * (Time -
#>      mu)^2/(2 * sig2^2)) * (ht - base2) + base2)
#> attr(,"parnames")
#> [1] "mu"      "ht"      "sig1"    "sig2"    "base1"   "base2"
#>
```

```
#> $params
#>      mu      ht      sig1      sig2      base1      base2
#> 428.000000 0.215909 152.000000 396.000000 0.011364 0.022727
```

We will now create an entirely new function that is not included in `bdots` to demonstrate that it works the same; the only change we will make is to substitute in the values for `y` and `time` without using `str2lang`. For our data set here, the corresponding values to `y` and `time` are "Fixations" and "Time", respectively

```
doubleGauss2 <- function(dat, y, time, params = NULL, concave = TRUE, ...) {

  if (is.null(params)) {
    ## Instead of defining our own, just reuse the one in bdots
    params <- bdots::dgaussPars(dat, y, time, concave)
  }
  else {
    if (length(params) != 6)
      stop("doubleGauss requires 6 parameters be specified for refitting")
    if (!all(names(params) %in% c("mu", "ht", "sig1", "sig2",
                                   "base1", "base2"))) {
      stop("doubleGauss parameters for refitting must be correctly labeled")
    }
  }

  ## Here, we use Fixations and Time directly
  ff <- bquote(Fixations ~ (Time < mu) * (exp(-1 * (Time - mu)^2 /
    (2 * sig1^2)) * (ht - base1) + base1) + (mu <= Time) *
    (exp(-1 * (Time - mu)^2 / (2 * sig2^2)) * (ht - base2) + base2))
  return(list(formula = ff, params = params))
}

same_fit_different_day <- bfit(data = cohort_unrelated,
  subject = "Subject",
  time = "Time",
  y = "Fixations",
  group = c("DB_cond", "LookType"),
  curveType = doubleGauss2(concave = TRUE),
  cores = 2)
```

Seeds have not yet been implemented, so there is some possibility that the resulting parameters are slightly different; however, using the `coef` function, we can roughly confirm their equivalence

```
## Original fit
head(coef(fit))
#>      mu      ht      sig1      sig2      base1      base2
#> [1,] 429.76 0.19860 159.89 314.64 0.0097098 0.033761
#> [2,] 634.93 0.26350 303.81 215.38 -0.0206361 0.028924
#> [3,] 647.07 0.25438 518.96 255.99 -0.2130875 0.013682
#> [4,] 723.05 0.25821 392.95 252.94 -0.0548262 0.031973
#> [5,] 501.48 0.22477 500.85 158.42 -0.3316790 0.025227
#> [6,] 460.72 0.30677 382.73 166.08 -0.2433086 0.039922

## "New" fit
head(coef(same_fit_different_day))
#>      mu      ht      sig1      sig2      base1      base2
#> [1,] 424.04 0.19850 154.21 319.47 0.011365 0.033636
```

```
#> [2,] 634.81 0.26351 303.66 215.43 -0.020586 0.028933  
#> [3,] 646.94 0.25444 517.65 256.00 -0.211651 0.013571  
#> [4,] 723.09 0.25821 393.00 252.90 -0.054852 0.031975  
#> [5,] 501.61 0.22479 500.95 158.31 -0.332169 0.025229  
#> [6,] 460.74 0.30680 382.52 165.99 -0.242859 0.039933
```