BLtrimmer usage and output

2022-09-09

```
library(MeltR)
library(tidyverse)

## -- Attaching packages --------------------------------------- tidyverse 1.3.1 --

## v ggplot2 3.4.0      v purrr   0.3.4
## v tibble  3.1.8      v dplyr   1.0.9
## v tidyr   1.2.0      v stringr 1.4.0
## v readr   2.1.2      v forcats 0.5.1

## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
devtools::load_all()
```

```
## i Loading meltR.A.paper
```

```
df = df.absorbance %>% filter(Experiment == "CROWD DP1")
meltR.A.fit =meltR.A(df,
        NucAcid = c("RNA", "CGCGCG"),
        Mmodel = "Homoduplex.2State",
        concT = 80,
        fitTs = c(15, 70),
        wavelength = 280,
        Silent = T)

Trimmed = BLTrimmer(meltR.A.fit,
                    Trim.method = "floating",
                    Assess.method = 3,
                    no.trim.range = c(0.15, 0.85),
                    quantile.threshold = 0.1,
                    n.ranges.float = 6,
                    range.step.float = 4,
                    n.combinations = 1000)
```

```
## [1] "You are trying to test 1000 baseline combinations"
## [1] "Do you think this is possible?"
## [1] "Fitting 1000 combinations of 6 different baselines per sample"
##    |                                                                 |
```

```
Trimmed$Ensemble.energies
```

```
##               Method     dH       CI95.dH     dS          CI95.dS    dG
## 1  1 Individual fits -56.00 -57.03 to -55.06 -154.40 -157.66 to -151.49 -8.11
## 2 2 Tm versus ln[Ct] -55.92 -57.08 to -54.85 -154.18 -157.85 to -150.87 -8.10
## 3        3 Global fit -56.74 -57.79 to -55.78 -156.53 -159.69 to -153.77 -8.19
##          CI95.dG Tm_at_0.1mM CI95.Tm_at_0.1mM
## 1 -8.15 to -8.07       51.09    50.88 to 51.23
## 2 -8.15 to -8.05       51.05    50.85 to 51.18
## 3  -8.27 to -8.1       51.39    51.01 to 51.7
```