

# 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	-55.86	-57.04 to -54.82	-153.96	-157.72 to -150.69	-8.11
## 2	2	Tm versus ln[Ct]	-55.70	-56.8 to -54.4	-153.48	-156.95 to -149.45	-8.09
## 3	3	Global fit	-56.70	-57.82 to -55.59	-156.38	-159.77 to -152.95	-8.19
##		CI95.dG	Tm_at_0.1mM	CI95.Tm_at_0.1mM			
## 1		-8.15 to -8.07	51.12	50.89 to 51.26			
## 2		-8.14 to -8.05	51.07	50.83 to 51.22			
## 3		-8.28 to -8.12	51.41	51.07 to 51.74			