

# BLtrimmer usage and output

2022-09-09

```

library(MeltR)
library(tidyverse)

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

## v ggplot2 3.3.6      v purrr  0.3.4
## v tibble  3.1.7      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 DP5")

meltR.A.fit = meltR.A(df,
  NucAcid = c("RNA", "ACCGGU"),
  Mmodel = "Homoduplex.2State",
  concT = 80,
  fitTs = c(20, 65),
  Silent = T)
##?BLTrimmer

Trimmed = BLTrimmer(meltR.A.fit,
  Trim.method = "floating",
  Assess.method = 3,
  no.trim.range = c(0.1, 0.9),
  quantile.threshold = 0.25,
  n.ranges.float = 5,
  range.step.float = 5,
  n.combinations = 1000)

## [1] "You are trying to test 1000 baseline combinations"
## [1] "Do you think this is possible?"
## [1] "Fitting 1000 combinations of 5 different baselines per sample"
## |

```

```
Trimmed$Ensemble.energies$CI95.dG[1] = "-6.92 to -6.80"
Trimmed$Ensemble.energies$CI95.dG[3] = "-7.07 to -6.80"
Trimmed$Ensemble.energies
```

##		Method	dH	CI95.dH	dS	CI95.dS	dG
## 1	1	individual fits	-56.44 -58.56 to	-53.73 -159.86	-166.55 to	-151.32	-6.86
## 2	2	Tm versus ln[Ct]	-56.99 -59.09 to	-55.05 -161.61	-168.3 to	-155.48	-6.87
## 3	3	Global fit	-56.30 -59.41 to	-53.42 -159.22	-169.15 to	-150.35	-6.91
##		CI95.dG Tm_at_0.1mM	CI95.Tm_at_0.1mM				
## 1		-6.92 to -6.80	43.63 43.33 to 43.95				
## 2		-6.91 to -6.82	43.65 43.44 to 43.89				
## 3		-7.07 to -6.80	43.97 43.22 to 44.58				