

BLtrimmer usage and output

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```
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

##		Method	dH	CI95.dH	dS	CI95.dS	dG
## 1	1	individual fits	-56.58	-58.72 to -54.43	-160.31	-167.02 to -153.41	-6.86
## 2	2	Tm versus ln[Ct]	-57.15	-59.07 to -54.97	-162.11	-168.25 to -155.2	-6.87
## 3	3	Global fit	-56.55	-60.04 to -53.53	-160.02	-171.51 to -150.57	-6.92
##		CI95.dG	Tm_at_0.1mM	CI95.Tm_at_0.1mM			
## 1		-6.92 to -6.8	43.62	43.32 to 43.91			
## 2		-6.91 to -6.82	43.64	43.43 to 43.87			
## 3		-7.08 to -6.78	43.96	43.16 to 44.58			