

# meltR.A usage and output

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```
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(df,
  NucAcid = c("RNA", "CGCGCG"),
  Mmodel = "Homoduplex.2State",
  concT = 80,
  fitTs = c(15, 70),
  wavelength = 280)

## [1] "Individual curves"
## [1] "dH and dG are in kcal/mol and dS is in cal/mol/K. Tms are in deg Celsius"
## Sample      Ct      dH      dS      dG      Tm
## 9      12 1.55e-05 -56.16 -156.83 -7.52 40.86
## 6       8 2.10e-05 -52.79 -145.06 -7.80 44.00
## 3       4 3.13e-05 -54.56 -150.10 -8.01 46.45
## 8      11 6.85e-05 -53.23 -147.90 -7.36 45.66
## 5       7 9.66e-05 -55.50 -154.06 -7.72 48.72
## 2       3 1.57e-04 -54.44 -150.32 -7.81 51.39
## 7      10 2.34e-04 -55.57 -154.58 -7.62 51.44
## 4       6 3.95e-04 -55.71 -154.16 -7.89 55.05
## 1       2 6.89e-04 -56.61 -157.03 -7.91 56.97
## [1] "Summary"
## [1] "dH and dG are in kcal/mol and dS is in cal/mol/K. Tms are in deg Celsius"
##      Method      dH SE.dH      dS SE.dS      dG SE.dG Tm_at_0.1mM
## 1 1 individual fits -54.95  1.30 -152.23  4.11 -7.74  0.21      49.09
## 2 2 Tm versus ln[Ct] -53.16  4.64 -146.69 14.42 -7.66  0.19      49.04
## 3 3 Global fit -55.38  0.17 -153.41  0.52 -7.80  0.01      49.37
## SE.Tm_at_0.1mM
## 1      3.81
## 2      0.42
## 3      0.04
## [1] "%error between methods"
##      dH      dS      dG
## 1 4.1 4.5 1.8
```