Preparation data and set up R for analysis

R is a language and environment for statistical computing and graphics. MIAMI data can be anlayzed by using R source which can be download from MIAMI site (http://grc.dept.med.gunma-u.ac.jp/~gene/indexe.html).

(1) Labeling control sample with Cy3 and case sample with Cy5.
(2) Hybridization and wash.
(3) Scan with appropriate PMT to avoid saturated spots and feature extraction using Agilent scanner (CGH setting).
(4) Install and setup R from (http://cran.r-project.org/).
(5) Download the R source file (Lm_Prot_AJ_Cmp2_NDC.R) from MIAMI site (http://grc.dept.med.gunma-u.ac.jp/~gene/indexe.html).

How to analyze Agilent scanner data with R

(1) Start R.
(2) Load source ” Lm_Prot_AJ_Cmp2_NDC.R” with file menu.
(3) Change directory to your data folder by file menu and press enter.
(4) Input the file name for Hpa II-cleavage difference and press enter.
(5) Input the file name for Msp I-cleavage difference and press enter.
(6) Input a name added to output files and press enter.
(7) After several minutes, calculation will be ended with the notification of “R process all finished.”.
(8) Output files will be made in the same folder as your data files. Following are the detail of the files.

Res: Data file of the results.
Hyper: List of hypermethylated probes when the control sample is labeled with Cy3.
Hypo: List of hypomethylated probes when the cotrol sample is labeled with Cy3.
Statics: Statics file.
UCSC: File which can be used for UCSC genome browser (http://genome.ucsc.edu/cgi-bin/hgGateway).

Definitions of terms in files

ProbeName	
GeneName	
gProcessedSignal_A	Hpa II signal of control
rProcessedSignal_A	Hpa II signal of case
gProcessedSignal_B	Msp I signal of control
rProcessedSignal_B	Msp I signal of case
Flags_A	
Flags_B	
ControlType	
ProbeUID	
SystematicName	
Description	
PValueA	Pvalue of log[(rProcessedSignal_A)/(gProcessedSignal_A)]
PValueB	Pvalue of log[(rProcessedSignal_B)/(gProcessedSignal_B)]
Cy3A	Hpa II signal of control (Normalized)
Cy5A	Hpa II signal of case (Normalized)
Cy3B	Msp I signal of control (Normalized)
Cy5B	Msp I signal of case (Normalized)
A	Cy3A/Cy5A
B	Cy3B/Cy5B
logA	
logB	
DRL	Horizontal distance from the regression line
D10	10^(DRL)
judge	judge=1(hypermethylated): D10>5, A>5, 0.5<B<2
	judge=−1(hypomethylated): D10<0.2, A<0.2, 0.5<B<2
	judge=0: If Judge is not equal to 1 or −1, then 0.