基礎生物学研究所　ゲノムインフォマティクス・トレーニングコース　2015秋

RNA-seqの解析パイプライン

RNA-seq Analysis Pipelines

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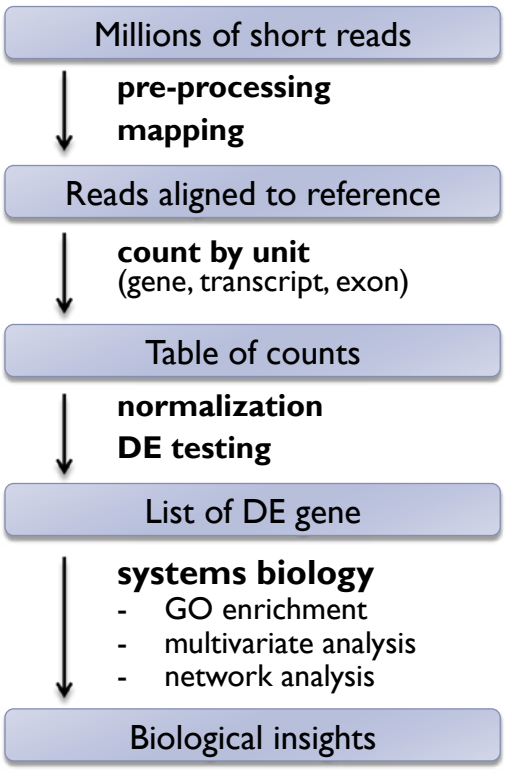
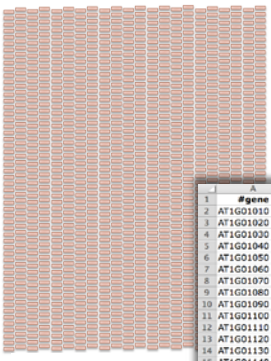
RNA-seq analysis pipeline for DE

Differential Expression analysis





NGS reads

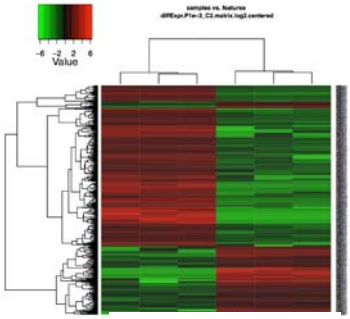
#gene	m1	m2	m3	h1	h2	h3
AT1G01010	35	77	40	46	64	60
AT1G01020	43	45	32	43	39	49
AT1G01030	16	24	26	27	35	20
AT1G01040	72	43	64	66	25	90
AT1G01050	49	78	90	67	45	60
AT1G01060	0	15	2	0	21	8
AT1G01070	16	34	6	9	20	1
AT1G01080	170	191	382	127	98	184
AT1G01090	291	346	563	171	116	453
AT1G01100	113	125	246	78	27	361
AT1G01110	0	1	1	0	0	0
AT1G01120	226	189	270	147	83	174
AT1G01130	9	11	1	0	2	0
AT1G01140	181	120	142	161	73	0
AT1G01150	0	2	0	0	0	0
AT1G01160	117	125	215	86	46	0
AT1G01170	74	57	82	36	22	0
AT1G01180	46	7	26	24	18	0
AT1G01190	0	3	2	1	2	0
AT1G01200	5	0	2	0	0	0
AT1G01210	178	203	98	205	83	0
AT1G01220	26	49	40	21	15	0
AT1G01225	4	10	6	6	0	0
AT1G01230	72	51	58	70	18	0
AT1G01240	81	89	45	62	24	0
AT1G01250	1	1	5	1	2	0
AT1G01260	15	52	37	33	27	0
AT1G01290	7	16	23	30	5	0
AT1G01300	75	115	232	89	109	0

Table of counts

gene	signal (A)	logFC (M)	p-value	FDR
AT5G48430	-9.17	6.30	3.7E-27	9.8E-23
AT2G08986	-9.15	5.04	2.8E-21	3.6E-17
AT5G31702	-9.74	5.68	5.0E-21	4.3E-17
AT1G51850	-10.07	5.32	2.2E-19	1.4E-15
AT2G39380	-9.82	4.97	2.9E-19	1.5E-15
AT2G44370	-10.23	5.48	1.1E-18	4.7E-15
AT3G46280	-8.19	4.93	1.3E-18	5.0E-15
AT3G55150	-10.44	5.86	1.8E-18	5.8E-15
AT2G19190	-8.70	4.55	8.5E-18	2.5E-14
AT1G51820	-9.40	4.40	1.3E-17	3.3E-14
AT2G39530	-9.16	4.36	1.7E-17	4.1E-14
AT1G40104	-9.58	4.61	2.2E-17	4.9E-14
AT2G30750	-9.97	4.64	1.5E-16	3.0E-13
AT2G17740	-9.12	4.18	1.8E-16	3.3E-13
AT2G07981	-10.07	4.75	1.0E-15	1.8E-12
AT1G30720	-9.21	3.91	3.5E-15	5.8E-12
AT5G31720	-9.12	3.76	1.9E-14	2.7E-11
AT1G51800	-8.47	3.99	1.9E-14	2.7E-11
AT1G30720	-9.06	3.75	4.7E-14	6.5E-11
AT4G12500	-6.58	4.39	1.5E-13	1.9E-10
AT1G07160	-10.76	5.02	2.0E-13	2.5E-10
AT2G39200	-7.57	3.98	6.0E-13	7.2E-10
AT2G10600	-9.30	3.50	8.8E-13	1.0E-09
AT1G65500	-9.60	3.50	9.6E-13	1.0E-09
AT5G39580	-9.24	3.45	1.3E-12	1.3E-09
AT5G44380	-9.51	3.45	1.7E-12	1.7E-09
AT5G13220	-7.20	3.88	2.8E-12	2.7E-09
AT2G45220	-8.45	3.54	3.9E-12	3.6E-09
AT1G30730	-9.80	3.45	6.0E-12	5.4E-09
AT1G64170	-9.91	3.39	1.2E-11	1.1E-08
AT4G20860	-8.10	3.49	1.5E-11	1.2E-08
AT4G23550	-10.08	3.49	1.5E-11	1.2E-08
AT4G12490	-6.75	3.88	1.6E-11	1.2E-08
AT5G64120	-7.09	3.76	2.1E-11	1.6E-08

List of DE genes
Table of significance score

Biological insights



Systems biology:
clustering and
network analysis

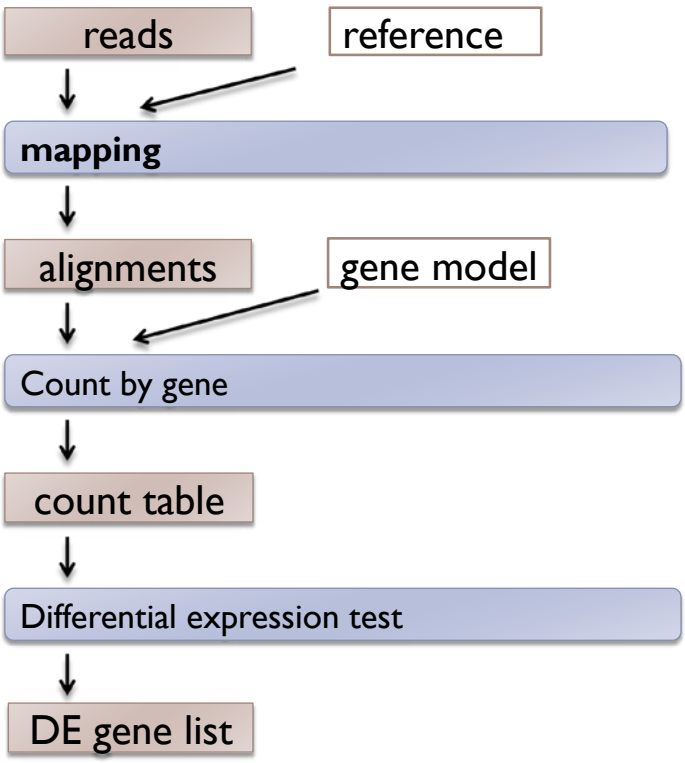
RNA-seq analysis pipeline for DE

	data type	format
Millions of short reads	sequences	fastq
pre-processing **mapping**		
Reads aligned to reference	alignment	SAM/BAM
count by unit (gene, transcript, exon)		
Table of counts	table	text (tab delimited)
normalization **DE testing**		
List of DE gene	various	various
systems biology - GO enrichment - multivariate analysis - network analysis		
Biological insights		

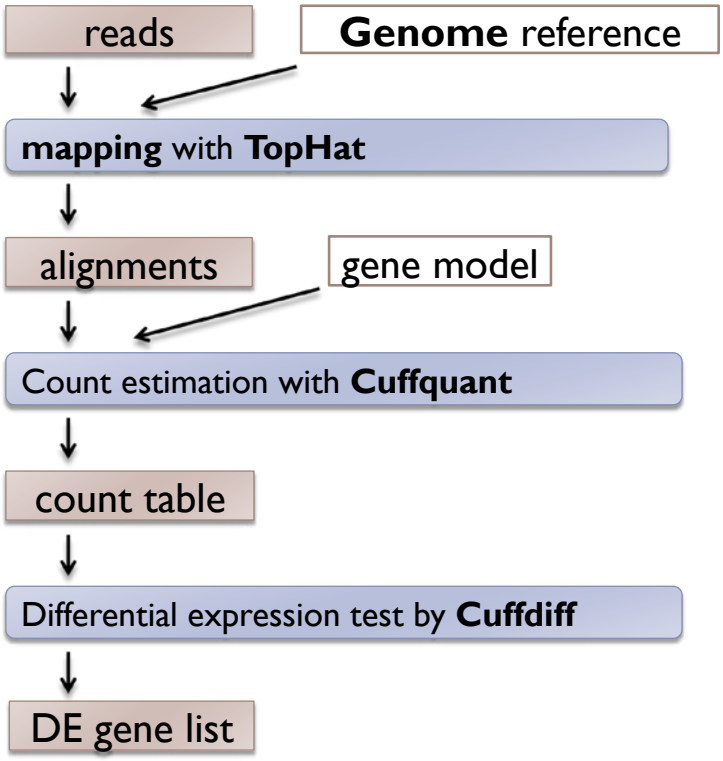
Two Basic Pipelines

- Choice of reference
  - **Genome** – standard for genome-known species
  - **Transcript** – the only way for genome-unknown species
    -- can be used for genome-known species

Common workflow



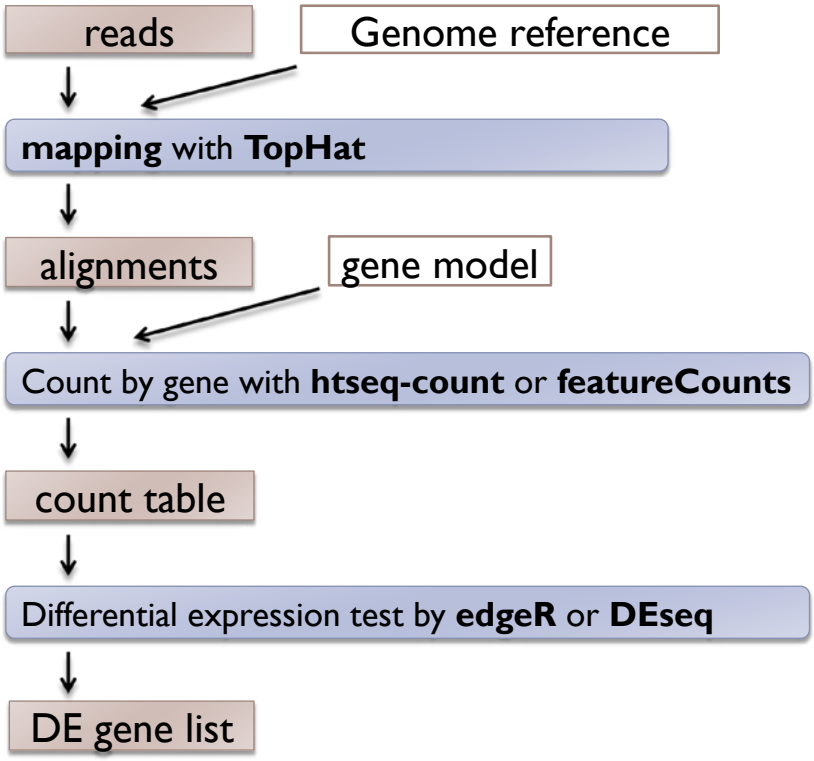
A Pipeline: Genome-based (1)



"Tuxido pipeline"

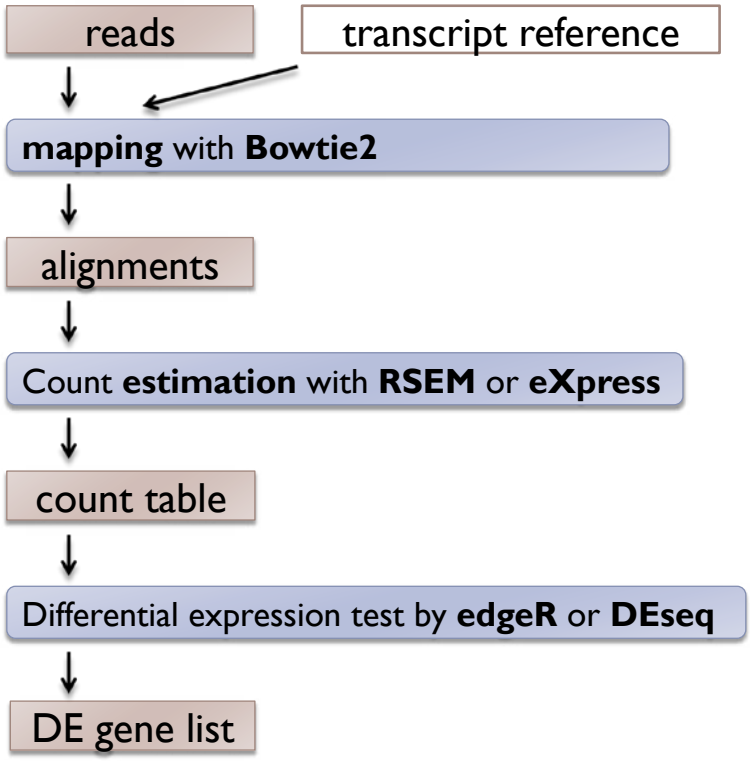
Novel gene modeling by Cufflinks is not included in this pipeline.

A Pipeline: Genome-based (2)

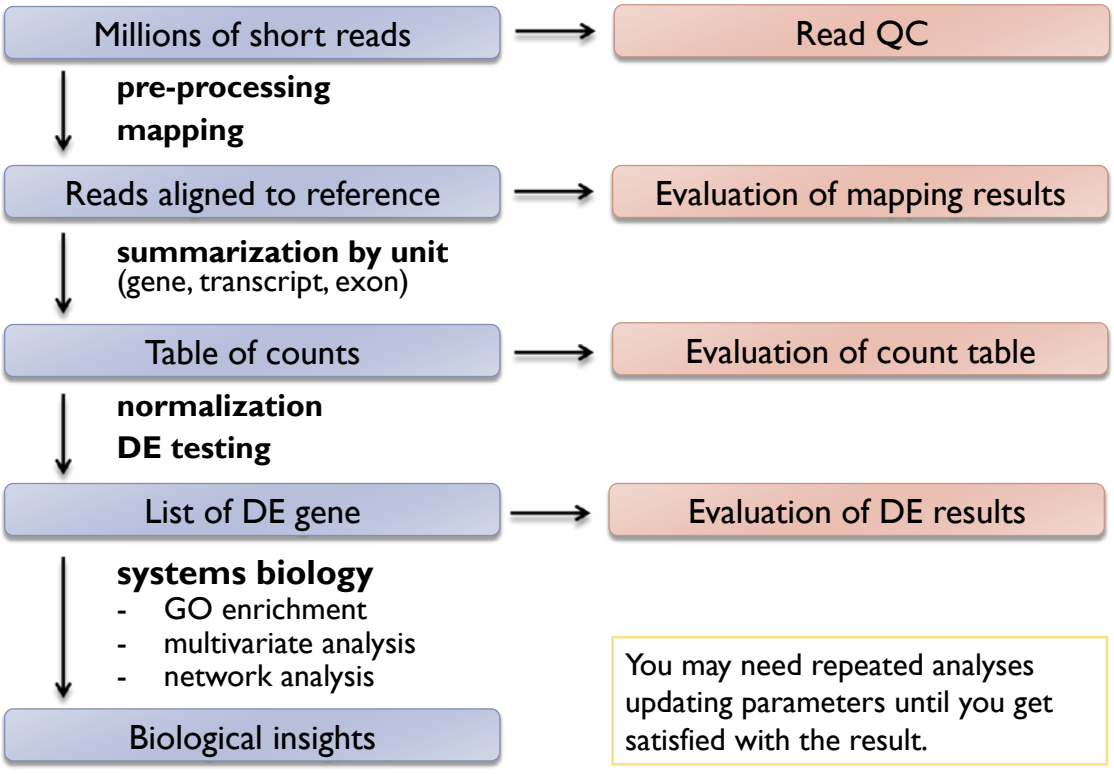


Anders S, et al. (2013) *Nat Protoc*

A Pipeline: Transcript-based

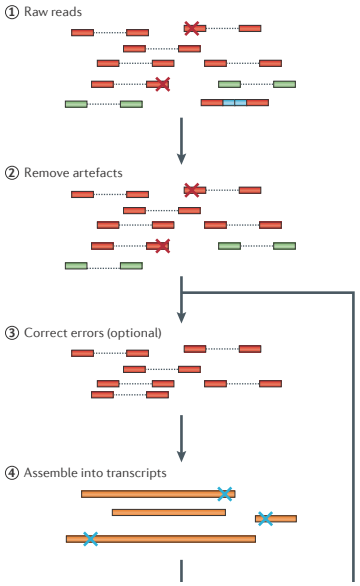


Check Points



Read QC and Pre-processing

- Read QC
  - Tools: FastQC etc.
- Pre-processing
  - Filter or trim by base quality
  - Remove artifacts
    - adaptors
    - low complexity reads
    - PCR duplications (optional)
  - Remove rRNA and other contaminations (optional)
  - Sequence error correction (optional)
  - Tools: cutadapt, trimmomatic

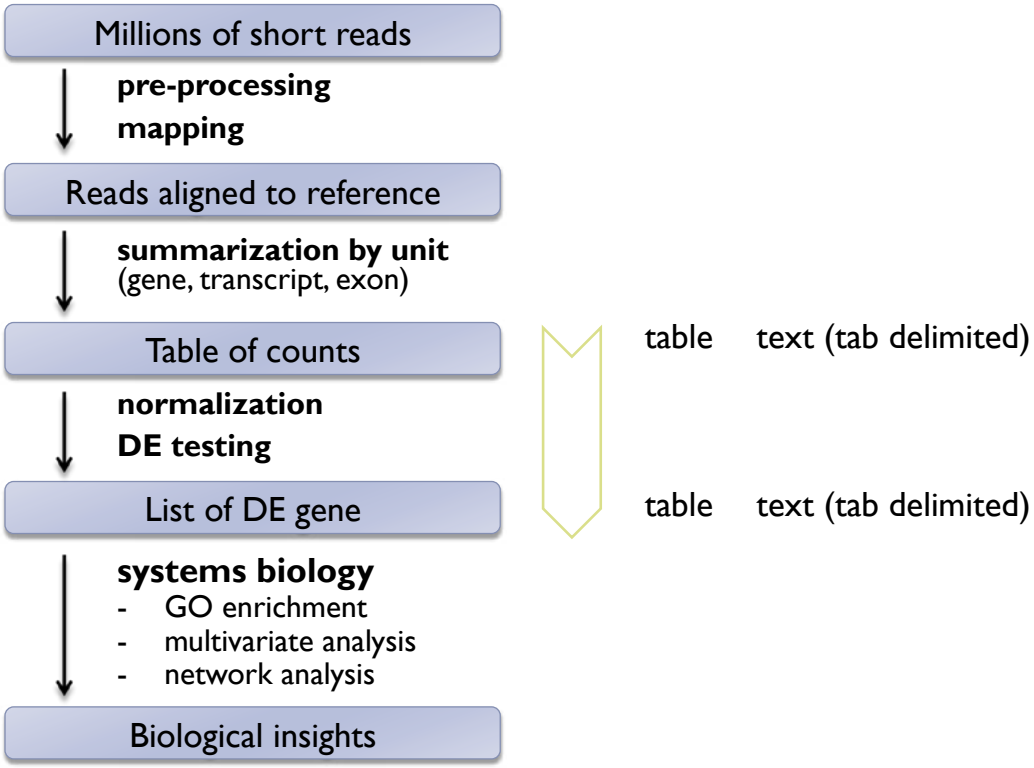


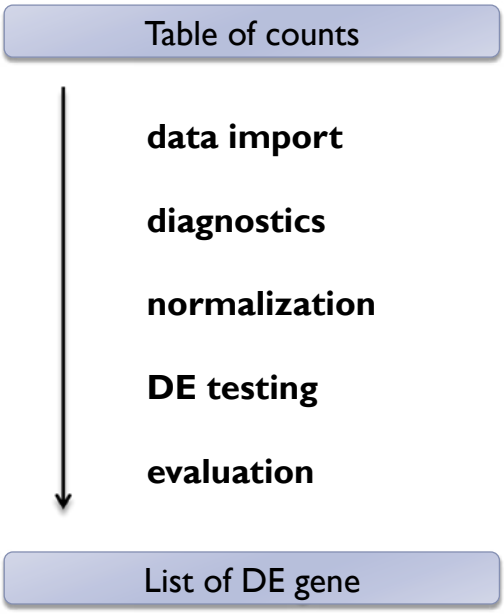
Martin et al (2011) *Nat Rev Genet*

Evaluation of mapping results

- Evaluation of SAM/BAM file
- Check statistics
- Visualization

RNA-seq analysis pipeline for DE





Import count table / diagnostics

Look into the input data first.

- Quick view of the table (tools: R, MS Excel etc.)
  - Check: Format, data structure, data size etc.
- Scatter plot (tools: R, MS Excel etc.)

Input

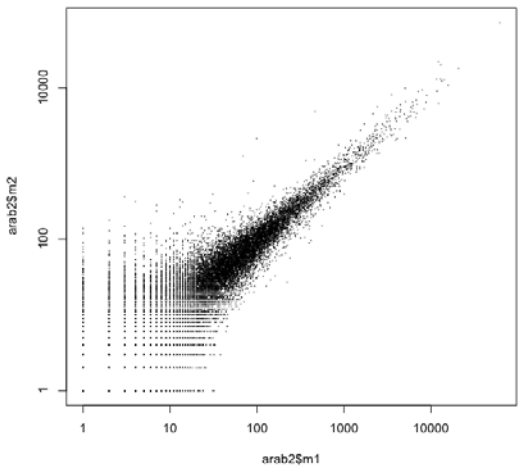
- Typical primary data = matrix of #genes x #samples

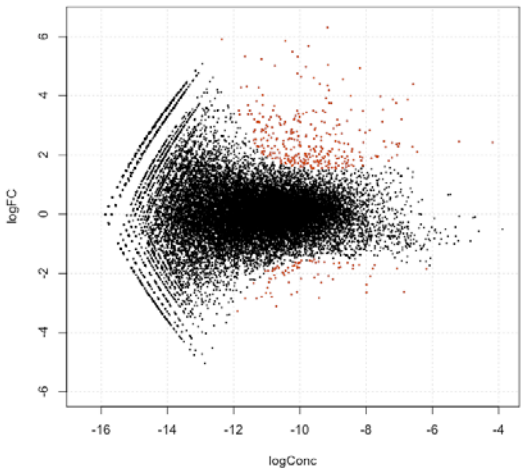
column x number of samples (libraries)

row x number of genes (probes)

	A	B	C	D	E	F	G
1	#gene	m1	m2	m3	h1	h2	h3
2	AT1G01010	35	77	40	46	64	60
3	AT1G01020	43	45	32	43	39	49
4	AT1G01030	16	24	26	27	35	20
5	AT1G01040	72	43	64	66	25	90
6	AT1G01050	49	78	90	67	45	60
7	AT1G01060	0	15	2	0	21	8
8	AT1G01070	16	34	6	9	20	1
9	AT1G01080	170	191	382	127	98	184
10	AT1G01090	291	346	563	171	116	453
11	AT1G01100	113	125	246	78	27	361
12	AT1G01110	0	1	1	0	0	0
13	AT1G01120	228	189	270	147	83	174
14	AT1G01130	9	11	1	0	2	9
15	AT1G01140	181	120	142	161	73	134
16	AT1G01150	0	2	0	0	0	0
17	AT1G01160	117	125	215	86	46	212
18	AT1G01170	74	57	82	36	22	29
19	AT1G01180	46	7	26	24	18	58
20	AT1G01190	0	3	2	1	2	2
21	AT1G01200	5	0	2	0	0	0
22	AT1G01210	178	203	98	205	83	143
23	AT1G01220	26	49	40	21	15	34
24	AT1G01225	4	10	6	6	0	3
25	AT1G01230	72	51	58	70	18	77
26	AT1G01240	81	89	45	62	24	33
27	AT1G01250	1	1	5	1	2	2
28	AT1G01260	15	52	37	33	27	54
29	AT1G01290	7	16	23	30	5	19
30	AT1G01300	75	115	232	89	109	224

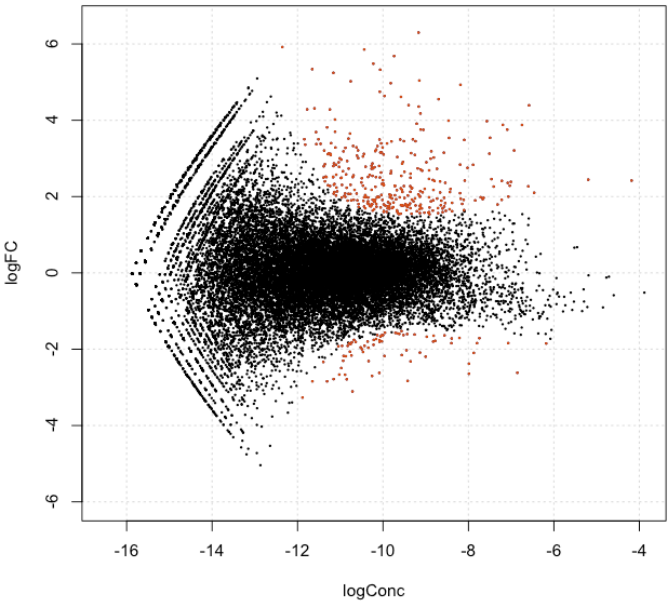
Diagnostics: Scatter plot & MA plot





MA plot

M



A

M: log fold-change
A: log intensity average

$$M = log_2(R/G) = log_2(R) - log_2(G)$$
$$A = \frac{1}{2}log_2(RG) = \frac{1}{2}(log_2(R) + log_2(G))$$

R: expression level of sample 1
G: expression level of sample 2

Let's try: data import and quick check

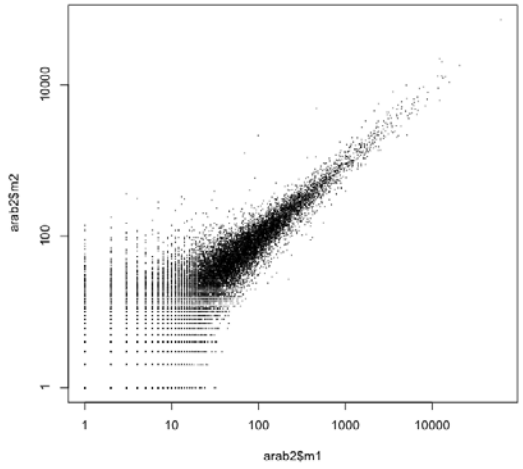
```
> dat <- read.delim("~/data/SS/arab2.txt", row.names=1)
> head(arab2)                              # look at the first several lines
          m1 m2 m3 h1 h2 h3                # for checking
AT1G01010 35 77 40 46 64 60
AT1G01020 43 45 32 43 39 49
AT1G01030 16 24 26 27 35 20
AT1G01040 72 43 64 66 25 90
AT1G01050 49 78 90 67 45 60
AT1G01060  0 15  2  0 21  8

> dim(dat)                                 # get numbers of rows and columns
[1] 26221     6

                                           # get column sums
> colSums(dat)
     m1      m2      m3      h1      h2      h3
1902032 1934029 3259705 2129854 1295304 3526579
```

Let's try: Scatter plot

```
> plot(dat$m1 + 1, arab2$m2 + 1, log="xy")
```



Scatter plot: R

```
>  pairs(dat, log="xy")
```

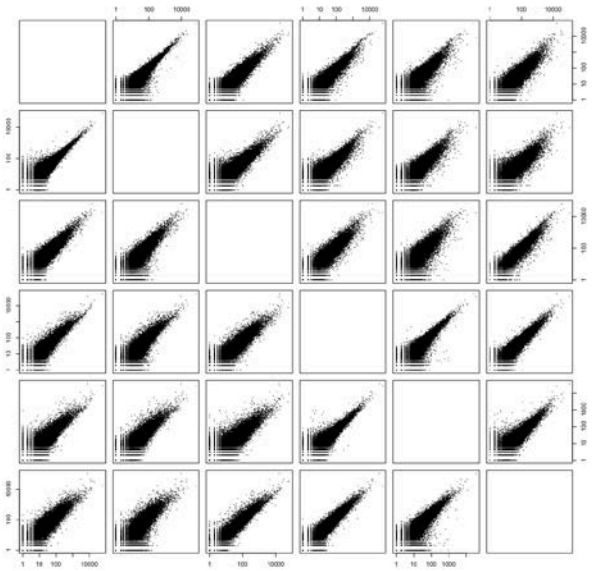


Table of counts

↓

data import

diagnostics

normalization

DE testing

evaluation

List of DE gene

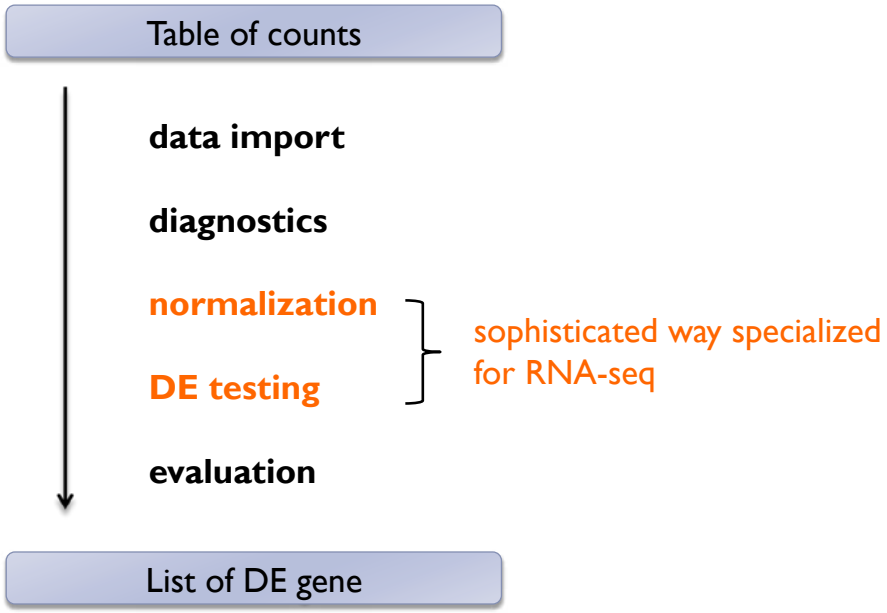
Normalization

What is normalization? Why it is required?

- Normalization means to adjust transcriptome data for effects which arise from variation in the technology rather than from biological differences between the RNA samples or between genes.
- Normalization is an essential step in the analysis of DE from RNA-seq data to make them really comparable.

Normalization: two types

- Between-libraries
  - Comparing expression (counts) of genes between libraries
- Within-library
  - Comparing expression (counts) of genes within a library (should be possible with NGS – in contrast to microarray)



DEG: RNA-seq specific issues

- RNA-seq count data is Non-Gaussian
- Normalization: composition effects
- N (biological replicates) is so small
- Multiple comparisons (多重検定の問題)

RNA-seq data is Non-Gaussian

- Microarray data
  - Log transform intensities
  - => Analyze as normally distributed random variables allowing parametric analysis
- RNA-seq data
  - Not normally distributed random variables
  - **Poisson distribution** for technical replicates
  - **Negative binomial distribution** for biological replicates.

RNA-seq issue: Normalization

- Simple normalization
  - RPM or RPKM works well, but not best
- Composition effects
  - A small number of highly expressed genes can consume a significant amount of the total sequence.
  - Strategies
    - estimate scaling factors from data and statistical models
    - quantile normalization
    - …

Implemation examples: edgeR and Cuffdiff

edgeR

- **Model**: An over dispersed Poisson model, **negative binomial (NB) model** is used
- **Normalization: TMM method** (trimmed mean of M values; Robinson et al., 2010), RLE (Anders et al., 2010) and upperquantile (Bullard et al., 2010)

Cuffdiff

- **Model**: FPKM, Geometric, quartile
- **Normalization:** Pooled (default), per-condition, blind, Poisson

(example) Cuffdiff

- Model
  - FPKM, Geometric, quartile
- Normalization
  - Pooled (default), per-condition, blind, Poisson (not recommended)

http://cufflinks.cbcb.umd.edu/manual.html#dispersion_meth

RNA-seq analysis pipeline for DE