edX

Course > Section 1: Biology b... > Introduction to Mic... > Microarray Assess...

Microarray Assessment
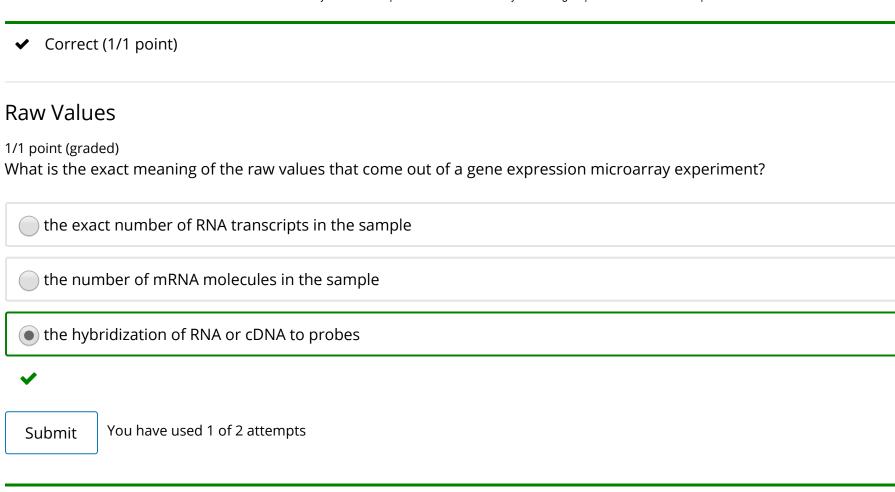## Assessment

1/1 point (graded)
Which best describes the general method of gene expression microarrays?

⊙ The microarray probes create copies of DNA through replication in a manner which is proportional to the gene expression.

⊙ The genes with the most copies in the sample hybridize to other genes with high intensities and are removed from the sample.

◉ More copies of a gene in a sample results in higher light intensity at the corresponding probe.

✔

Submit	You have used 2 of 2 attempts

✔ Correct (1/1 point)

Raw Values

1/1 point (graded)
What is the exact meaning of the raw values that come out of a gene expression microarray experiment?

◯ the exact number of RNA transcripts in the sample

◯ the number of mRNA molecules in the sample

⦿ the hybridization of RNA or cDNA to probes

✔

| Submit | You have used 1 of 2 attempts |

✔ Correct (1/1 point)

Microarray use

1/1 point (graded)
Which of the following aims of a study would benefit from the use of gene expression microarrays?

○ looking for the genetic mutation which causes a rare monogenic disorder affecting 50 patients

◉ classifying tumor samples from various patients into distinct phenotypic classes

○ finding the protein binding sites of the estrogen receptor in breast cancer cell lines

✔

Submit   You have used 2 of 2 attempts

✔ Correct (1/1 point)

Using a SummarizedExperiment

0/1 point (graded)
This code chunk constructs a SummarizedExperiment container for expression data on samples taken from different tissues. We'll learn more about this container design later on. For now, just follow the instructions below, adding packages to your installation if any are missing, using biocLite(). For example, acquire the tissuesGeneExpression package using biocLite("genomicsclass/tissuesGeneExpression") if you don't already have it.

```
library(tissuesGeneExpression)
data(tissuesGeneExpression)
library(SummarizedExperiment)
tissSE = SummarizedExperiment(list(rma=e))
colData(tissSE) = DataFrame(tab)
library(hgu133a.db)
sym = mapIds(hgu133a.db, keys=rownames(tissSE), column="SYMBOL", keytype="PROBEID")
nm = mapIds(hgu133a.db, keys=rownames(tissSE), column="GENENAME", keytype="PROBEID")
rowData(tissSE) = DataFrame(symbol=sym, genename=nm)
```

We can use

```
grep("GAPDH", rowData(tissSE)$symbol, value=TRUE)
```

to count the number of array features that measure expression of gene GAPDH.

How many features in this SummarizedExperiment measure expression of gene H2AFX?
Use the 'symbol' field of the rowData, and watch out for NA in arithmetic computations.

189   ✖ **Answer:** 4

189

Explanation
sum(rowData(tissSE)$symbol=="H2AFX", na.rm=TRUE)

Submit   You have used 5 of 5 attempts

ⓘ Answers are displayed within the problem

Comparing expression distributions

1/1 point (graded)

Verify that 205436_s_at is the affymetrix code for H2AFX and then consider the following plot:

```
par(las=2, mar=c(10,4,2,2))
boxplot(as.numeric(assay(tissSE["205436_s_at",]))~tissSE$Tissue)
```

Which of the following relationships are suggested by this plot?

○ Expression of H2AFX is greater in cerebellum than in hippocampus.

◉ Expression of H2AFX is greater in hippocampus than in cerebellum.

○ H2AFX is not expressed in brain.

○ H2AFX is not expressed in placenta.

✔

| Submit | You have used 1 of 5 attempts

✔ Correct (1/1 point)