**Annotation** is the process of giving context to your data using *external* information.

This can be done in many ways, but it usually involves linking your data to *online databases*. 
Example: annotating a probeset on the Affymetrix HGU95av2 microarray.

Affymetrix identifier 39730_at

ENTREZ identifier 25

Affymetrix identifier 1635_at
Example: annotating a genomic interval.

Genome coordinates
chr7:27,136,000-27,137,000
Some annotation is just experimental data from other groups.
How to annotate 100-10,000 items? Need to do this programmatically. And easily!
Two main approaches in Bioconductor:

**Annotation packages**: (ex. hgu95av2.db) This is “preprocessed” and “packaged” annotation.

**Query online resources**: like UCSC or ENSEMBL.