Next-generation sequencing (NGS), also known as high-throughput sequencing, is the catch-all term used to describe a number of different modern sequencing technologies including:

* Illumina (Solexa) sequencing
* Roche 454 sequencing
* Ion torrent: Proton / PGM sequencing
* SOLiD sequencing

These recent technologies allow us to sequence DNA and RNA much more quickly and cheaply than the previously used Sanger sequencing, and as such have revolutionised the study of genomics and molecular biology.

ep·i·ge·net·ics

the study of changes in organisms caused by modification of gene expression rather than alteration of the genetic code itself.

DNA methylation/ Histone modification

A **histone modification** is a covalent post-translational modification (PTM) to histone proteins which includes [**methylation**](http://www.whatisepigenetics.com/glossary/methylation/), [**phosphorylation**](http://www.whatisepigenetics.com/glossary/phosphorylation/), [**acetylation**](http://www.whatisepigenetics.com/glossary/acetylation/), ubiquitylation, and sumoylation.

Conversion rate=number of goal achieved/number of visitors

**Nonparametric** tests are also called distribution-free tests because they don't assume that your data follow a specific distribution. You may have heard that you should use **nonparametric** tests when your data don't meet the assumptions of the **parametric** test, especially the assumption about normally distributed data.

Describe standard deviation to a five year old.

Standard deviation measures the spread of things. Larger standard deviation means that things are more spread away. For example, standard deviation for 1 and 9 is larger than the standard deviation for 1 and 2 since 1 and 9 are further apart.

Mean measures the average of a group of number. Let’s say we have a group of number 1 to 5, the mean can be calculated by two steps. First we have to sum our numbers ,which results in 15. The second step requires us to divide this sum by the total number of our observations. We have 5 number in this case, so 15 has to be divided by 5, which gives us 3 for the mean.

Median is the middle number if you arrange all the number you have in order. For example if we have 5,2 and 3. We have to place these 3 numbers in order first, which are 2,3 and 5. So in this case the median is the middle number 3. If we have 5,2,3 and 4. We still arrange them first in order, which are 2,3,4,5. In this case the middle numbers are 3 and 4. So we have to take a average between 3 and 4 find the median

Mode is the number that occurs most frequently. For example, if we have 1,1,2,2,3,3,3. The mode is 3 since it occurs three times while 1 and 2 only occurs 2 times.

What is a p-value?

P value normally returns a probability. It is built under a hypothesis test. Lets say we want to test if the expression of certain gene would differ among cancer patient and control. SO our null hupothesis would be that this different is 0, therefore there is no difference at all under null hupothesos. In this case the p value is the probability of seeing the alternative hypothesis among gene expression level given the null hypothesis is true. If p value is really small, this means the null hypothesis may occur mostly by chance. Therefore, the majority of our data would not have the same value as the null.