FirePat stages for processing

FirePat processor requires two expression datasets.

Expression datasets:

a data matrix containing:

\* expression levels for each entry (sRNA/loci/gene) from a set of samples.

\* Initialises the expression levels to 1.0 and assumes client will calculate

\* these later, or otherwise not interested in them.

Workbench contains the expression matrix code already. This can be found in the package: uk.ac.uea.cmp.srnaworkbench.data.correlation

FirePat Processing happens within the FirePat class found in the package:

uk.ac.uea.cmp.srnaworkbench.tools.firepat

Processing stages run as follows (text in black is already completed code):

1. Build differential expression parameters.
2. Run differential expression calculator on both input sets
3. Build expression correlation parameters
4. Run expression correlation algorithm on differential expression sets
5. Split: need to generate correlation data suitable for clustering from CorrelationList resEC. Talk with Irina
6. Build correlated pair clustering parameters object
7. Fill in the missing params. Some extra params required for final output (see code in uk.ac.uea.cmp.srnaworkbench.tools.cpc) talk with Irina
8. Perform heirachical clustering and then kmeans clustering.
9. log ratios: Talk with Irina
10. Create fancy output. Workbench already has skeleton code for a Version 3 style interface. This could be easily replaced with a Version 4 interface (see developer guide)