R library for Bayesian Network Testing (BNT)

The files:

ProcessDataScript.txt
GeneSetAnalysisScript.txt
GSEA_BN_LIB.txt
MST_LIB.txt

contain R source code which can be used to run the algorithms described in the manuscript "A Hypothesis Test for Equality of Bayesian Network Models" (Almudevar 2009). The data used was obtained from the website www.broad.mit.edu/gsea, and is described in *Subramanian et al (2005) Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles, PNAS, 102, 15545-15550* and *Subramanian et al (2007) GSEA-P: a desktop application for Gene Set Enrichment Analysis, Bioinformatics, 23, 3251-3253.*

The files **GSEA_BN_LIB.txt** and **MST_LIB.txt** contain subroutines, and can be read into the R environment using commands:

```
source("GSEA_BN_LIB.txt")
source("MST_LIB.txt")
```

The file **ProcessDataScript.txt** contains script which may be used to convert data downloaded from www.broad.mit.edu/gsea into R objects which may be used by the BNT algorithms. Refer to that file for more documentation.

The file **GeneSetAnalysisScript.txt** contains script used to set up, run and summarize the BNT algorithms. Data object formats are defined, and further documentation is provided in that file.