

FIG. 1: Comparison of the analytical results with resampling simulations. Expected number of false discoveries calculated in this work (solid line) and estimated by resampling runs (dotted lines) of 100 random test sets of size 10, 100 and 500 taken from all annotated genes of the Affymetrix HG-133A chip as a reference set.

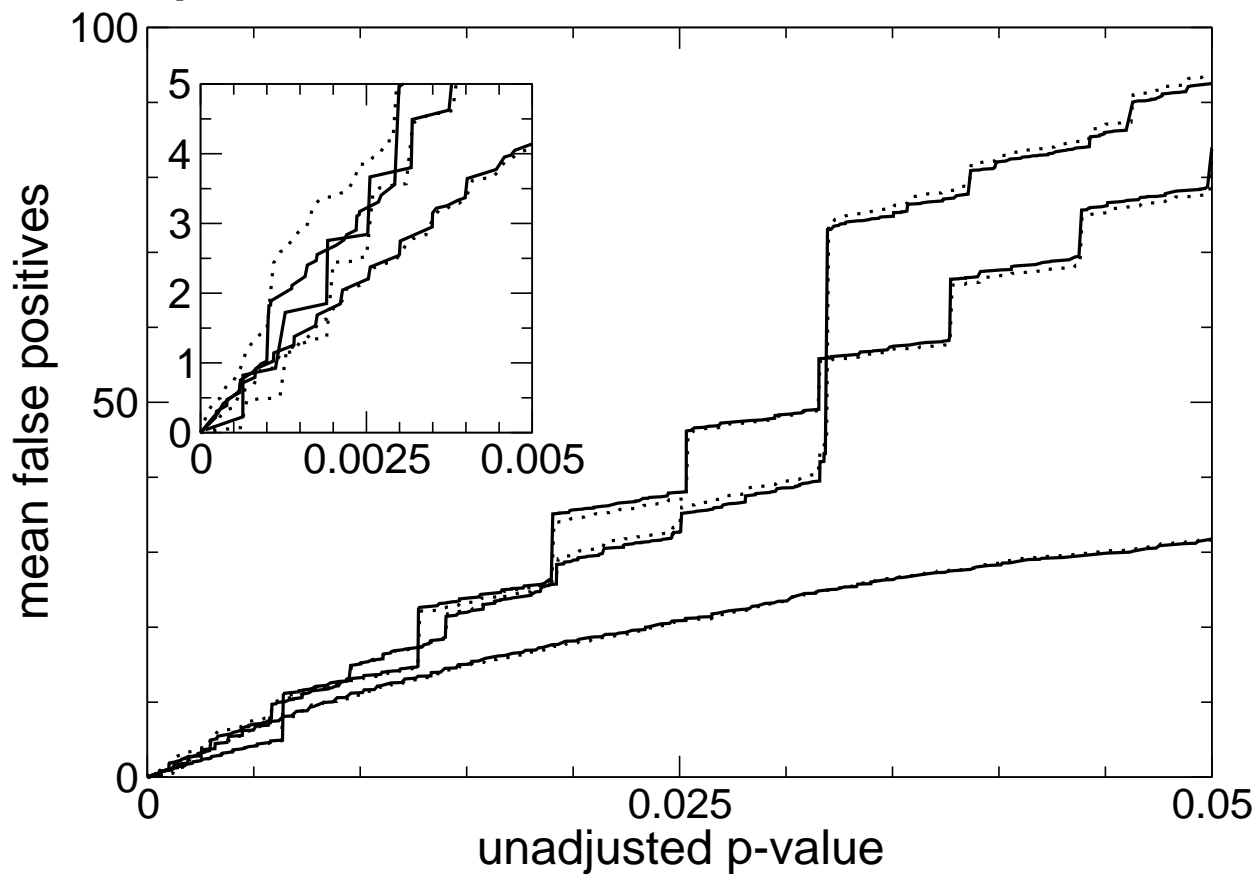


TABLE I: Significantly enriched terms ($FDR \leq 0.05$) of the five clusters G1/S, S, G2, G2/M, and M/G1 that are unspecific with respect to the categorization by the cell cycle categorizations gap phases, replication, and mitosis.

| ID | GO term | adjusted p-values to control FDR for the groups according to Whitfield et al. | | | | |
|--------------|--|--|---------------------|---------------------|---------------------|-------|
| | | G1/S | S | G2 | G2/M | M/G1 |
| 75 | cell cycle checkpoint | | | $5.8 \cdot 10^{-3}$ | | |
| 9719 | response to endogenous stimulus | 0.012 | $5.9 \cdot 10^{-3}$ | | | |
| 6275 | regulation of DNA replication | $1 \cdot 10^{-4}$ | | | | |
| 74 | regulation of cell cycle | 0.02 | | $3.4 \cdot 10^{-6}$ | $7.9 \cdot 10^{-5}$ | |
| 16728 | oxidoreductase activity, acting on CH2 groups, disulfide as acceptor | | $7.9 \cdot 10^{-3}$ | | | |
| 16725 | oxidoreductase activity, acting on CH2 groups | | $7.9 \cdot 10^{-3}$ | | | |
| 5634 | nucleus | $8.8 \cdot 10^{-5}$ | | $7.4 \cdot 10^{-5}$ | 0.039 | |
| 6139 | nucleobase, nucleoside, nucleotide and nucleic acid metabolism | $6.3 \cdot 10^{-5}$ | $8.4 \cdot 10^{-4}$ | | | |
| 278 | mitotic cell cycle | $1.2 \cdot 10^{-7}$ | $2.2 \cdot 10^{-4}$ | $9.5 \cdot 10^{-9}$ | $6.5 \cdot 10^{-7}$ | |
| 5622 | intracellular | | | $2.4 \cdot 10^{-3}$ | | |
| 67 | DNA replication and chromosome cycle | $1.2 \cdot 10^{-7}$ | $4.9 \cdot 10^{-6}$ | $2.8 \cdot 10^{-3}$ | | |
| 6259 | DNA metabolism | $2.9 \cdot 10^{-7}$ | $5.2 \cdot 10^{-8}$ | | | |
| 8301 | DNA bending activity | | | | 0.028 | |
| 9262 | deoxyribonucleotide metabolism | | $8.4 \cdot 10^{-4}$ | | | |
| 5694 | chromosome | | $2.7 \cdot 10^{-4}$ | $3.5 \cdot 10^{-4}$ | | |
| 9987 | cellular process | | | 0.028 | 0.029 | |
| 8283 | cell proliferation | $7.5 \cdot 10^{-4}$ | 0.012 | $1.9 \cdot 10^{-7}$ | $8.5 \cdot 10^{-5}$ | |
| 8151 | cell growth and/or maintenance | | | $2.9 \cdot 10^{-3}$ | | |
| 7049 | cell cycle | $6 \cdot 10^{-5}$ | $2.7 \cdot 10^{-4}$ | $9.5 \cdot 10^{-9}$ | $2.4 \cdot 10^{-6}$ | |
| 8122 | amine oxidase (copper-containing) activity | | | | | 0.032 |
| 3677 | DNA binding | 0.02 | $4.2 \cdot 10^{-4}$ | | | |
| 42267 | natural killer cell mediated cytolysis | | | 0.011 | | |
| 3683 | lamin/chromatin binding | | | 0.011 | | |
| 7089 | start control point of mitotic cell cycle | | | 0.02 | | |
| 16043 | cell organization and biogenesis | | | 0.02 | | |
| 785 | chromatin | | | 0.025 | | |
| 6996 | organelle organization and biogenesis | | | 0.025 | | |
| 5521 | lamin binding | | | 0.027 | | |
| 7050 | cell cycle arrest | | | 0.032 | | |
| 4861 | cyclin-dependent protein kinase inhibitor activity | | | 0.034 | | |
| 5099 | Ras GTPase activator activity | | | 0.034 | | |
| 786 | nucleosome | | 0.0059 | 0.04 | | |
| 17076 | purine nucleotide binding | | | 0.042 | | |
| 7028 | cytoplasm organization and biogenesis | | | 0.042 | | |
| 166 | nucleotide binding | | | 0.046 | | |
| 6334 | nucleosome assembly | | | $9.1 \cdot 10^{-3}$ | | |
| 9186 | deoxyribonucleoside diphosphate metabolism | | 0.011 | | | |
| 6545 | glycine biosynthesis | | 0.014 | | | |
| 4146 | dihydrofolate reductase activity | | 0.014 | | | |
| 9132 | nucleoside diphosphate metabolism | | 0.019 | | | |
| 3676 | nucleic acid binding | | 0.023 | | | |
| 6544 | glycine metabolism | | 0.037 | | | |
| 9117 | nucleotide metabolism | | 0.037 | | | |
| 5524 | ATP binding | | 0.042 | | | |
| 42623 | ATPase activity, coupled | | 0.043 | | | |
| 3684 | damaged DNA binding | | 0.044 | | | |
| 30554 | adenyl nucleotide binding | | 0.044 | | | |
| 8094 | DNA dependent ATPase activity | 0.031 | | | | |