

A classification of tasks for the systematic study of immune response using functional genomics data

Supplemental data file 1 – Classification of relevant information

C HEDELER^{1,2*}, N. W. PATON¹, J. M. BEHNKE³, J. E. BRADLEY³, M. G. HAMSHERE³, K. J. ELSE²

¹*School of Computer Science, The University of Manchester, Oxford Road, Manchester, M13 9PL, UK*

²*Faculty of Life Sciences, Michael Smith Building, University of Manchester, Oxford Road, Manchester, M13 9PT, UK*

³*School of Biology, Nottingham University, Nottingham, NG7 2RD, UK*

Email: C Hedeler - chedeler@cs.manchester.ac.uk;

*Corresponding author

1 Classification of relevant information

1.1 Genome

IID	Data	Data sources	Reference
G-SEQ	Sequence		
G-SEQ-DNA	DNA sequence	ENSEMBL	(Hubbard <i>et al.</i> , 2002)
G-SEQ-PP	Protein sequence	ENSEMBL	
G-SEQ-TRANS	Transcripts (alternative)	ENSEMBL	
G-SEQ-EXON	Exons, Introns	ENSEMBL	
G-SEQ-FEAT	Feature (UTR)	ENSEMBL	
G-SEQ-EST	EST		

Table 1. Genome data - Sequence

IID	Data	Data sources	Reference
G-LOC	Location		
G-LOC-CHR	Chromosomal location	ENSEMBL, MGD	(Blake <i>et al.</i> , 2003)
G-LOC-MARK	Marker	ENSEMBL, MGD, uniSTS	http://www.ncbi.nlm.nih.gov/entrez/
G-LOC-BP	bp position	ENSEMBL	
G-LOC-CM	cM position	MGD	

Table 2. Genome data - Location

IID	Data	Data sources	Reference
G-STR	Strain		
G-STR-SNP	SNP	ENSEMBL, dbSNP	(Wheeler <i>et al.</i> , 2003)
G-STR-HAP	Haplotype		(Wade <i>et al.</i> , 2002)
G-STR-PHENO	Phenotype classification	MGD	
G-STR-ALL	Alleles	MGD	

Table 3. Genome data - Strain

IID	Data	Data sources	Reference
G-FA	Functional annotation		
G-FA-GO	<i>Gene Ontology Annotation</i>	Gene Ontology Consortium, MGD	(The Gene Ontology Consortium, 2000)
G-FA-GO-MF	Molecular Function	GO, MGD	
G-FA-GO-BP	Biological Process	GO, MGD	
G-FA-GO-CC	Cellular Component	GO, MGD	
G-FA-GO-HS	Hierarchical structure	GO	
G-FA-GO-SS	Semantic similarity		(Lord <i>et al.</i> , 2003)
G-FA-SPKW	<i>SwissProt Keywords</i>	SwissProt	(Boeckmann <i>et al.</i> , 2003)
G-FA-EC	<i>Enzyme numbers</i>	LIGAND	(Kanehisa <i>et al.</i> , 2002)
G-FA-EC-HS	Hierarchical structure	LIGAND	
G-FA-PF	<i>Protein families</i>		
G-FA-PF-ENS	Ensembl protein family	ENSEMBL	
G-FA-PF-IP	InterPro	InterPro	(Mulder <i>et al.</i> , 2003)
G-FA-PF-PRO	Prosite	Prosite	(Hulo <i>et al.</i> , 2004)
G-FA-PF-PFAM	PFAM	PFAM	(Bateman <i>et al.</i> , 2002)
G-FA-PF-PRI	PRINTS	PRINTS	(Attwood <i>et al.</i> , 2003)
G-FA-PF-SM	Smart	Smart	(Letunic <i>et al.</i> , 2002)
G-FA-PF-TIGR	TIGRFAMs	TIGRFAMs	http://www.tigr.org/TIGRFAMs/
G-FA-PF-PIR	PIR	PIR	(Wu <i>et al.</i> , 2003)
G-FA-RIF	<i>GeneRIF: Gene References into Function</i>	LocusLink	http://www.ncbi.nlm.nih.gov/LocusLink/

Table 4. Genome data - Functional annotation

IID	Data	Data sources	Reference
G-SC	Species comparison		
G-SC-HM	Homology matches	ENSEMBL	

Table 5. Genome data - Species comparison

1.2 Transcriptome

IID	Data	Data sources	Reference
T-MD	Microarray description	SMD, GEO	(Gollub <i>et al.</i> , 2003), (Wheeler <i>et al.</i> , 2003)
T-MD-GL	Gene list		
T-MD-MT	Microarray type (Affy, glass)		
T-MD-ST	Spot type (cDNA, oligo)		
T-ECOND	Experimental condition Strain, tissue, timepoint, treatment, infection with pathogen, growth condition	SMD, GEO	
T-R	Result	SMD, GEO	
T-R-EL	Expression levels		
T-R-TC	Timecourse		

Table 6. Transcriptome data

1.3 Proteome

IID	Data	Data sources	Reference
P-ECOND	Experimental condition Strain, tissue, timepoint, treatment, infection with pathogen, growth condition	SWISS-2DPAGE	http://us.expasy.org/ch2d/
P-R	Result	SWISS-2DPAGE	
M-R-P	Protein list	SWISS-2DPAGE	

Table 7. Metabolome data

1.4 Metabolome

IID	Data	Data sources	Reference
M-MP	Metabolic pathways		
M-MP-CP	classification of pathways		
M-MP-LG	list of genes	KEGG	(Kanehisa <i>et al.</i> , 2002)
M-MP-OG	order of genes	KEGG	

Table 8. Metabolome data

1.5 Interactome

IID	Data	Data sources	Reference
I-UT	Used technique		
I-PPI	Observed protein-protein interaction		
I-COMPL	Observed complexes		

Table 9. Interactome data

1.6 Control

IID	Data	Data sources	Reference
C-CMRP	Cellular, molecular, regulatory pathways	BioCarta, KEGG	http://www.biocarta.com/
C-CMRP-CP	classification of pathways	BioCarta, KEGG	
C-CMRP-LP	list of proteins	BioCarta	
C-CMRP-OP	order of proteins	BioCarta	
C-CMRP-RP	interaction of proteins	BioCarta	

Table 10. Control data

References

- Attwood, T., Bradley, P., Flower, D., Gaulton, A., Maudling, N., Mitchell, A., Moulton, G., Nordle, A., Paine, K., Taylor, P., Uddin, A., and Zygouri, C. (2003). PRINTS and its automatic supplement, prePRINTS. *Nucleic Acids Research*, **31**, 400–402.
- Bateman, A., Birney, E., Cerruti, L., Durbin, R., Etwiler, L., Eddy, S., Griffiths-Jones, S., Howe, K., Marshall, M., and Sonnhammer, E. (2002). The Pfam Protein Families Database. *Nucleic Acids Research*, **30**, 276–280.
- Blake, J. A., Richardson, J., Bult, C., Kadin, J., Eppig, J., et al. (2003). MGD: The Mouse Genome Database. *Nucleic Acids Research*, **31**, 193–195.
- Boeckmann, B., Bairoch, A., Apweiler, R., Blatter, M., Estreicher, A., Gasteiger, E., Martin, M., Michoud, K., O'Donovan, C., Phan, I., Pilbouth, S., and Schneider, M. (2003). The SWISS-PROT protein knowledgebase and its supplement TrEMBL in 2003. *Nucleic Acids Research*, **31**, 365–370.
- Gollub, J., Ball, C. A., Binkley, G., Demeter, J., Finkelstein, D. B., Hebert, J. M., Hernandez-Boussard, T., Jin, H., Kaloper, M., Matese, J. C., et al. (2003). The Stanford Microarray Database: data access and quality assessment tools. *Nucleic Acids Research*, **31**, 94–96.
- Hubbard, T., Barker, D., Birney, E., Cameron, G., Chen, Y., Clark, L., Cox, T., Cuff, J., Curwen, V., Down, T., et al. (2002). The Ensembl genome database project. *Nucleic Acids Research, 2002*, **30**, 38–41.
- Hulo, N., Sigrist, C., Le Sauz, V., Langendijk-Genevaux, P., Bordoli, L., Gattiker, A., De Castro, E., Bucher, P., and Bairoch, A. (2004). Recent improvements to the PROSITE database. *Nucleic Acids Research*, **32**, D134–D137.
- Kanehisa, M., Goto, S., Kawashima, S., and Nakaya, A. (2002). The KEGG databases at GenomeNet. *Nucleic Acids Research*, **30**, 42–46.
- Letunic, I., Goodstadt, L., Dickens, N., Doerks, T., Schultz, J., Mott, R., Ciccarelli, F., Copley, R., Ponting, C., and Bork, P. (2002). Recent improvements to the SMART domain-based sequence annotation resource. *Nucleic Acids Research*, **1** (242–244).
- Lord, P. W., Stevens, R. D., Brass, A., and Goble, C. A. (2003). Investigating semantic similarity measures across the Gene Ontology: the relationship between sequence and annotation. *Bioinformatics*, **19**, 1275–1283.
- Mulder, N., Apweiler, R., Attwood, T., Bairoch, A., Barrell, D., Bateman, A., Binns, D., Biswas, M., Bradley, P., Bork, P., et al. (2003). The InterPro Database, 2003 brings increased coverage and new features. *Nucleic Acids Research*, **31**, 315–318.
- The Gene Ontology Consortium (2000). Gene Ontology: tool for the unification of biology. *Nature Genetics*, **25**, 25–29.
- Wade, C. M., III, E. J. K., Kirby, A. W., Zody, M. C., Mullikin, J. C., Lander, E. S., Lindblad-Toh, K., and Daly, M. J. (2002). The mosaic structure of variation in the laboratory mouse genome. *Nature*, **420**, 574–578.
- Wheeler, D. L., Church, D. M., Federhen, S., Lash, A. E., Madden, T. L., Pontius, J. U., Schuler, G. D., Schriml, L. M., Sequeira, E., Tatusova, T. A., and Wagner, L. (2003). Database resources of the National Center for Biotechnology. *Nucleic Acids Research*, **31**, 28–33.
- Wu, C. H., Yeh, L.-S. L., Huang, H., Arminski, L., Castro-Alvear, J., Chen, Y., Hu, Z.-Z., Ledley, R. S., Kourtesis, P., Suzek, B. E., Vinayaka, C. R., Zhang, J., and Barker, W. C. (2003). The Protein Information Resource. *Nucleic Acids Research*, **31**, 345–347.