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Some Prote Sprinzak	ein Interacti (et al., <i>JMB</i> , 327:91	on Data S 9-923, 2003	Set vir Antional University of Singapore
Experimental method category ^a	Number of interacting pair	s Co-localization ^b (%)	Co-cellular-role ^b (%)
All: All methods A: Small scale Y2H A0: GY2H Uetz <i>et al.</i> (published results) A1: GY2H Uetz <i>et al.</i> (unpublished results) A2: GY2H Ito <i>et al.</i> (core) A3: GY2H Ito <i>et al.</i> (all) B: Physical methods C: Genetic methods D1: Biochemical, <i>in vitro</i> D2: Biochemical, chromatography E1: Immunological, direct E2: Immunological, indirect 2M: Two different methods 3M: Three different methods	9347 1861 956 516 798 3655 71 1052 614 648 1025 34 2360 1212 570	$\begin{array}{c} 64\\ 73\\ 66\\ 53\\ 64\\ 41\\ 98\\ 77\\ 87\\ 93\\ 90\\ 100\\ 87\\ 92\\ 95\\ \end{array}$	49 62 45 33 40 15 95 75 79 88 90 93 85 94 93
and four units of interious	Large	disagreemen	t betw methods
 GY2H: genome-sca 2M, 3M, 4M: interse 	ale Y2H ection of 2, 3, 4 m	ethods	
nvited talk at Bioinformatica Indica 200)8	Copyrig	ght 2008 © Limsoon Wong



А	re We There Ye	et?
	Coverage	Data quality
DNA genome sequence	99% of genome sequence	99.9% correct
mRNA profiling	80-90% of transcripts represented	90% of spots are good data
Protein interaction data	10-30% of interactions catalogued	50-70% of interactions are spurious
		Slide credit: See-Kiong Ng























A New Interaction Generality Saito et al., *Bioinformatics*, 19:756--763, 2003

The improved interaction generality measure $ig_2^{\mathcal{G}}(X \leftrightarrow Y)$ is defined as a weighted sum of the 5 local topological configurations $\tau_1, ..., \tau_5$ as

$$ig_2^{\mathcal{G}}(X \leftrightarrow Y) = \sum_{i=1}^5 \lambda_i * |\{X' \mid X' \leftrightarrow Y' \in \mathcal{G}, \ Y' \in \{X,Y\}, \ \tau_i^{\mathcal{G}}(X',X \leftrightarrow Y)\}|$$

where λ_i is the weight for configuration τ_i , and $\tau_i^{\mathcal{G}}(X^i, X \leftrightarrow Y)$ means X^i is in configuration τ_i in graph \mathcal{G} wrt $X \leftrightarrow Y$.

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