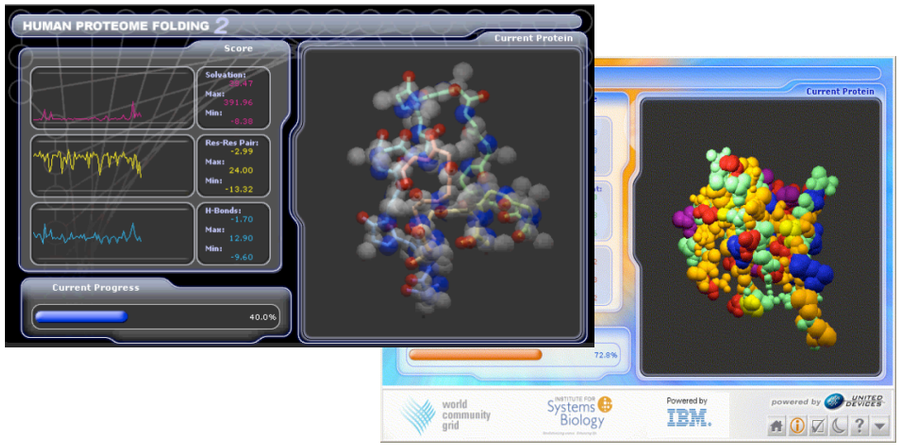
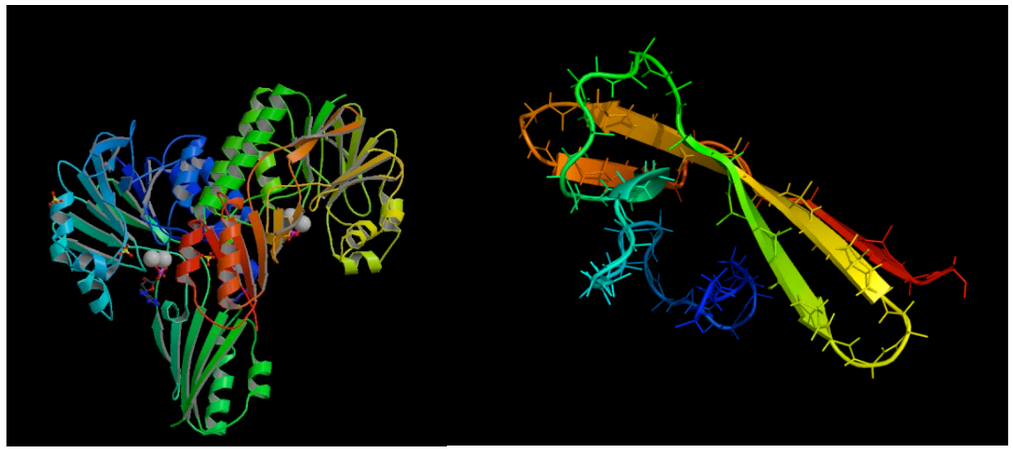
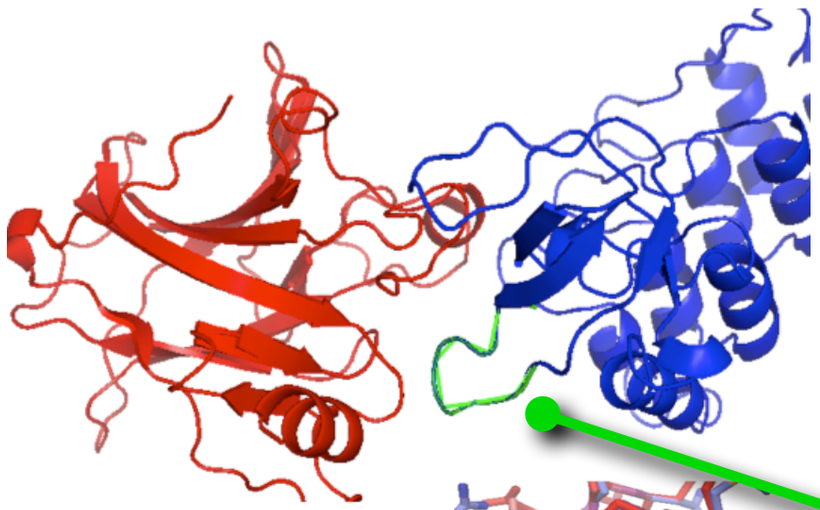
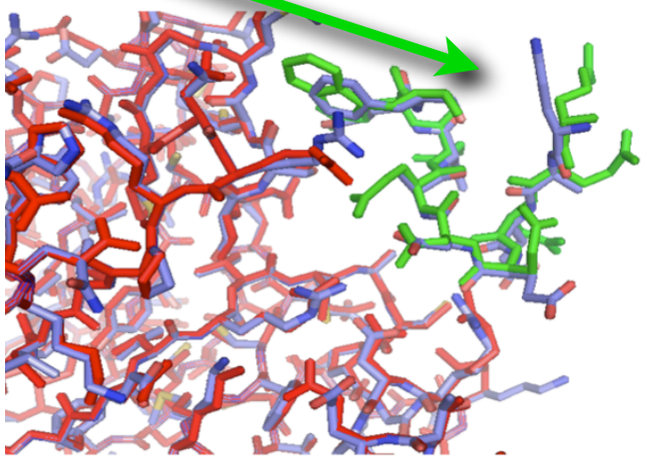
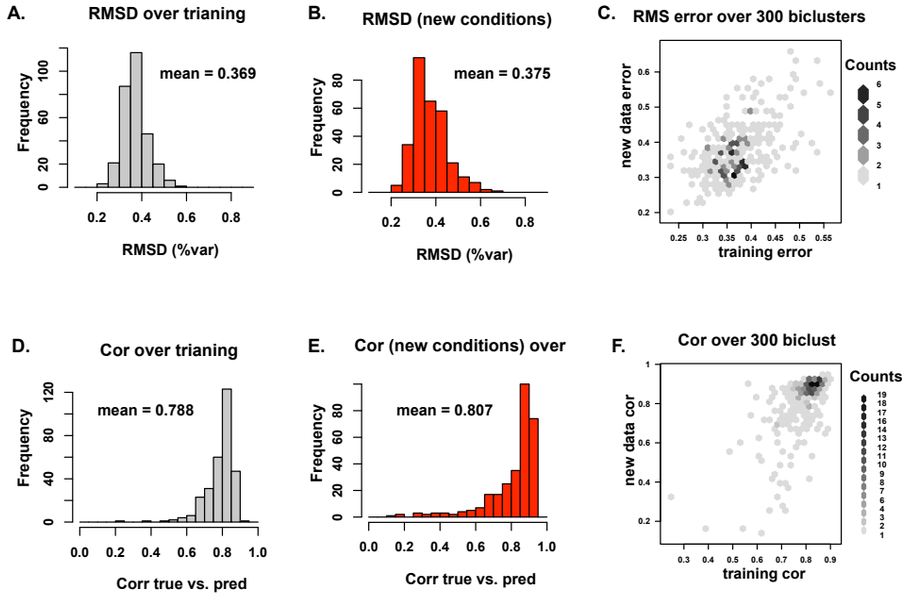
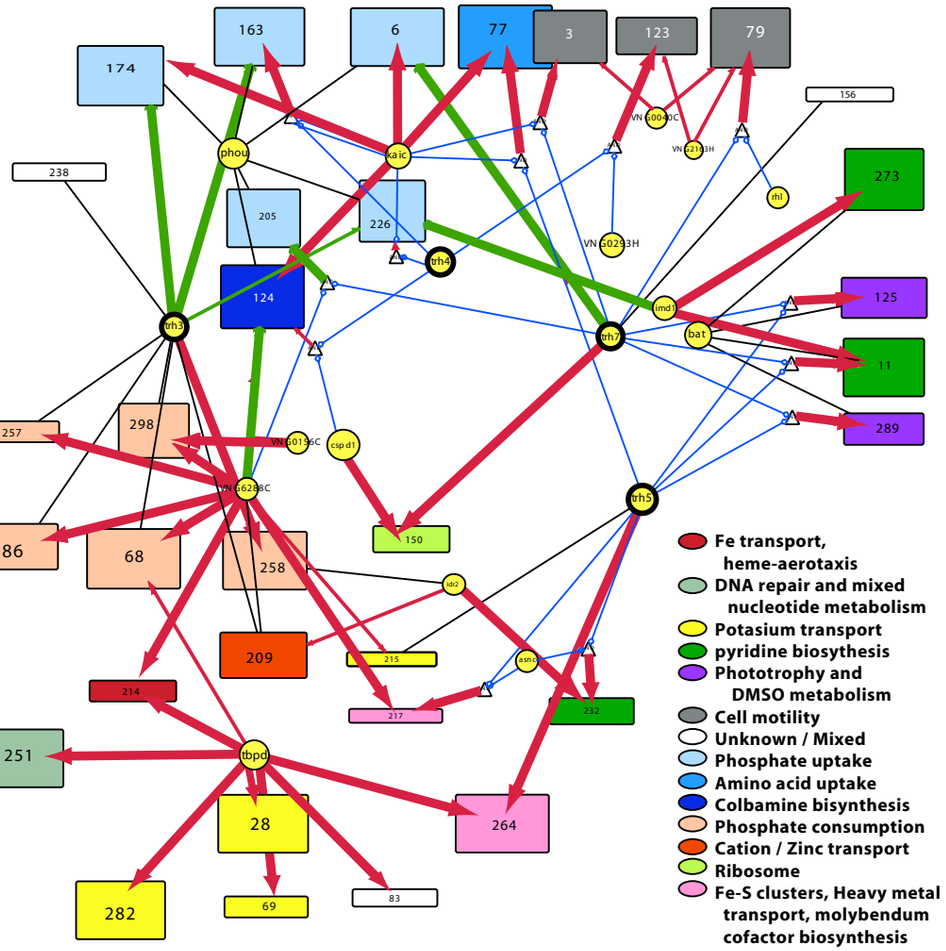

HUMAN PROTEOME FOLDING 2
Score
Current Protein
Current Progress
40.0%
Current Protein
72.8%
world community grid
Systems Biology
Powered by
IBM
powered by UNITED DEVICES

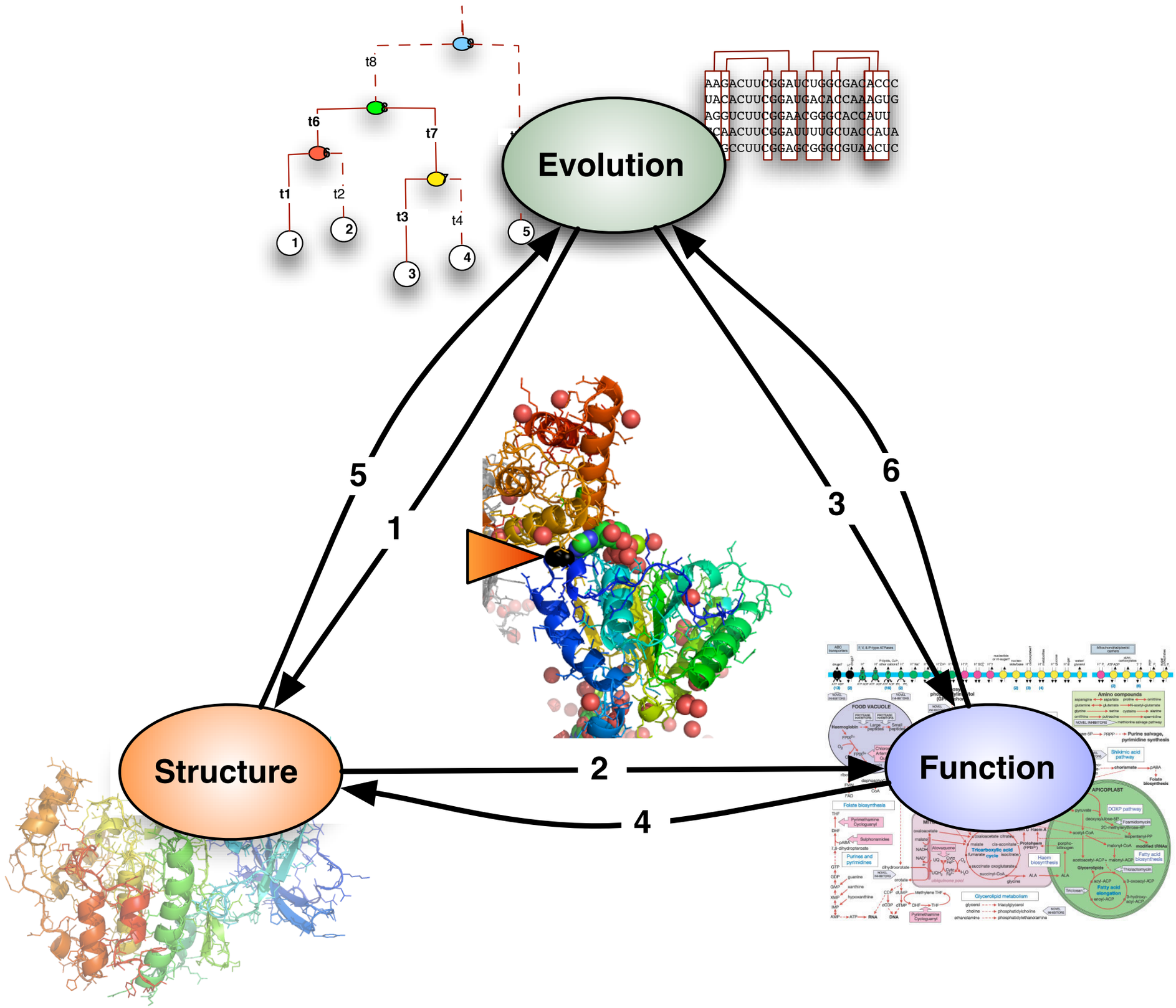


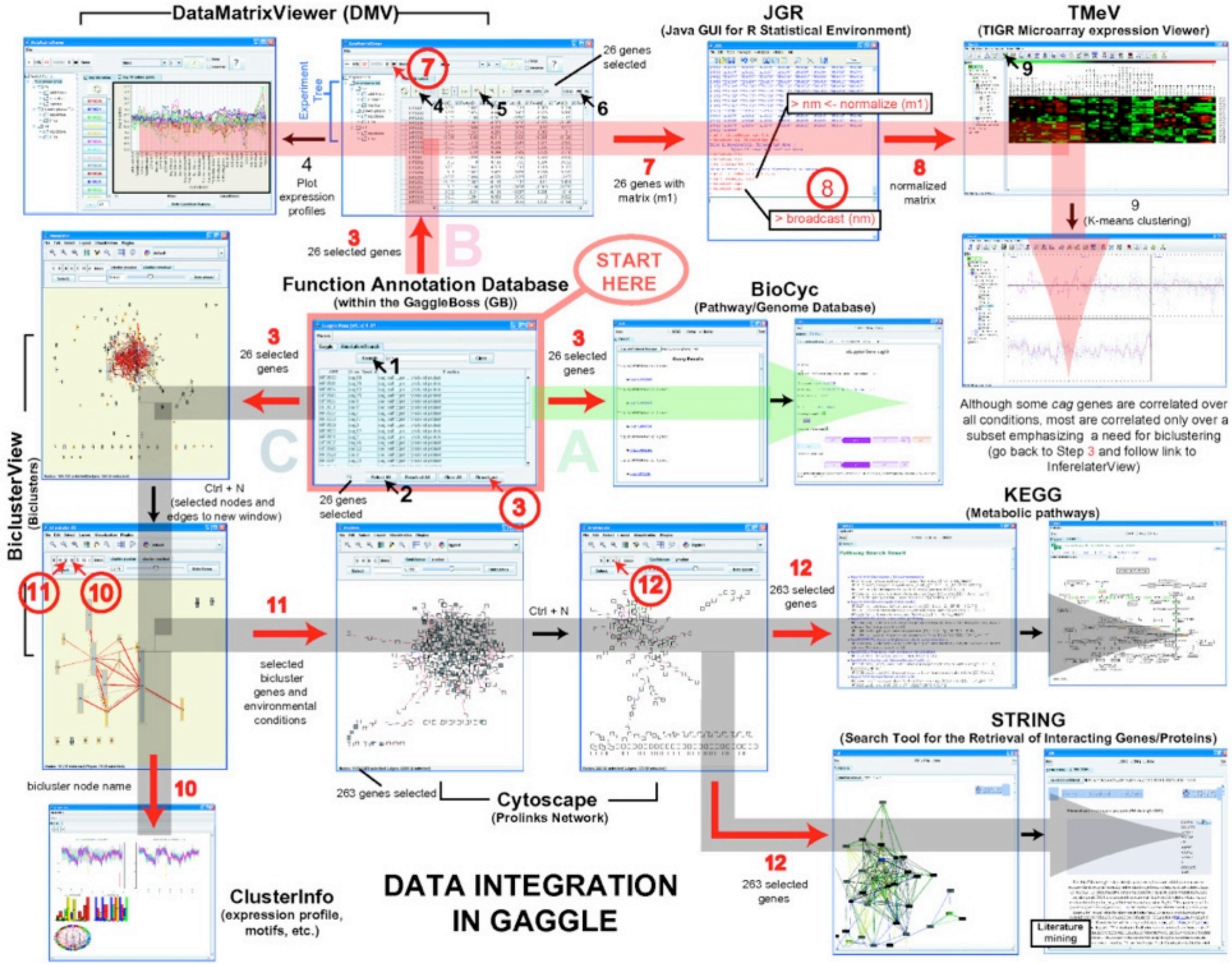





A.
RMSD over trianing
mean = 0.369
Frequency
RMSD (%var)
B.
RMSD (new conditions)
mean = 0.375
Frequency
RMSD (%var)
C.
RMS error over 300 biclusters
new data error
training error
Counts
D.
Cor over trianing
mean = 0.788
Frequency
Corr true vs. pred
E.
Cor (new conditions) over
mean = 0.807
Frequency
Corr true vs. pred
F.
Cor over 300 biclust
new data cor
training cor
Counts


163
6
77
3
123
79
174
156
238
273
205
226
124
125
11
289
257
298
86
68
258
150
209
215
214
217
232
251
28
264
282
69
83
phou
kaic
trh4
trh3
trh7
trh5
imdl
bat
rhl
csp d1
ttbpd
Fe transport, heme-aerotaxis
DNA repair and mixed nucleotide metabolism
Potasium transport
pyridine biosythesis
Phototrophy and DMSO metabolism
Cell motility
Unknown / Mixed
Phosphate uptake
Amino acid uptake
Colbamine bisynthesis
Phosphate consumption
Cation / Zinc transport
Ribosome
Fe-S clusters, Heavy metal transport, molybendum cofactor biosynthesis


t8
t6
t7
t1
t2
t3
t4
1
2
3
4
5
6
7
8
9
Evolution
AAGACUUCGGAUCUGGCGACACCC
UACACUUCGGAUGACACCAAAGUG
AGGUCUUCGGAACGGGCACCAUU
CAACUUCGGAUUUUGCUACCAUA
GCCUUCGGAGCGGGCGUAACUC
5
1
3
6
Structure
2
4
Function



Shannon, Bonneau, Baliga, 2006