

GWAS QC;
VEGAS: SNP-
gene mapping

MGS
GWAS Affy6
GWAS Affy500k
GWAS

Gene-based
association Gene-based
association Gene-based
association

dmGWAS: each
gene with P -
value as a seed
to search
significant
modules

MGS-weighted
PPI Affy6-
weighted PPI Affy500k-
weighted PPI

InWeb PPI

Dynamically
search modules Dynamically
search modules Dynamically
search modules

$P(Z_m) < 0.05$;
Cross evaluation

Module evaluation
in Affy6 or
Affy500K Module evaluation
in MGS or
Affy500K Module
evaluation in
MGS or Affy6

Merged modules

Initial: use each node as seed

Calculate module score Z_m

Expand the module by adding
neighborhood interactors, calculate
score for new module Z_{m+1}

Add the gene into the module if
 $Z_{m+1} > Z_m(1+r)$ until no gene can
satisfy $Z_{m+1} > Z_m(1+r)$

Get a module for each seed

Calculate P -value for each module
Get modules with $P(Z_m) < 0.05$

Calculate $P(Z_m)$ in evaluation
datasets for the genes in each
module, get $P(Z_{m(eval)}) < 0.05$ in at
least one evaluation dataset.