S2 File

Semantics used to infer regulatory networks from wheat -omics data

QNS1: Discover rules between highly abundant molecules and N/S supply or development phase.

FINDRULES
SCOPE t1 IN Omic_data
HAVING high : $t1.ATT > 0.5$ OVER ALL MINUS sample, Nitrogen, Sulfur, Phase_1,
Phase_2, Phase_3
AND NoNitrogen : $t1.ATT = 0$ OVER Nitrogen
AND Nitrogen : $t1.ATT = 15 \text{ OVER Nitrogen}$
AND NoSulfur : $t1.ATT = 0.2 \text{ OVER Sulfur}$
AND Sulfur: $t1.ATT = 2 \text{ OVER Sulfur}$
AND Cellularization : <i>t</i> 1.ATT = 1 OVER Phase_1
AND Storage : $t1.ATT = 1 \text{ OVER Phase}_2$
AND Senescence : $t1.ATT = 1 \text{ OVER Phase}_3;$

QNS2: Discover rules between not abundant molecules and N/S supply or development phase.

FINDRULES SCOPE t1 IN Omic_data HAVING high : t1.ATT < -0.5 OVER ALL MINUS sample, Nitrogen, Sulfur, Phase_1, Phase_2, Phase_3 AND NoNitrogen : t1.ATT = 0 OVER Nitrogen AND Nitrogen : t1.ATT=15 OVER Nitrogen AND NoSulfur : t1.ATT = 0.2 OVER Sulfur AND Sulfur: t1.ATT = 2 OVER Sulfur AND Cellularization : t1.ATT = 1 OVER Phase_1 AND Storage : t1.ATT = 1 OVER Phase_2; AND Senescence : t1.ATT = 1 OVER Phase_3;