SSGA and MSGA: two seed-growing algorithms for constructing collaborative subnetworks

Xiaohui Ji[1, 2], Su Chen[2], Jun Cheng Li[3], Wenping Deng[4], Zhigang Wei[2] and Hairong Wei [4, 5, 6*]
[1]College of Information and Computer Engineering, [2]State Key Lab of Forest Genetics and Breeding, Northeast Forestry University, Harbin, Heilongjiang 150040, People's Republic of China.
[3] Guangdong Key Laboratory for Innovative Development and Utilization of Forest Plant Germplasm, South China Agricultural University, Guangzhou 510642, People's Republic of China
[4] School of Forest Resources and Environmental Science, Michigan Technological University, Houghton, MI 49931, United States of America. [5] Department of Computer Science, Michigan Technological University, Houghton, MI 49931, United States of America. [6]Life Science and Technology Institute, Michigan Technological University, Houghton, MI 49931, United States of America.

* Correspondence author: Hairong Wei (hairong@mtu.edu)
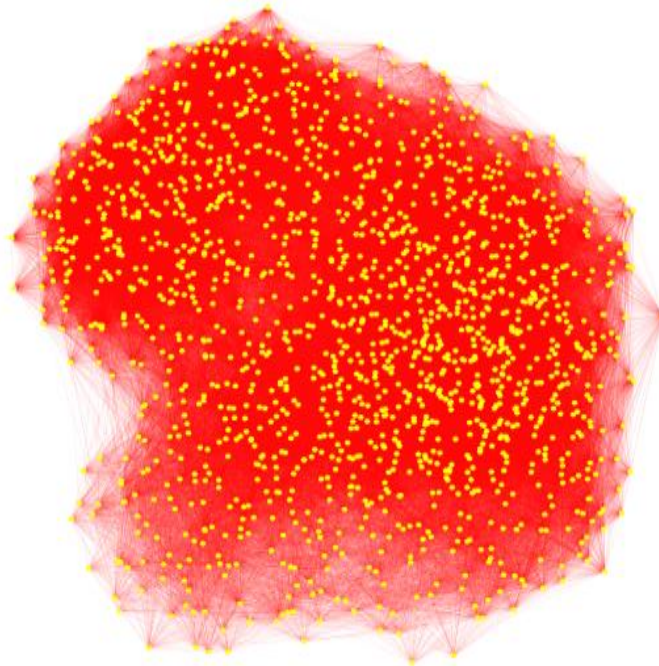
Supplementary Figure 1. The whole collaborative network constructed with Spearman rank correlation for algorithm development. The network was built with 108 normalized microarray chip data described in Nie et al BMC Systems Biology20115:53 DOI: 10.1186/1752-0509-5-53
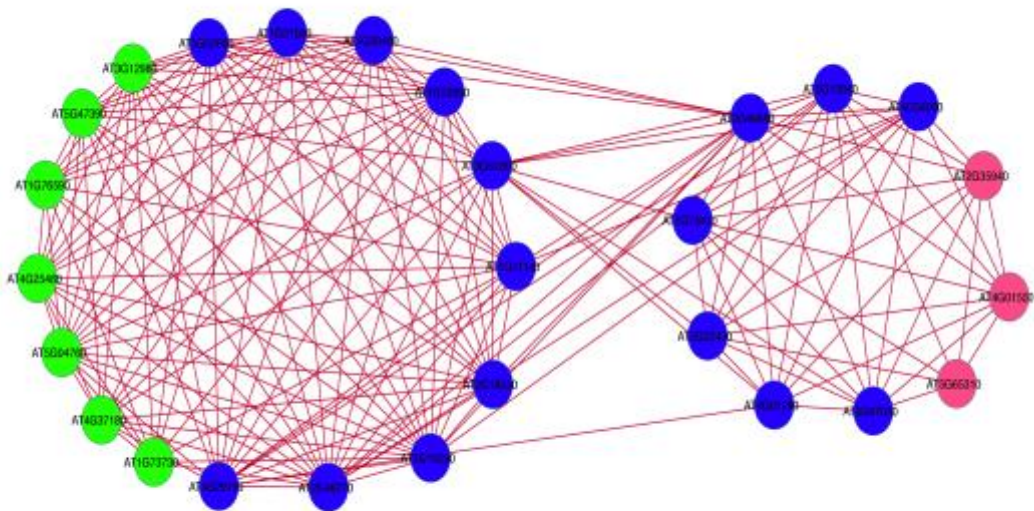
Supplementary Figure 2. Transcription factors (blue nodes) in the Subnetwork 11 derived from Triple-Link algorithm were split into Subnetworks 16 (left) and 18 (right) by SSGA. Green and pink colored nodes are new transcription factors shown up in the Subnetworks 16 and 18 respectively.
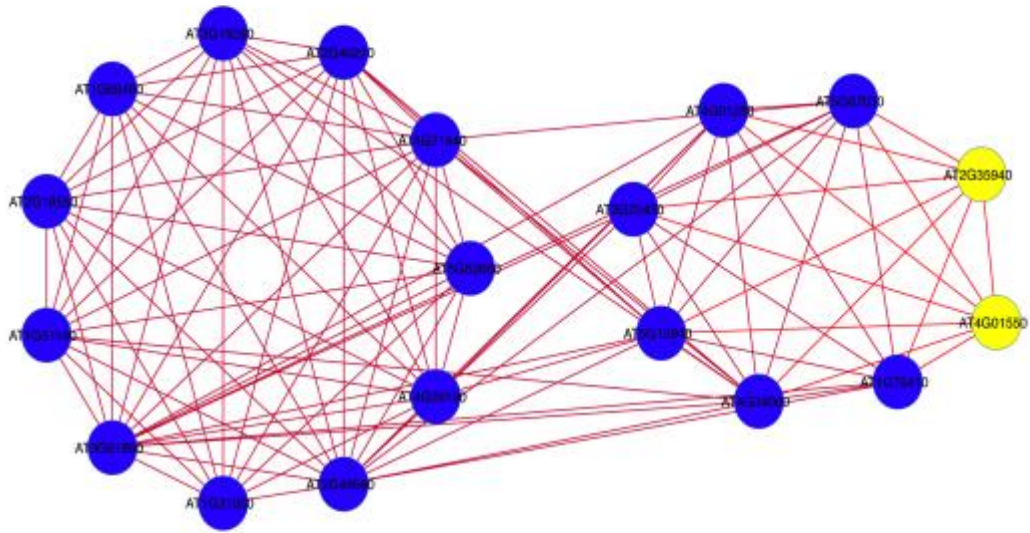
Supplementary Figure 3. Transcription factors (blue nodes) in the Subnetwork 11 derived from Triple-Link algorithm were split into Subnetworks 16 (left) and 8 (right) by MSGA. Yellow colored nodes are new transcription factors shown up in the Subnetwork 8.
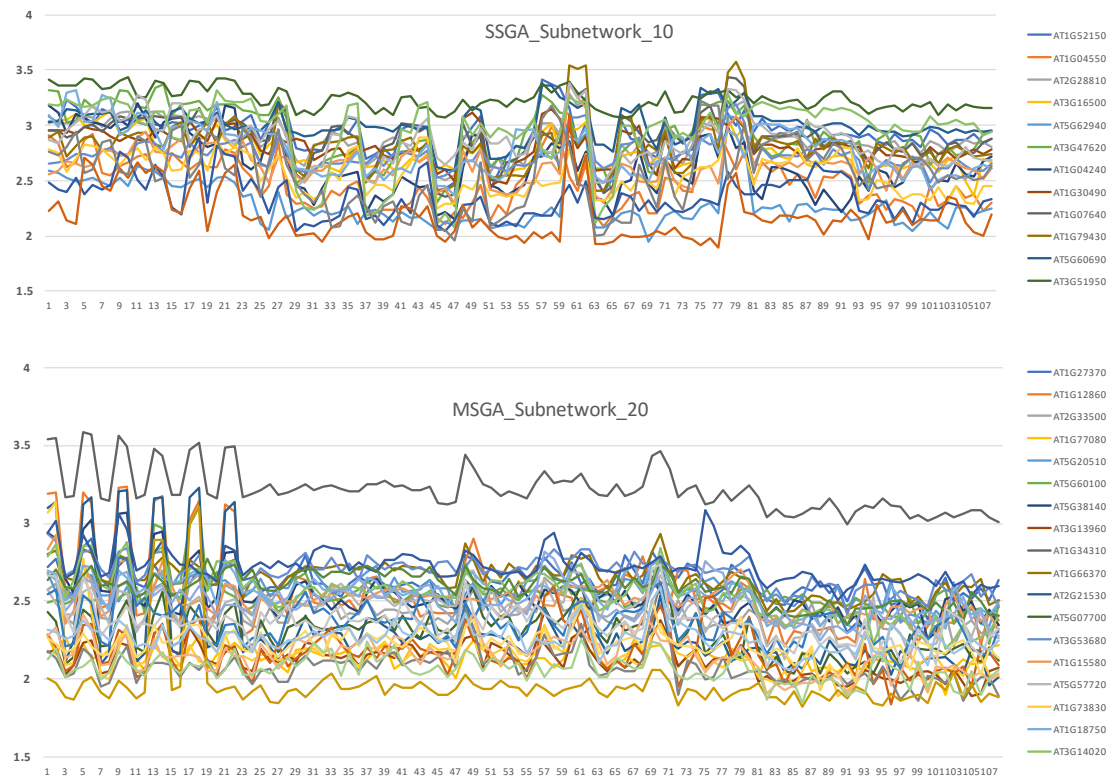
Supplementary Figure 4. The profiles of all genes in two randomly chosen subnetworks, one from SSGA and the other one from MSGA, were shown to display the loosely coordinated TFs within the same subnetworks.

Supplementary Figure 5. The variation of average number of connections per node (blue) and average edge weight (red) within each subnetwork (number of nodes ≥ 5). Each blue point represents an average number of connections between a subnetwork node and all other intra-subnetwork nodes divided by the number of nodes in the subnetwork. Each Red point represents an average edge weight of all edges within a subnetwork. The collaborative networks for decomposition and construction of subnetworks were constructed through a coexpression analysis between each transcription factor and all genomic genes using Spearman rank correlation, Weighted rank correlation, Hoeffding's D measure, Pearson, or Kendall, which was followed by building shared coordination matrices.

Supplementary Figure 6. The degrees of all regulatory genes in the collaborative network built using Spearman rank correlation and 108 normalized microarray chip data described in Nie et al BMC Systems Biology20115:53 DOI: 10.1186/1752-0509-5-53.

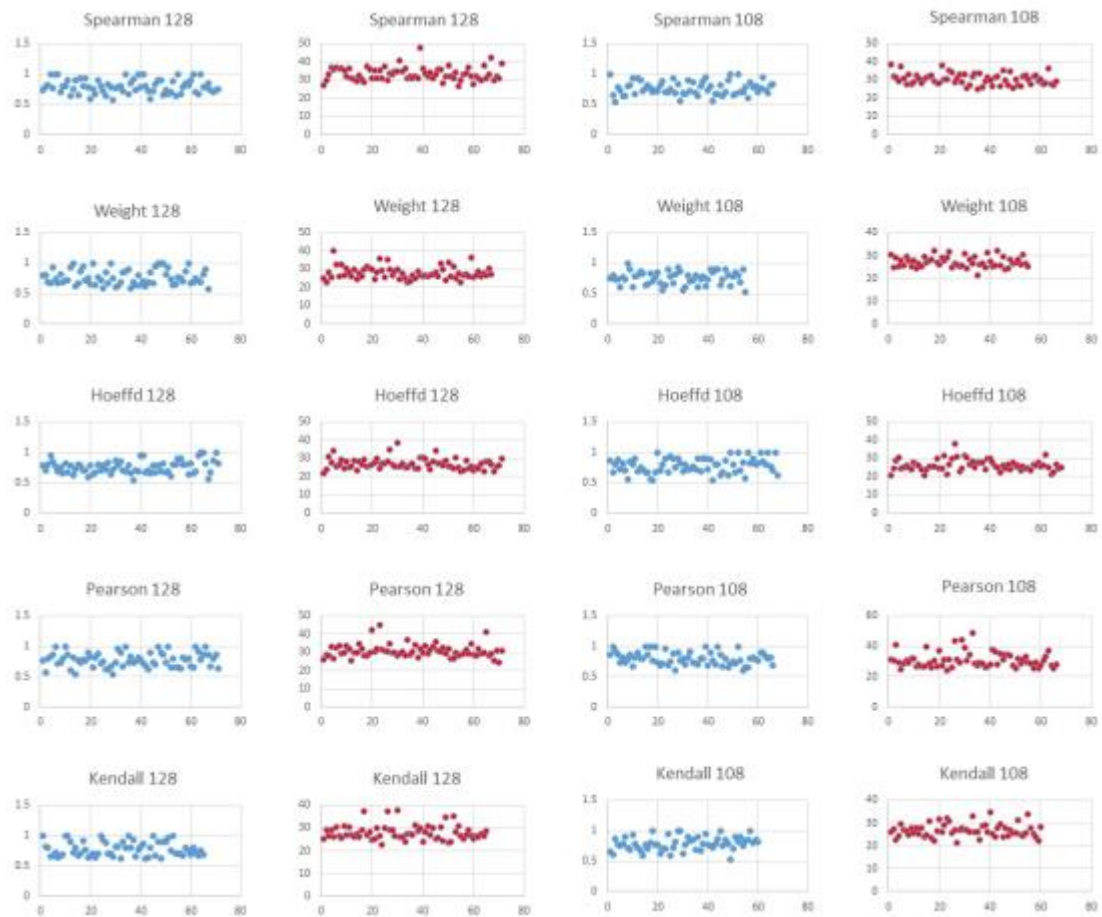Supplementary Figure 7. The times of connectivity numbers in the collaborative network built using Spearman rank correlation and 108 normalized microarray chip data described in Nie et al BMC Systems Biology20115:53 DOI: 10.1186/1752-0509-5-53.

Supplementary Table 1. The Subnetwork functions of SSGA result.

Gene	Symbol	Description	Evidence
Subnetwork 1		**Function: control the root hair growth**	
AT1G27740	RSL4	Postmitotic cell growth in root-hair cells	[1]
AT5G58010	LRL3	Roothairless1	[2]
AT5G19790	RAP2.11	Ethylene response factor controlling root growth	[3]
AT5G25810	TINY	ERF/AP2 TF control cell expansion in root	[4]
AT2G28160	FRU	Regulates iron uptake responses in outer cells of root	[5]
AT1G66470	RHD6	Early root hair formation	[6]
AT1G57560	MYB50	myb domain protein 50	
AT1G30650	WRKY14	WRKY DNA-binding protein 14	[7]
AT5G60120	TOE2	target of early activation tagged (EAT) 2	
Subnetwork 5		**Function: control root vascular development, second wall growth development**	
AT1G71930	VND7	Regulates xylem vessel formation	[8]
AT5G12870	MYB46	Target of SND1, control second wall biosynthesis	[9]
AT4G28500	SND2	Vascular cell differentiation	[10]
AT4G00220	LBD30	A central regulator of auxin distribution and signaling in root	[11]
AT1G63910	MYB103	Second wall growth	[12]
AT1G12260	VND4	Switches for protoxylem and metaxylem vessel formation	[13]
AT1G68810	bHLH	Root vascular initial	[14]
AT2G45420	LBD18	Lateral root and tracheary element formation	[15]
AT1G66230	MYB20	Second wall growth	[16]
AT1G73410	MYB54	Second wall growth	[16]
AT1G17950	MYB52	Second wall growth	[16]
AT3G21270	DOF2	Early stages of vascular development	[17]
AT1G01780	PLIM2b	LIM domain-containing protein	
AT1G80730	ZFP1	zinc-finger protein 1	[18]

Supplementary Table 2. The Subnetwork functions of MSGA result.

Gene	Symbol	Description	Evidence
Subnetwork 2	**Function: control root cap development and orientation of cell division plane**		
AT2G37260	WRKY44	Differentiation of trichomes and root hairless cells	[19]
AT1G74500	TMO7	Embryonic root initiation	[20]
AT2G30340	LBD13	Expressed in cells at the adaxial base of lateral roots	[21]
AT4G31920	RR10	response regulator 10	[22]
AT2G29060	---	scarecrow transcription factor family protein	
AT5G14750	WER1	WEREWOLF 1	[23]
AT1G33280	NAC015	BRN1, SMB control root cap maturation	[24]
AT4G10350	NAC070	BRN2, SMB control root cap maturation	[24]
AT2G40470	LBD15	Expressed in cells at the adaxial base of lateral roots	[21]
AT5G39820	NAC094	Apical meristem protein, function unknown	[1]
AT1G21340	---	Dof-type zinc finger DNA-binding protein	
AT5G57420	IAA33	IAA is involved in root development	[25]
AT1G26870	FEZ	FEZ and SMB control root stem cells in cap	[26]
AT1G77200	---	DREB subfamily A-4 of ERF/AP2 transcription factor	
AT1G36060	---	Controls Cell Dedifferentiation	[27]
AT1G66350	RGL1	Root epidermal differentiation	[28]
AT1G79580	SMB	FEZ and SMB control root stem cells	[24]
Subnetwork 4	**Function: control root cell cycle & growth**		
AT2G22840	GRF1	Growth factor expressed in root	[29]
AT4G37740	GRF2	Growth factor expressed in root	[29]
AT2G36400	GRF3	Growth factor expressed in root	[29]
AT3G01330	E2L2	Cyclin D/retinoblastoma/E2F pathway	[30]
AT5G24330	SDG34	Cell cycle regulation of late G1 to S phase	[31]
AT1G34355	PS1	Parallel spindle 1 involved in meiosis	[32]

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