

==> 0-human\_HI\_2012\_preliminary\_CCA/CCA\_out/human\_HI\_2012\_preliminary.txt <==

data1: ../CCA\_in/gcv\_list\_matched-to\_indicator\_list.csv

data2: ../CCA\_in/indicator\_list\_matched-to\_gcv\_list.csv

instance-name mismatches: 0

x-transform: (none)

y-transform: (none)

not normalizing x-rows

not normalizing y-rows

scaling X and Y

no weights given, assuming all ones

robust covariance-estimation method: None

instances: 3262

independent variables: 29 (29 before removing zero-variance variables)

dependent variables: 14 (14 before removing zero-variance variables)

regularization type: given

regularization lambda1: 0.001

regularization lambda2: 0.001

canonical correlations: 0.206723079981208, 0.147612652170657, 0.115443417013443,  
0.0721010187870098, 0.0678683502142033, 0.0612118691183185, 0.0513859104573886,  
0.0390326623761603, 0.0203550180566923, 0.0188378768970548, 0.0117138121081867,  
0.00977594445261574, 0.00229184005790305, 4.11135350962948e-12

p-values (asymptotic Wilks): 0.999611453889118, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1

p-values (asymptotic Hotelling): 0.999440508379085, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1

p-values (asymptotic Pillai): 0.999731630588338, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1

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match 1 :

canonical correlation: 0.206723079981208

canonical root: 0.042734431796917

shared variance X: 0.0194460030879943

shared variance Y: 0.0722187903289318

redundancy index X: 0.000831013892686528

redundancy index Y: 0.00308622896976758

"x"

"sig\_11" -0.00120671427343512

"sig\_14" -0.00314965881598565

"sig\_17" -0.00419243761214134

"sig\_22" -0.00465865277050862

"sig\_4" -0.00500691232691375

"sig\_12" -0.0063710126520796

"sig\_23" -0.00711992651910206

"sig\_18" -0.0104422039868064

"sig\_6" -0.0107276346579718

"sig\_26" -0.0108891318587959

"sig\_24" -0.0110774398438986

"sig\_19" -0.0122456462859324

"sig\_10" -0.014670416824843

"sig\_7" -0.0149679221522128

"sig\_27" -0.0171095201366061

"sig\_25" -0.0184779538372171

"sig\_28" -0.0185658378574391

"sig\_1" -0.0241407310733882

"sig\_13" -0.0275968393148867

"sig\_21" -0.028017261791614  
"sig\_16" -0.0324948437267477  
"sig\_20" -0.0329020173044324  
"sig\_29" -0.0347095985748757  
"sig\_8" -0.036342381796606  
"sig\_2" -0.0426009141248841  
"sig\_3" -0.0433523544631845  
"sig\_9" -0.0455307163827973  
"sig\_15" -0.0544047547961567  
"sig\_5" -0.0579196362491496  
-----  
"x"  
"cell.organization.and.biogenesis" 0.0216618590654488  
"cell.cycle.and.proliferation" 0.0175324008552528  
"death" 0.0152634243902104  
"protein.metabolism" 0.0148646382703586  
"stress.response" 0.0110679238114312  
"other.metabolic.processes" 0.00911234096698411  
"signal.transduction" 0.00558028412703987  
"DNA.metabolism" 0.00475978868566922  
"transport" 0.0037958078496125  
"cell.cell.signaling" 0.00351480526749924  
"RNA.metabolism" 0.00295950785942282  
"other.biological.processes" 0.00182605433574208  
"developmental.processes" -0.0449510692768564  
"cell.adhesion" -0.214809779696109

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==> 1-human\_i2d\_full\_CCA/CCA\_out/human\_i2d\_full.txt <==

data1: ../CCA\_in/gcv\_list\_matched-to\_indicator\_list.csv

data2: ../CCA\_in/indicator\_list\_matched-to\_gcv\_list.csv

instance-name mismatches: 0

x-transform: (none)

y-transform: (none)

not normalizing x-rows

not normalizing y-rows

scaling X and Y

no weights given, assuming all ones

robust covariance-estimation method: None

instances: 11824

independent variables: 29 (29 before removing zero-variance variables)

dependent variables: 14 (14 before removing zero-variance variables)

regularization type: given

regularization lambda1: 0.001

regularization lambda2: 0.001

canonical correlations: 0.192817429326585, 0.0965470343255822, 0.0707393194728759,  
0.0465633681479094, 0.040420281770981, 0.0313070575368282, 0.0287117851357318,  
0.0225895848183581, 0.0181165088946409, 0.0165499163768614, 0.0100982144566696,  
0.00386664111522486, 0.00121508662908237, 1.06190511108932e-11

p-values (asymptotic Wilks): 0, 0.999998835343346, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1

p-values (asymptotic Hotelling): 0, 0.999998725213363, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1

p-values (asymptotic Pillai): 0, 0.999998930722582, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1

---

match 1 :

canonical correlation: 0.192817429326585

canonical root: 0.0371785610521125

shared variance X: 0.139022184215527

shared variance Y: 0.0783243296878116

redundancy index X: 0.005168644763455

redundancy index Y: 0.00291198587316409

"x"

"sig\_8" 0.156570375170777

"sig\_29" 0.147595608756204

"sig\_28" 0.146445493226234

"sig\_2" 0.134749325386025

"sig\_26" 0.110854916048875

"sig\_7" 0.106850200510262

"sig\_27" 0.0881708807880575

"sig\_23" 0.0640151099584672

"sig\_24" 0.0622791145874277

"sig\_1" 0.055357718500308

"sig\_22" 0.0539316237002693

"sig\_6" 0.0537041236559418

"sig\_25" 0.050007616019724

"sig\_5" 0.0445395964788531

"sig\_18" 0.0360753490235308

"sig\_17" 0.0326307706131563

"sig\_21" 0.0303854622728897

"sig\_19" 0.0276574070900695

"sig\_3" 0.0182536813595501

"sig\_4" 0.0171528757426264

"sig\_14" 0.0147948227024832

"sig\_15" 0.0134262307080674

"sig\_13" 0.0121075767076754

"sig\_20" 0.0117907804482356

"sig\_16" 0.0115932392361632

"sig\_12" 0.0111772521028839

"sig\_11" 0.00425893174013389

"sig\_9" 0.00306471346185928

"sig\_10" 0.0026420295636139

-----

"x"

"protein.metabolism" 0.191119067122117

"cell.cycle.and.proliferation" 0.00645593473635202

"RNA.metabolism" 0.00551161800135311

"other.metabolic.processes" -0.00541342075775608

"DNA.metabolism" -0.00846505376992217

"cell.organization.and.biogenesis" -0.0110094757793993

"cell.adhesion" -0.0151771932592363

"death" -0.0158829650600743

"cell.cell.signaling" -0.0167353634339866

"stress.response" -0.0180429852870266

"signal.transduction" -0.0292823691188659

"transport" -0.0316966251381463  
"other.biological.processes" -0.0354819582105481  
"developmental.processes" -0.0373897644911509

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==> 2-human\_i2d\_hc\_CCA/CCA\_out/human\_i2d\_hc.txt <==

data1: ../CCA\_in/gcv\_list\_matched-to\_indicator\_list.csv

data2: ../CCA\_in/indicator\_list\_matched-to\_gcv\_list.csv

instance-name mismatches: 0

x-transform: (none)

y-transform: (none)

not normalizing x-rows

not normalizing y-rows

scaling X and Y

no weights given, assuming all ones

robust covariance-estimation method: None

instances: 8623

independent variables: 29 (29 before removing zero-variance variables)

dependent variables: 14 (14 before removing zero-variance variables)

regularization type: given

regularization lambda1: 0.001

regularization lambda2: 0.001

canonical correlations: 0.158469994979046, 0.11543635544056, 0.0772836280646526,  
0.0702601665250415, 0.0483336381389128, 0.0440788961172898, 0.0331273463456733,  
0.0262729216314226, 0.0240476148805155, 0.0175965202078741, 0.0141131263969192,  
0.00745666913932046, 0.00559416148946001, 6.21584718972518e-12

p-values (asymptotic Wilks): 0.00252070708287766, 0.999905687346829, 1, 1, 1, 1, 1, 1, 1, 1, 1,  
1, 1

p-values (asymptotic Hotelling): 0.00198699810352854, 0.999895796391142, 1, 1, 1, 1, 1, 1, 1, 1,  
1, 1, 1, 1

p-values (asymptotic Pillai): 0.00317595685457639, 0.99991417144405, 1, 1, 1, 1, 1, 1, 1, 1, 1,  
1, 1

---

match 1 :

canonical correlation: 0.158469994979046

canonical root: 0.025112739308659

shared variance X: 0.0843394138182706

shared variance Y: 0.0768147466476277

redundancy index X: 0.00211799371266334

redundancy index Y: 0.00192902870762256

"x"

"sig\_28" -0.0119062320243425

"sig\_29" -0.0143045635770186

"sig\_22" -0.0147594552804987

"sig\_26" -0.0166677591612906

"sig\_8" -0.0209630218182657

"sig\_11" -0.0220483694474096

"sig\_14" -0.0262513182731647

"sig\_17" -0.0270777853880929

"sig\_18" -0.0294784368092719

"sig\_4" -0.0328041797039679

"sig\_23" -0.0332915227568785

```

"sig_24" -0.0363113795743376
"sig_7" -0.0383198207169688
"sig_13" -0.0390518735992712
"sig_27" -0.0406411446558964
"sig_12" -0.041404066448652
"sig_19" -0.0417592021843706
"sig_15" -0.0420586850042297
"sig_10" -0.0434589355496161
"sig_21" -0.0477577901310387
"sig_9" -0.0481160710880356
"sig_6" -0.0491583513336417
"sig_20" -0.0519587464734773
"sig_25" -0.060271028889127
"sig_3" -0.0609291412809264
"sig_16" -0.0630183070809746
"sig_2" -0.0651986623219251
"sig_1" -0.0696144171484156
"sig_5" -0.0826595888182245
-----
"x"
"other.metabolic.processes" 0.0577370592785656
"transport" 0.0304258503717386
"protein.metabolism" 0.0275404840567749
"cell.organization.and.biogenesis" 0.0197115463285709
"cell.cell.signaling" 0.0145459762584342
"cell.adhesion" 0.00798905640762276
"signal.transduction" 0.00755160362383596
"DNA.metabolism" 0.00273615538491305
"stress.response" 0.00132197087457651
"other.biological.processes" 0.00115014221783991
"developmental.processes" 0.000185735138073838
"RNA.metabolism" -0.018384276994062
"cell.cycle.and.proliferation" -0.0275864530484533
"death" -0.150681891589344

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==> 3-human_ppi_56k_CCA/CCA_out/human_ppi_56k.txt <==
data1: ../CCA_in/gcv_list_matched-to_indicator_list.csv
data2: ../CCA_in/indicator_list_matched-to_gcv_list.csv
instance-name mismatches: 0
x-transform: (none)
y-transform: (none)
not normalizing x-rows
not normalizing y-rows
scaling X and Y
no weights given, assuming all ones
robust covariance-estimation method: None
instances: 9492
independent variables: 29 (29 before removing zero-variance variables)
dependent variables: 14 (14 before removing zero-variance variables)
regularization type: given
regularization lambda1: 0.001

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regularization lambda2: 0.001  
canonical correlations: 0.155502366337325, 0.122330153085332, 0.0721916469525734,  
0.0658286999903781, 0.0507591882016145, 0.0447629091342856, 0.0334643409447025,  
0.0252407133585192, 0.0232387976018107, 0.0186153798269275, 0.0141235633714565,  
0.0130588510816304, 0.0080157971708303, 9.95723445506514e-12  
p-values (asymptotic Wilks): 1.2048099118811e-05, 0.987868860836005, 0.999999999999997, 1,  
1, 1, 1, 1, 1, 1, 1, 1, 1  
p-values (asymptotic Hotelling): 8.48291405330936e-06, 0.986805681344013,  
0.999999999999997, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1  
p-values (asymptotic Pillai): 1.69757655874569e-05, 0.988812942230048, 0.999999999999997, 1,  
1, 1, 1, 1, 1, 1, 1, 1, 1

---

match 1 :

canonical correlation: 0.155502366337325  
canonical root: 0.0241809859365076  
shared variance X: 0.0870751525262858  
shared variance Y: 0.0770069978574192  
redundancy index X: 0.00210556303865737  
redundancy index Y: 0.00186210513220293

"x"

"sig\_11" -0.026784802933832  
"sig\_14" -0.0288886028081594  
"sig\_17" -0.0306259680080317  
"sig\_21" -0.0314830876613935  
"sig\_25" -0.0317026566863245  
"sig\_27" -0.0320674320245462  
"sig\_24" -0.0321108638894928  
"sig\_12" -0.0327918397376766  
"sig\_16" -0.0332374224817281  
"sig\_19" -0.0338165170323861  
"sig\_20" -0.0345037685100623  
"sig\_18" -0.0347490713711972  
"sig\_22" -0.0350056852276918  
"sig\_10" -0.035614007988589  
"sig\_15" -0.0360029304889873  
"sig\_23" -0.0367118612918546  
"sig\_26" -0.0380475414953398  
"sig\_13" -0.0394063147912216  
"sig\_9" -0.0425992857572804  
"sig\_4" -0.0430682710918634  
"sig\_28" -0.0435298646523559  
"sig\_5" -0.0461792408675793  
"sig\_6" -0.0462117522072392  
"sig\_3" -0.0488412651834434  
"sig\_7" -0.0499351619842475  
"sig\_1" -0.0681076890184487  
"sig\_8" -0.071701548908936  
"sig\_29" -0.0721921026141832  
"sig\_2" -0.0816038161136185

-----  
"x"

"other.metabolic.processes" 0.056972399906057

"transport" 0.0411734541804025  
"protein.metabolism" 0.0247592305748396  
"cell.cell.signaling" 0.0175015211841763  
"cell.organization.and.biogenesis" 0.0145870683161458  
"developmental.processes" 0.0143830418152403  
"signal.transduction" 0.0119598573165771  
"cell.adhesion" 0.00820072615765368  
"stress.response" 0.00620450723272041  
"other.biological.processes" 0.00191852149973519  
"DNA.metabolism" -0.00567393530573056  
"cell.cycle.and.proliferation" -0.0155296169120109  
"RNA.metabolism" -0.065515997126898  
"death" -0.130453937016065

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==> 4-biogrid\_human\_ppi\_noUBC\_full\_CCA/CCA\_out/biogrid\_human\_ppi\_noUBC\_full.txt  
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data1: ../CCA\_in/gcv\_list\_matched-to\_indicator\_list.csv  
data2: ../CCA\_in/indicator\_list\_matched-to\_gcv\_list.csv  
instance-name mismatches: 0  
x-transform: (none)  
y-transform: (none)  
not normalizing x-rows  
not normalizing y-rows  
scaling X and Y  
no weights given, assuming all ones  
robust covariance-estimation method: None  
instances: 11539  
independent variables: 29 (29 before removing zero-variance variables)  
dependent variables: 14 (14 before removing zero-variance variables)  
regularization type: given  
regularization lambda1: 0.001  
regularization lambda2: 0.001  
canonical correlations: 0.236950341937738, 0.0871589838129494, 0.0532885506341267,  
0.0495151706857958, 0.044512988016526, 0.0371122205970379, 0.0316618934605753,  
0.0241484838871384, 0.0183881131151198, 0.013068781634366, 0.00662841499320093,  
0.00388683438944895, 0.000496612765960135, 1.08887717374405e-11  
p-values (asymptotic Wilks): 0, 0.999999999984925, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1  
p-values (asymptotic Hotelling): 0, 0.999999999983843, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1  
p-values (asymptotic Pillai): 0, 0.999999999985839, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1

---

match 1 :  
canonical correlation: 0.236950341937738  
canonical root: 0.056145464544411  
shared variance X: 0.197581271321833  
shared variance Y: 0.0786587512336516  
redundancy index X: 0.0110932922636396  
redundancy index Y: 0.00441633212849663  
"x"  
"sig\_11" -0.0070770419166052  
"sig\_14" -0.0140711653216073  
"sig\_10" -0.0174887608095644

"sig\_4" -0.0202676452696141  
 "sig\_9" -0.0247251633119841  
 "sig\_16" -0.0377705621072966  
 "sig\_12" -0.0378098566409724  
 "sig\_13" -0.0435633706341271  
 "sig\_3" -0.04898098726946  
 "sig\_17" -0.0519135433207063  
 "sig\_20" -0.0584313976243124  
 "sig\_15" -0.0635040709981089  
 "sig\_18" -0.0671237084176427  
 "sig\_19" -0.0786758241071425  
 "sig\_1" -0.0851022859876499  
 "sig\_22" -0.0854233804588473  
 "sig\_6" -0.0951146668692336  
 "sig\_21" -0.0959056513350244  
 "sig\_23" -0.100012277417367  
 "sig\_5" -0.112611511918066  
 "sig\_25" -0.120091707009029  
 "sig\_24" -0.126949553736189  
 "sig\_27" -0.142534512311281  
 "sig\_26" -0.149869042253716  
 "sig\_7" -0.158077201198269  
 "sig\_28" -0.162009560802856  
 "sig\_29" -0.173875086596927  
 "sig\_8" -0.179771932670619  
 "sig\_2" -0.183029721939835  
 -----  
 "x"  
 "transport" 0.0401331925929093  
 "cell.organization.and.biogenesis" 0.0327476269031693  
 "other.metabolic.processes" 0.0306884873124966  
 "other.biological.processes" 0.0285974638203856  
 "developmental.processes" 0.0267731376388543  
 "signal.transduction" 0.022790063251574  
 "stress.response" 0.02063129627154  
 "RNA.metabolism" 0.0163600157752575  
 "cell.cell.signaling" 0.015445030285537  
 "cell.adhesion" 0.0135374395490533  
 "DNA.metabolism" 0.0086792843745809  
 "death" 0.00467341735093078  
 "cell.cycle.and.proliferation" -0.00104858382524773  
 "protein.metabolism" -0.241513731202962

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==> 5-biogrid\_human\_ppi\_hc\_CCA/CCA\_out/biogrid\_human\_ppi\_hc.txt <==

data1: ../CCA\_in/gcv\_list\_matched-to\_indicator\_list.csv  
 data2: ../CCA\_in/indicator\_list\_matched-to\_gcv\_list.csv  
 instance-name mismatches: 0  
 x-transform: (none)  
 y-transform: (none)  
 not normalizing x-rows  
 not normalizing y-rows



scaling X and Y  
no weights given, assuming all ones  
robust covariance-estimation method: None  
instances: 7005  
independent variables: 29 (29 before removing zero-variance variables)  
dependent variables: 14 (14 before removing zero-variance variables)  
regularization type: given  
regularization lambda1: 0.001  
regularization lambda2: 0.001  
canonical correlations: 0.259203382837973, 0.105463296530231, 0.0734249953496146,  
0.0604353183929021, 0.0455769363239592, 0.0352639505555099, 0.0276243782427665,  
0.0217172327011541, 0.017036806882873, 0.00775284955592884, 0.00453626833240375,  
0.00263883280967739, 0.00103639950546324, 1.83926339532982e-12  
p-values (asymptotic Wilks): 1.57651669496772e-14, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1  
p-values (asymptotic Hotelling): 8.88178419700125e-16, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1  
p-values (asymptotic Pillai): 2.5157653738006e-13, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1

---

match 1 :  
canonical correlation: 0.259203382837973  
canonical root: 0.0671863936746485  
shared variance X: 0.0598109484194785  
shared variance Y: 0.0799898899141395  
redundancy index X: 0.00401848192656518  
redundancy index Y: 0.00537423223376318

"x"  
"sig\_15" 0.00260280240089236  
"sig\_9" 0.00252305583149569  
"sig\_20" 0.00246642779019045  
"sig\_16" 0.00242865577057703  
"sig\_10" 0.00220472299707353  
"sig\_13" 0.00217533857525897  
"sig\_12" 0.00214515138768351  
"sig\_3" 0.00213216597437075  
"sig\_19" 0.00126337736659486  
"sig\_21" 0.00107349396744511  
"sig\_5" -0.000911276259850539  
"sig\_25" -0.00530342665329895  
"sig\_18" -0.00791468063786719  
"sig\_24" -0.0111103956901261  
"sig\_22" -0.0112278643201106  
"sig\_17" -0.0112820611965511  
"sig\_6" -0.0116878687124547  
"sig\_1" -0.0119001400708926  
"sig\_14" -0.0186112062389635  
"sig\_4" -0.019726379866063  
"sig\_23" -0.020212532634804  
"sig\_11" -0.0219124074418505  
"sig\_27" -0.050170545855492  
"sig\_7" -0.0547959483167961  
"sig\_26" -0.0648747742193664  
"sig\_2" -0.121948932386978  
"sig\_28" -0.13589527539024

"sig\_8" -0.179278748178528  
"sig\_29" -0.184297815284909  
-----  
"x"  
"other.biological.processes" 0.0473959473405863  
"other.metabolic.processes" 0.0422726566255688  
"transport" 0.0408521308146745  
"cell.organization.and.biogenesis" 0.0294666845847446  
"signal.transduction" 0.0287593798906555  
"stress.response" 0.0258601134592973  
"developmental.processes" 0.022122903055576  
"RNA.metabolism" 0.0161663448411842  
"death" 0.0143356784936169  
"cell.cell.signaling" 0.0114668921243357  
"cell.adhesion" 0.0101164046322496  
"DNA.metabolism" 0.00454250430486669  
"cell.cycle.and.proliferation" 0.0034684792856061  
"protein.metabolism" -0.263661004746923

---

==> 6-yeast\_apms\_collins\_boone\_CCA/CCA\_out/yeast\_apms\_collins.txt <==

data1: ../CCA\_in/gcv\_list\_matched-to\_indicator\_list.csv

data2: ../CCA\_in/indicator\_list\_matched-to\_gcv\_list.csv

instance-name mismatches: 0

x-transform: (none)

y-transform: (none)

not normalizing x-rows

not normalizing y-rows

scaling X and Y

no weights given, assuming all ones

robust covariance-estimation method: None

instances: 1241

independent variables: 29 (29 before removing zero-variance variables)

dependent variables: 14 (14 before removing zero-variance variables)

regularization type: given

regularization lambda1: 0.001

regularization lambda2: 0.001

canonical correlations: 0.530126834561433, 0.361843921516991, 0.206925060942331,  
0.0452633417280611, 0.0210188150930933, 0.00999697197910705, 0.00441740692233176,  
0.0029567357858866, 0.00248619978944194, 0.000811599077584253, 0.000293452376832328,  
0.000121400848920915, 1.99583453190023e-05, 4.68702703621409e-12

p-values (asymptotic Wilks): 7.05413505386332e-12, 0.99999999767416, 1, 1, 1, 1, 1, 1, 1, 1, 1,  
1, 1

p-values (asymptotic Hotelling): 0, 0.999999948510477, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1

p-values (asymptotic Pillai): 1.35840490078643e-07, 0.999999999904449, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,  
1, 1

---

match 1 :

canonical correlation: 0.530126834561433

canonical root: 0.281034460722125

shared variance X: 0.497721553582597

shared variance Y: 0.0811137498774557

redundancy index X: 0.139876908400864  
redundancy index Y: 0.0227957589539601  
"x"

"sig\_9" -0.212189480521127  
"sig\_10" -0.23169736846479  
"sig\_13" -0.232821245542862  
"sig\_11" -0.273160142436031  
"sig\_12" -0.292685740106294  
"sig\_15" -0.293876049989637  
"sig\_18" -0.296045033770591  
"sig\_14" -0.302255014933251  
"sig\_16" -0.304908840874617  
"sig\_3" -0.329827658812634  
"sig\_19" -0.329876959356558  
"sig\_21" -0.343057910908779  
"sig\_17" -0.354993407571703  
"sig\_20" -0.363364202312918  
"sig\_4" -0.364511835103225  
"sig\_23" -0.376791679199217  
"sig\_25" -0.393313656591054  
"sig\_24" -0.396594900291068  
"sig\_22" -0.403435045705139  
"sig\_6" -0.4095493068112  
"sig\_5" -0.416556791006977  
"sig\_27" -0.421970977216574  
"sig\_26" -0.426165690577217  
"sig\_28" -0.44429555896716  
"sig\_1" -0.453051926929247  
"sig\_7" -0.454313584962548  
"sig\_29" -0.46430615776707  
"sig\_8" -0.479142491460243  
"sig\_2" -0.499532936369011

-----

"x"  
"Golgi.endosome.vacuole.sorting" 0.111655921978258  
"Metabolism.mitochondria" 0.0950477649048382  
"DNA.replication...repair.HR.cohesion" 0.0949749193203341  
"Chromatin.transcription" 0.0808908170932502  
"Cell.polarity.morphogenesis" 0.0799677241526446  
"Signaling.stress.response" 0.0716519088009494  
"Chrom..seg..kinetoch..spindle.microtub." 0.066696597773356  
"Protein.folding...glycosylation.cell.wall" 0.0566941389415309  
"ER.Golgi.traffic" 0.0562878541332071  
"Nuclear.cytoplasmic.transport" 0.0424185802893814  
"Cell.cycle.progression.meiosis" 0.0101030282088361  
"Protein.degradation.proteosome" 0.00767401924632755  
"RNA.processing" -0.0475609645756522  
"Ribosome.translation" -0.508987082686986

---

==> 7-yeast\_biogrid\_genetic\_boone\_CCA/CCA\_out/yeast\_biogrid\_genetic.txt <==  
data1: ../CCA\_in/gcv\_list\_matched-to\_indicator\_list.csv

data2: ../CCA\_in/indicator\_list\_matched-to\_gcv\_list.csv  
instance-name mismatches: 0  
x-transform: (none)  
y-transform: (none)  
not normalizing x-rows  
not normalizing y-rows  
scaling X and Y  
no weights given, assuming all ones  
robust covariance-estimation method: None  
instances: 3194  
independent variables: 29 (29 before removing zero-variance variables)  
dependent variables: 14 (14 before removing zero-variance variables)  
regularization type: given  
regularization lambda1: 0.001  
regularization lambda2: 0.001  
canonical correlations: 0.345898747530568, 0.225253241302983, 0.192166372706951,  
0.152207771368256, 0.125467954333461, 0.0838134364268649, 0.0414587398071686,  
0.0349862906272815, 0.0267829805194673, 0.0204493876758583, 0.0133903458974968,  
0.00780910965545125, 0.00468155216669138, 3.66692195078349e-12  
p-values (asymptotic Wilks): 0, 0.0022897950861186, 0.96274721478692, 0.999999999803514, 1,  
1, 1, 1, 1, 1, 1, 1, 1, 1  
p-values (asymptotic Hotelling): 0, 0.00140322624264066, 0.954461092089526,  
0.999999999732645, 1, 1, 1, 1, 1, 1, 1, 1, 1  
p-values (asymptotic Pillai): 0, 0.00359336909789421, 0.969147469427546, 0.999999999845346,  
1, 1, 1, 1, 1, 1, 1, 1, 1

---

match 1 :

canonical correlation: 0.345898747530568  
canonical root: 0.119645943543215  
shared variance X: 0.22401408775993  
shared variance Y: 0.0802124263544652  
redundancy index X: 0.0268023768970095  
redundancy index Y: 0.00959709143507066  
"x"

"sig\_11" -0.0551769634216806  
"sig\_10" -0.0881022932088438  
"sig\_9" -0.0921700695229395  
"sig\_14" -0.10259516324479  
"sig\_16" -0.11486409875365  
"sig\_13" -0.117355102815521  
"sig\_12" -0.117809704835365  
"sig\_15" -0.117830736805456  
"sig\_4" -0.120009433616735  
"sig\_3" -0.133039386074082  
"sig\_20" -0.137327306466373  
"sig\_18" -0.139299917258546  
"sig\_17" -0.139351536301352  
"sig\_21" -0.142043755220121  
"sig\_19" -0.144161490286786  
"sig\_25" -0.164290225528346  
"sig\_5" -0.165378699840157  
"sig\_22" -0.165421846375952

```

"sig_24" -0.166340022106763
"sig_6" -0.167983901367485
"sig_23" -0.169263770994989
"sig_1" -0.177760143478368
"sig_27" -0.184914003335098
"sig_26" -0.190232437320193
"sig_7" -0.201196864769798
"sig_28" -0.209521009110606
"sig_2" -0.232243524038129
"sig_29" -0.232692589398075
"sig_8" -0.234253259522763
-----
"x"
"Metabolism.mitochondria" 0.147874525297607
"Ribosome.translation" 0.0753500601829054
"Cell.polarity.morphogenesis" 0.0594431695713238
"RNA.processing" 0.0567141147811023
"Protein.folding...glycosylation.cell.wall" 0.0463691470645248
"Signaling.stress.response" 0.0403017597131823
"Cell.cycle.progression.meiosis" 0.035408954689929
"Nuclear.cytoplasmic.transport" 0.0180588923787346
"Golgi.endosome.vacuole.sorting" 0.0167303035785614
"Protein.degradation.proteosome" -0.00324927490158622
"ER.Golgi.traffic" -0.0155264565216734
"Chrom..seg..kinetoch..spindle.microtub." -0.0310708153407769
"DNA.replication...repair.HR.cohesion" -0.219151127981763
"Chromatin.transcription" -0.232418063465632

```

---

==> 8-yeast\_lc\_boone\_CCA/CCA\_out/yeast\_lc.txt <==

data1: ../CCA\_in/gcv\_list\_matched-to\_indicator\_list.csv

data2: ../CCA\_in/indicator\_list\_matched-to\_gcv\_list.csv

instance-name mismatches: 0

x-transform: (none)

y-transform: (none)

not normalizing x-rows

not normalizing y-rows

scaling X and Y

no weights given, assuming all ones

robust covariance-estimation method: None

instances: 1245

independent variables: 29 (29 before removing zero-variance variables)

dependent variables: 14 (14 before removing zero-variance variables)

regularization type: given

regularization lambda1: 0.001

regularization lambda2: 0.001

canonical correlations: 0.364346353486098, 0.222732183779795, 0.177725185619804,  
0.147228316519833, 0.135506136504788, 0.07263882212047, 0.0594040385010535,  
0.0473100108137332, 0.0353817037766459, 0.0241701346239287, 0.0158033901670125,  
0.0127684243717899, 0.00462442529683922, 4.42407935929931e-12

p-values (asymptotic Wilks): 0.991481808403308, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1

p-values (asymptotic Hotelling): 0.977068242726224, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1

p-values (asymptotic Pillai): 0.997099104532471, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1

---

match 1 :

canonical correlation: 0.364346353486098

canonical root: 0.132748265298617

shared variance X: 0.232935469112896

shared variance Y: 0.0846578280295998

redundancy index X: 0.0309217794512565

redundancy index Y: 0.011238179814878

"x"

"sig\_11" -0.108993021133359

"sig\_20" -0.128827634641015

"sig\_12" -0.132602397049258

"sig\_18" -0.13788260863897

"sig\_13" -0.145220858017979

"sig\_14" -0.145453620426178

"sig\_16" -0.145964790818549

"sig\_15" -0.147117776651623

"sig\_10" -0.147264377436303

"sig\_19" -0.147847728531907

"sig\_9" -0.148712701637112

"sig\_23" -0.152510815485891

"sig\_17" -0.155248068898286

"sig\_24" -0.158023520176441

"sig\_21" -0.160178174770615

"sig\_4" -0.170322453892581

"sig\_25" -0.171051381102332

"sig\_26" -0.171300987313395

"sig\_3" -0.172303285952746

"sig\_22" -0.175482439741081

"sig\_5" -0.177068521486826

"sig\_6" -0.180418166200231

"sig\_27" -0.18404850553849

"sig\_28" -0.191498722532155

"sig\_29" -0.194208317124702

"sig\_7" -0.209302456320386

"sig\_8" -0.218367154575864

"sig\_1" -0.229296955772637

"sig\_2" -0.263039563642853

-----

"x"

"DNA.replication...repair.HR.cohesion" 0.104901909531929

"Golgi.endosome.vacuole.sorting" 0.0989970446915004

"Cell.polarity.morphogenesis" 0.0821743169306519

"Metabolism.mitochondria" 0.0712839282449141

"Signaling.stress.response" 0.0651391942323962

"Protein.folding...glycosylation.cell.wall" 0.0430905486286769

"Protein.degradation.proteosome" 0.0329617267125309

"Cell.cycle.progression.meiosis" 0.0274932246757048

"Ribosome.translation" 0.0262923723476164

"ER.Golgi.traffic" 0.0262415363158927

"Chrom..seg..kinetoch..spindle.microtub." 0.0111831134802526

"Nuclear.cytoplasmic.transport" 0.0063461797663747  
"RNA.processing" -0.020482606895401  
"Chromatin.transcription" -0.352522976691121

---

==> 9-yeast\_y2h\_union\_yu\_ito\_uetz\_boone\_CCA/CCA\_out/yeast\_y2h\_union\_yu\_ito\_uetz.txt  
<==

data1: ../CCA\_in/gcv\_list\_matched-to\_indicator\_list.csv  
data2: ../CCA\_in/indicator\_list\_matched-to\_gcv\_list.csv  
instance-name mismatches: 0  
the following columns had zero variance and were not kept: sig\_18, sig\_19, sig\_20, sig\_22, sig\_24,  
sig\_25, sig\_26, sig\_27, sig\_29  
x-transform: (none)  
y-transform: (none)  
not normalizing x-rows  
not normalizing y-rows  
scaling X and Y  
no weights given, assuming all ones  
robust covariance-estimation method: None  
instances: 1217  
independent variables: 20 (29 before removing zero-variance variables)  
dependent variables: 14 (14 before removing zero-variance variables)  
regularization type: given  
regularization lambda1: 0.001  
regularization lambda2: 0.001  
canonical correlations: 0.149550141688948, 0.139353246579411, 0.113439033199888,  
0.100294568637644, 0.0968547516555907, 0.0700456135387205, 0.0542661457263749,  
0.029036216582858, 0.0156620370452622, 0.0126385244850273, 0.00427848827679673,  
0.000284133230115921, 1.31528718041907e-12, 5.99415906153189e-15  
p-values (asymptotic Wilks): 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1  
p-values (asymptotic Hotelling): 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1  
p-values (asymptotic Pillai): 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1

---

match 1 :  
canonical correlation: 0.149550141688948  
canonical root: 0.0223652448791845  
shared variance X: 0.0698006135730673  
shared variance Y: 0.0773340832648852  
redundancy index X: 0.00156110781527898  
redundancy index Y: 0.0017295957097264  
"x"  
"sig\_16" 0.0480990366969199  
"sig\_15" 0.0472827249457309  
"sig\_10" 0.0472121227336458  
"sig\_9" 0.0470242371232134  
"sig\_3" 0.0462517948495082  
"sig\_5" 0.0427178172642452  
"sig\_11" 0.0375616834081254  
"sig\_4" 0.0270195977318146  
"sig\_13" 0.0223313017420621  
"sig\_8" 0.0131045459667852  
"sig\_12" 0.0131045459667852

"sig\_21" 0.0131045459667852  
 "sig\_23" 0.0131045459667852  
 "sig\_28" 0.0131045459667852  
 "sig\_1" 0.00791297882596256  
 "sig\_7" -0.0355230660421116  
 "sig\_2" -0.0412286025962996  
 "sig\_6" -0.0429641384590762  
 "sig\_17" -0.0511201548035703  
 "sig\_14" -0.0764419155096765  
 -----  
 "x"  
 "Ribosome.translation" 0.0648126557653644  
 "DNA.replication...repair.HR.cohesion" 0.0379432279049965  
 "Metabolism.mitochondria" 0.0282423353443325  
 "Protein.folding...glycosylation.cell.wall" 0.0184544380514178  
 "Protein.degradation.proteosome" 0.0144113833068616  
 "Chromatin.transcription" 0.0104698510144167  
 "Cell.cycle.progression.meiosis" 0.0104661586609085  
 "RNA.processing" 0.00977878601504888  
 "ER.Golgi.traffic" 0.0015763292100546  
 "Signaling.stress.response" 0.00140859589996155  
 "Golgi.endosome.vacuole.sorting" -0.00628212751290403  
 "Chrom..seg..kinetoch..spindle.microtub." -0.0187755252543441  
 "Nuclear.cytoplasmic.transport" -0.0444780694015933  
 "Cell.polarity.morphogenesis" -0.125684759889509

---

==> 10-

**biogrid\_yeast\_ppi\_noYLL039C\_full\_boone\_CCA/CCA\_out/biogrid\_yeast\_ppi\_noYLL039C\_full.txt <==**

data1: ../CCA\_in/gcv\_list\_matched-to\_indicator\_list.csv

data2: ../CCA\_in/indicator\_list\_matched-to\_gcv\_list.csv

instance-name mismatches: 0

x-transform: (none)

y-transform: (none)

not normalizing x-rows

not normalizing y-rows

scaling X and Y

no weights given, assuming all ones

robust covariance-estimation method: None

instances: 3213

independent variables: 29 (29 before removing zero-variance variables)

dependent variables: 14 (14 before removing zero-variance variables)

regularization type: given

regularization lambda1: 0.001

regularization lambda2: 0.001

canonical correlations: 0.45880430741723, 0.334360215431518, 0.1420314043403,  
 0.132113078886416, 0.126037346446307, 0.0858490466766794, 0.0751817045510912,  
 0.0495975179653885, 0.0251233141995856, 0.0202085926434529, 0.00669445592243282,  
 0.00523369061950981, 0.00172734205429482, 2.59750328836361e-12

p-values (asymptotic Wilks): 0, 3.95239396766556e-14, 0.9999925714824, 0.999999999834122, 1,



1, 1, 1, 1, 1, 1, 1, 1, 1

p-values (asymptotic Hotelling): 0, 6.66133814775094e-16, 0.999991294598666,  
0.999999999799288, 1, 1, 1, 1, 1, 1, 1, 1, 1

p-values (asymptotic Pillai): 0, 1.39732669879322e-12, 0.999993443367027, 0.999999999853165,  
1, 1, 1, 1, 1, 1, 1, 1, 1, 1

---

match 1 :

canonical correlation: 0.45880430741723

canonical root: 0.210501392504605

shared variance X: 0.146950744641231

shared variance Y: 0.0793050041353958

redundancy index X: 0.0309333363765677

redundancy index Y: 0.0166938138030842

"x"

"sig\_11" -0.0335008490033594

"sig\_14" -0.0391537348322753

"sig\_10" -0.0409595646198318

"sig\_4" -0.0426056194541177

"sig\_9" -0.0499901600190122

"sig\_16" -0.0545855659016712

"sig\_20" -0.0564132469786062

"sig\_12" -0.0570348147961002

"sig\_17" -0.0668197918344551

"sig\_3" -0.0741528141430949

"sig\_13" -0.0758506944969938

"sig\_22" -0.0836100209712914

"sig\_15" -0.0868136570402509

"sig\_18" -0.1024025656627

"sig\_19" -0.105622260347412

"sig\_1" -0.119007594487353

"sig\_21" -0.128874211571179

"sig\_6" -0.131148971139729

"sig\_23" -0.1450657878404

"sig\_5" -0.172067047001145

"sig\_24" -0.191165208583122

"sig\_25" -0.191580063628038

"sig\_26" -0.253455034820029

"sig\_27" -0.264910205957605

"sig\_7" -0.275508344217967

"sig\_28" -0.289739702115225

"sig\_29" -0.299368501765292

"sig\_8" -0.324296804477194

"sig\_2" -0.345230081760038

-----

"x"

"Metabolism.mitochondria" 0.158613705213679

"Golgi.endosome.vacuole.sorting" 0.0917174364025812

"Protein.folding...glycosylation.cell.wall" 0.0879435513193002

"Cell.polarity.morphogenesis" 0.0780618327851984

"DNA.replication...repair.HR.cohesion" 0.0767868682121237

"Signaling.stress.response" 0.0651268670024973

"ER.Golgi.traffic" 0.0500043262291588

"Chrom..seg..kinetoch..spindle.microtub." 0.0486399094923175  
"Cell.cycle.progression.meiosis" 0.0394419673356677  
"Nuclear.cytoplasmic.transport" -0.0100198222843484  
"Protein.degradation.proteosome" -0.0157390822678899  
"Chromatin.transcription" -0.0283716381202604  
"RNA.processing" -0.240026232630838  
"Ribosome.translation" -0.352812642444517

---

==> 11-biogrid\_yeast\_ppi\_hc\_boone\_CCA/CCA\_out/biogrid\_yeast\_ppi\_hc.txt <==

data1: ../CCA\_in/gcv\_list\_matched-to\_indicator\_list.csv

data2: ../CCA\_in/indicator\_list\_matched-to\_gcv\_list.csv

instance-name mismatches: 0

x-transform: (none)

y-transform: (none)

not normalizing x-rows

not normalizing y-rows

scaling X and Y

no weights given, assuming all ones

robust covariance-estimation method: None

instances: 2574

independent variables: 29 (29 before removing zero-variance variables)

dependent variables: 14 (14 before removing zero-variance variables)

regularization type: given

regularization lambda1: 0.001

regularization lambda2: 0.001

canonical correlations: 0.480627179279578, 0.352528060869427, 0.270443084759021,  
0.151403419086887, 0.0815863199453, 0.0709716081173748, 0.0613185769398159,  
0.0432744905634365, 0.0108699833330386, 0.00878904002122636, 0.00333002191987313,  
0.00202123923726412, 0.00120516810095203, 2.09204692548251e-12

p-values (asymptotic Wilks): 0, 0, 0.849357929016897, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1

p-values (asymptotic Hotelling): 0, 0, 0.780582736787638, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1

p-values (asymptotic Pillai): 0, 4.66293670342566e-15, 0.899189518236576, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1

---

match 1 :

canonical correlation: 0.480627179279578

canonical root: 0.231002485462244

shared variance X: 0.115565674552335

shared variance Y: 0.0801859937736547

redundancy index X: 0.02669595805571

redundancy index Y: 0.0185231638609742

"x"

"sig\_11" -0.0119779378405587

"sig\_4" -0.015018428077976

"sig\_14" -0.0164028680357963

"sig\_10" -0.0278177448848956

"sig\_17" -0.0911416140538267

"sig\_1" -0.113103369651705

"sig\_23" -0.119081755255454

"sig\_12" -0.123726418244095

"sig\_19" -0.127379065608306

"sig\_16" -0.136782050293979  
"sig\_9" -0.137854551520488  
"sig\_18" -0.139816705273713  
"sig\_15" -0.13997096292874  
"sig\_6" -0.146767426703034  
"sig\_20" -0.14789838467656  
"sig\_13" -0.152075171589064  
"sig\_22" -0.156927183812745  
"sig\_21" -0.162365023831832  
"sig\_3" -0.165003498173753  
"sig\_25" -0.167230519879966  
"sig\_24" -0.174202197302304  
"sig\_27" -0.176044279367578  
"sig\_26" -0.184355849663703  
"sig\_28" -0.187954744778803  
"sig\_29" -0.190331258989726  
"sig\_5" -0.195533698267289  
"sig\_7" -0.233129780389112  
"sig\_8" -0.251401123286975  
"sig\_2" -0.322635337534557

-----  
"x"

"Metabolism.mitochondria" 0.170694094856535  
"Cell.polarity.morphogenesis" 0.100732059796327  
"Protein.folding...glycosylation.cell.wall" 0.0946501617805622  
"Golgi.endosome.vacuole.sorting" 0.0875840454530169  
"Signaling.stress.response" 0.0854740180195598  
"DNA.replication...repair.HR.cohesion" 0.0833685291957366  
"ER.Golgi.traffic" 0.0566929205702521  
"Chrom..seg..kinetoch..spindle.microtub." 0.0561706696779016  
"Cell.cycle.progression.meiosis" 0.0439940011223377  
"Nuclear.cytoplasmic.transport" 0.0163091921704493  
"Ribosome.translation" 0.00935415395080078  
"Protein.degradation.proteosome" -0.0579729929892282  
"Chromatin.transcription" -0.246174503929106  
"RNA.processing" -0.357067691021968

---

==> 12-yeast\_apms\_collins\_merin\_CCA/CCA\_out/yeast\_apms\_collins.txt <==

data1: ../CCA\_in/gcv\_list\_matched-to\_indicator\_list.csv

data2: ../CCA\_in/indicator\_list\_matched-to\_gcv\_list.csv

instance-name mismatches: 0

x-transform: (none)

y-transform: (none)

not normalizing x-rows

not normalizing y-rows

scaling X and Y

no weights given, assuming all ones

robust covariance-estimation method: None

instances: 1566

independent variables: 29 (29 before removing zero-variance variables)

dependent variables: 13 (13 before removing zero-variance variables)

regularization type: given  
regularization lambda1: 0.001  
regularization lambda2: 0.001  
canonical correlations: 0.544892162389242, 0.248623359284329, 0.104546658209469,  
0.0698693547090216, 0.0471148670028552, 0.0333416064826747, 0.0171933571928798,  
0.00600785354494836, 0.00136441369687946, 0.00107901236678116, 0.000102163421900291,  
2.13174682863128e-05, 4.44110495008666e-12  
p-values (asymptotic Wilks): 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1  
p-values (asymptotic Hotelling): 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1  
p-values (asymptotic Pillai): 5.06950037504339e-12, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1

---

match 1 :  
canonical correlation: 0.544892162389242  
canonical root: 0.296907468633224  
shared variance X: 0.475784003049143  
shared variance Y: 0.0879401590091665  
redundancy index X: 0.141263823961503  
redundancy index Y: 0.0261100900026148

"x"  
"sig\_9" -0.212026065128185  
"sig\_13" -0.230801706957958  
"sig\_10" -0.235598148946088  
"sig\_11" -0.279105196502028  
"sig\_15" -0.289307378462571  
"sig\_18" -0.290827205805071  
"sig\_12" -0.296789663990839  
"sig\_14" -0.305178733410265  
"sig\_16" -0.306044842814076  
"sig\_3" -0.324791588613672  
"sig\_19" -0.329808702694567  
"sig\_21" -0.340181621625768  
"sig\_17" -0.35616237131605  
"sig\_4" -0.362012160247897  
"sig\_20" -0.363830057895866  
"sig\_23" -0.381028637991733  
"sig\_25" -0.392689647466987  
"sig\_24" -0.392722175847764  
"sig\_22" -0.399912734540233  
"sig\_6" -0.405766539047981  
"sig\_5" -0.411176114515425  
"sig\_27" -0.421748632800405  
"sig\_26" -0.42604088494671  
"sig\_1" -0.44138753874283  
"sig\_28" -0.447632062932571  
"sig\_7" -0.452477516146797  
"sig\_29" -0.476223678139649  
"sig\_8" -0.489675133977061  
"sig\_2" -0.505434908247228

-----  
"x"  
"X.O." 0.104102534665489  
"X.U." 0.100382845116751

"X.D." 0.0948091969757041  
"X.M." 0.0726108674631589  
"X.C." 0.0620774080694442  
"X.E." 0.0579127948652987  
"X.F." 0.0495838871365898  
"X.G." 0.0479167960833334  
"X.B." 0.0423225178542114  
"X.R." 0.0359243057574675  
"X.A." 0.0317350841760096  
"X.T." 0.0213862182416464  
"X.P." -0.542733791212077

---

==> 13-yeast\_biogrid\_genetic\_merin\_CCA/CCA\_out/yeast\_biogrid\_genetic.txt <==

data1: ../CCA\_in/gcv\_list\_matched-to\_indicator\_list.csv

data2: ../CCA\_in/indicator\_list\_matched-to\_gcv\_list.csv

instance-name mismatches: 0

x-transform: (none)

y-transform: (none)

not normalizing x-rows

not normalizing y-rows

scaling X and Y

no weights given, assuming all ones

robust covariance-estimation method: None

instances: 5306

independent variables: 29 (29 before removing zero-variance variables)

dependent variables: 13 (13 before removing zero-variance variables)

regularization type: given

regularization lambda1: 0.001

regularization lambda2: 0.001

canonical correlations: 0.272033583222785, 0.151545030565273, 0.143353396342569,  
0.0957295123246031, 0.0742020946607868, 0.0533581504908864, 0.0421084082690797,  
0.0377036171976486, 0.0246093004448181, 0.0149575309103221, 0.00720608149148486,  
0.0048670268350887, 3.48243532835279e-12

p-values (asymptotic Wilks): 0, 0.327797991346335, 0.999407290025711, 1, 1, 1, 1, 1, 1, 1, 1, 1

p-values (asymptotic Hotelling): 0, 0.306213621685667, 0.999312037519998, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1

p-values (asymptotic Pillai): 0, 0.349104759346362, 0.999482711575819, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1

---

match 1 :

canonical correlation: 0.272033583222785

canonical root: 0.0740022704010281

shared variance X: 0.163378333096137

shared variance Y: 0.0853314337854258

redundancy index X: 0.0120903675834496

redundancy index Y: 0.0063147198366965

"x"

"sig\_11" -0.00262967437205441

"sig\_14" -0.049311983082273

"sig\_4" -0.0532704055501834

"sig\_10" -0.0661533890570665

"sig\_9" -0.0709213361309097

"sig\_16" -0.0817144586609401  
"sig\_13" -0.0826254910595178  
"sig\_12" -0.0826629883438993  
"sig\_15" -0.083645913176941  
"sig\_17" -0.0878194977298463  
"sig\_18" -0.0883148566712501  
"sig\_20" -0.0933259098836352  
"sig\_21" -0.0946893386974427  
"sig\_19" -0.0956845849871249  
"sig\_22" -0.0984154578224395  
"sig\_3" -0.0999574016325162  
"sig\_24" -0.10265213928342  
"sig\_23" -0.104862635721159  
"sig\_25" -0.105627025872295  
"sig\_26" -0.112657685307225  
"sig\_27" -0.112857047086288  
"sig\_6" -0.114758351718993  
"sig\_5" -0.116591822398335  
"sig\_28" -0.122173047915417  
"sig\_7" -0.130978854128145  
"sig\_29" -0.134457286738909  
"sig\_1" -0.13664395479534  
"sig\_8" -0.147618530225976  
"sig\_2" -0.16768767702374

-----

"x"  
"X.U." 0.11238104942241  
"X.P." 0.0779337721788811  
"X.M." 0.0631428348998701  
"X.A." 0.0616085892988108  
"X.E." 0.0492631627666717  
"X.G." 0.0434931069938828  
"X.R." 0.0241704427706144  
"X.C." -0.0209318025847434  
"X.T." -0.0345589434654708  
"X.F." -0.0487092477178982  
"X.O." -0.0576520263604394  
"X.B." -0.1535634256477  
"X.D." -0.177386436699251

---

==> 14-yeast\_lc\_merin\_CCA/CCA\_out/yeast\_lc.txt <==

data1: ../CCA\_in/gcv\_list\_matched-to\_indicator\_list.csv

data2: ../CCA\_in/indicator\_list\_matched-to\_gcv\_list.csv

instance-name mismatches: 0

x-transform: (none)

y-transform: (none)

not normalizing x-rows

not normalizing y-rows

scaling X and Y

no weights given, assuming all ones

robust covariance-estimation method: None

instances: 1470  
independent variables: 29 (29 before removing zero-variance variables)  
dependent variables: 13 (13 before removing zero-variance variables)  
regularization type: given  
regularization lambda1: 0.001  
regularization lambda2: 0.001  
canonical correlations: 0.307324015965059, 0.2489499357079, 0.159516475924923,  
0.107485590940243, 0.0922502851579473, 0.0853852905632663, 0.0517908772834508,  
0.0341995451392947, 0.00660235146659546, 0.00150713103171687, 0.000849291997972973,  
5.64387302637781e-12, 1.21655306015563e-14  
p-values (asymptotic Wilks): 0.986410994510114, 0.999999999999983, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1  
p-values (asymptotic Hotelling): 0.973807772472913, 0.999999999999955, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1  
1, 1  
p-values (asymptotic Pillai): 0.993286915760317, 0.999999999999993, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1

---

match 1 :

canonical correlation: 0.307324015965059  
canonical root: 0.0944480507888919  
shared variance X: 0.296019620177441  
shared variance Y: 0.0846155921345776  
redundancy index X: 0.0279584761210275  
redundancy index Y: 0.00799177774345874

"x"

"sig\_20" -0.047851955591882  
"sig\_25" -0.085355592771275  
"sig\_16" -0.0856485945427644  
"sig\_5" -0.0925643874794808  
"sig\_11" -0.102036757939423  
"sig\_9" -0.103603681604107  
"sig\_10" -0.119489758473192  
"sig\_21" -0.122162301380042  
"sig\_12" -0.139952475895602  
"sig\_15" -0.144153129545997  
"sig\_3" -0.146888944668942  
"sig\_4" -0.149318581796754  
"sig\_13" -0.150073656921049  
"sig\_14" -0.157360390930831  
"sig\_27" -0.158984633255244  
"sig\_18" -0.160467685253807  
"sig\_19" -0.16407390997288  
"sig\_17" -0.168895069933171  
"sig\_22" -0.169339631166878  
"sig\_23" -0.175851384270726  
"sig\_24" -0.181701922100155  
"sig\_6" -0.183251209163566  
"sig\_1" -0.188263282264305  
"sig\_26" -0.189472954420694  
"sig\_7" -0.207124202472284  
"sig\_28" -0.21300370950767  
"sig\_29" -0.237852537805593  
"sig\_8" -0.243756847429461  
"sig\_2" -0.250266654303811

-----

"x"

"X.O." 0.0581923874636994

"X.C." 0.0486892433589521

"X.U." 0.046181143341328

"X.D." 0.0414279415789849

"X.F." 0.0362820011498663

"X.M." 0.0331857327369195

"X.A." 0.027089480818006

"X.R." 0.0245530973707528

"X.E." 0.0238625278905134

"X.P." 0.0195269537249107

"X.G." 0.00749958829079788

"X.T." -0.0203896260157444

"X.B." -0.306066369274566

---

==> 15-

**yeast\_y2h\_union\_yu\_ito\_uetz\_merin\_CCA/CCA\_out/yeast\_y2h\_union\_yu\_ito\_uetz.txt <==**

data1: ../CCA\_in/gcv\_list\_matched-to\_indicator\_list.csv

data2: ../CCA\_in/indicator\_list\_matched-to\_gcv\_list.csv

instance-name mismatches: 0

the following columns had zero variance and were not kept: sig\_18, sig\_20, sig\_24, sig\_25, sig\_27, sig\_29

x-transform: (none)

y-transform: (none)

not normalizing x-rows

not normalizing y-rows

scaling X and Y

no weights given, assuming all ones

robust covariance-estimation method: None

instances: 1882

independent variables: 23 (29 before removing zero-variance variables)

dependent variables: 13 (13 before removing zero-variance variables)

regularization type: given

regularization lambda1: 0.001

regularization lambda2: 0.001

canonical correlations: 0.277917235737594, 0.147002910498568, 0.130954816572809, 0.118435857542706, 0.105555454551125, 0.0953840769058755, 0.0901096376315554, 0.0556458216027103, 0.0314111649575372, 0.0240863598173141, 0.0100419312658175, 1.17959361364341e-12, 1.04708723308737e-14

p-values (asymptotic Wilks): 0.30609433415624, 0.999999905073447, 0.99999999830097, 0.9999999999613, 0.99999999999999, 1, 1, 1, 1, 1, 1, 1, 1

p-values (asymptotic Hotelling): 0.251354517566798, 0.999999902026883, 0.99999999824196, 0.99999999999596, 0.99999999999999, 1, 1, 1, 1, 1, 1, 1, 1

p-values (asymptotic Pillai): 0.363840945358908, 0.999999904586385, 0.99999999821541, 0.99999999999577, 0.99999999999999, 1, 1, 1, 1, 1, 1, 1, 1

---

match 1 :

canonical correlation: 0.277917235737594

canonical root: 0.0772379899200252

shared variance X: 0.142087079317262



shared variance Y: 0.0793639216288315  
redundancy index X: 0.0109745204000725  
redundancy index Y: 0.00612990977878135

"x"

"sig\_15" 0.00623989460300872  
"sig\_11" 0.0056314041540578  
"sig\_9" 0.00559562366615487  
"sig\_10" 0.00439336888191989  
"sig\_4" 0.00379509773565555  
"sig\_16" -0.00210153054397247  
"sig\_3" -0.00545584295940676  
"sig\_1" -0.0159918222121736  
"sig\_14" -0.0176064089210684  
"sig\_5" -0.0558392072569607  
"sig\_22" -0.0780529189493939  
"sig\_26" -0.0780529189493939  
"sig\_13" -0.111454352532523  
"sig\_7" -0.111559563838091  
"sig\_17" -0.118025022547727  
"sig\_19" -0.125698887852185  
"sig\_6" -0.126013421289528  
"sig\_12" -0.135517854535312  
"sig\_28" -0.138089167258585  
"sig\_21" -0.14083827874911  
"sig\_2" -0.178238659152607  
"sig\_23" -0.188103906736545  
"sig\_8" -0.196718012242962

-----

"x"

"X.U." 0.031217103728973  
"X.D." 0.0198221461062847  
"X.F." 0.0191019160572502  
"X.B." 0.0157866958247049  
"X.T." 0.014949975345475  
"X.O." 0.0143429343749548  
"X.C." 0.0109719552806429  
"X.P." 0.00832644895625454  
"X.E." 0.00538842617952655  
"X.G." 0.00516641466244076  
"X.A." 0.0051432199076593  
"X.M." 0.00250387767575605  
"X.R." -0.279451613238666

---

==> 16-

**biogrid\_yeast\_ppi\_noYLL039C\_full\_merin\_CCA/CCA\_out/biogrid\_yeast\_ppi\_noYLL039C\_full.txt** <==

data1: ../CCA\_in/gcv\_list\_matched-to\_indicator\_list.csv

data2: ../CCA\_in/indicator\_list\_matched-to\_gcv\_list.csv

instance-name mismatches: 0

x-transform: (none)

y-transform: (none)

not normalizing x-rows  
not normalizing y-rows  
scaling X and Y  
no weights given, assuming all ones  
robust covariance-estimation method: None  
instances: 5426  
independent variables: 29 (29 before removing zero-variance variables)  
dependent variables: 13 (13 before removing zero-variance variables)  
regularization type: given  
regularization lambda1: 0.001  
regularization lambda2: 0.001  
canonical correlations: 0.457793640216691, 0.2595970297473, 0.133669128165249,  
0.100625895821383, 0.0661686496315145, 0.0353136085033062, 0.0228192325479487,  
0.0159208153631233, 0.013363879119108, 0.00304678279056754, 0.00201204048964762,  
0.000800193678138186, 4.59461642728709e-12  
p-values (asymptotic Wilks): 0, 6.77236045021345e-14, 0.99999986626606, 1, 1, 1, 1, 1, 1, 1, 1,  
1  
p-values (asymptotic Hotelling): 0, 5.99520433297585e-15, 0.999999832606628, 1, 1, 1, 1, 1, 1, 1,  
1, 1, 1  
p-values (asymptotic Pillai): 0, 6.56585896763318e-13, 0.999999891170033, 1, 1, 1, 1, 1, 1, 1, 1,  
1

---

match 1 :

canonical correlation: 0.457793640216691  
canonical root: 0.209575017022849  
shared variance X: 0.187906774072764  
shared variance Y: 0.0831806542246869  
redundancy index X: 0.0393805653750081  
redundancy index Y: 0.0174325870251104

"x"

"sig\_10" -0.0326993725861056  
"sig\_11" -0.0359054072208462  
"sig\_14" -0.0384362519219121  
"sig\_4" -0.0387024997873069  
"sig\_9" -0.0389688289892214  
"sig\_12" -0.0527216984724671  
"sig\_16" -0.0531995931183881  
"sig\_20" -0.0639653777585132  
"sig\_3" -0.0652846004609765  
"sig\_17" -0.0666187224384383  
"sig\_13" -0.0735321755632051  
"sig\_22" -0.0813254193954455  
"sig\_15" -0.0831442185666287  
"sig\_18" -0.102397710589111  
"sig\_1" -0.112988145193408  
"sig\_19" -0.120262489929942  
"sig\_6" -0.135762040204614  
"sig\_21" -0.138437674464701  
"sig\_23" -0.17370013773394  
"sig\_5" -0.184341882559055  
"sig\_24" -0.213680407711576  
"sig\_25" -0.223800795369718

"sig\_26" -0.296035205302833  
 "sig\_7" -0.305690787155944  
 "sig\_27" -0.310887976184902  
 "sig\_28" -0.348435706498005  
 "sig\_2" -0.370431421774572  
 "sig\_29" -0.370990452689801  
 "sig\_8" -0.378489823251369

"X"  
 "X.U." 0.10778056797161  
 "X.M." 0.0761545516265312  
 "X.A." 0.0543393225353614  
 "X.E." 0.0400743387252687  
 "X.G." 0.0361501849555575  
 "X.R." 0.0349808309292134  
 "X.O." 0.0343116092017051  
 "X.C." 0.0338535923109098  
 "X.D." 0.0283799223527677  
 "X.F." 0.0276252683425219  
 "X.B." 0.0139298396422311  
 "X.T." -0.117212944705058  
 "X.P." -0.440679219008082

```
==> 17-biogrid_yeast_ppi_hc_merin_CCA/CCA_out/biogrid_yeast_ppi_hc.txt <==
```

```
data1: ../CCA_in/gcv_list_matched-to_indicator_list.csv
```

instance-name mismatches: 0

x-transform: (none)

y-transform: (none)

not normalizing x-rows

not normalizing y-rows

scaling X and Y

no weights given, assuming all ones

robust covariance-estimation method: None

instances: 3739

independent variables: 29 (29 before removing zero-variance variables)

dependent variables: 13 (13 before removing zero-variance variables)

regularization type: given

regularization lambda1: 0.001

regularization lambda2: 0.001

canonical correlations: 0.424493771565584, 0.233628261267086, 0.190279076195741,

0.10686030130993, 0.076884435076271, 0.0566560857280131, 0.045671531187661,

0.0292231671607533, 0.00374647602928837, 0.00289244317377023, 0.0017142604652321,

0.00137115740152111, 2.87395925446758e-12

p-values (asymptotic Wilks): 0, 0.000260974852365647, 0.999353801619981, 1, 1, 1, 1, 1, 1, 1, 1,

 $1, 1$ 

p-values (asymptotic Hotelling): 0, 0.000122849269693415, 0.999092856011398, 1, 1, 1, 1, 1, 1, 1,

1, 1, 1

p-values (asymptotic Pillai): 0, 0.000523929849900573, 0.999532961060552, 1, 1, 1, 1, 1, 1, 1,

$$1, 1$$

match 1 :  
canonical correlation: 0.424493771565584  
canonical root: 0.180194962097974  
shared variance X: 0.0352451644086494  
shared variance Y: 0.0840577489844797  
redundancy index X: 0.00635100106475346  
redundancy index Y: 0.0151467828922994

"x"

"sig\_11" 0.00615470207634573  
"sig\_4" 0.00504623777854404  
"sig\_14" 0.00442874775308286  
"sig\_10" 0.00384959851621533  
"sig\_9" 0.00131980902054059  
"sig\_16" 0.000254687723151294  
"sig\_20" -0.000286593984447435  
"sig\_12" -0.00999888477920179  
"sig\_3" -0.0113237855573394  
"sig\_15" -0.0128471431399962  
"sig\_13" -0.0178707390058732  
"sig\_17" -0.0230687440709742  
"sig\_1" -0.0329380822531339  
"sig\_23" -0.0430387257478965  
"sig\_19" -0.04477162249344  
"sig\_6" -0.0525594098676211  
"sig\_21" -0.0564164462738961  
"sig\_5" -0.0595007916680764  
"sig\_25" -0.0638289751081469  
"sig\_18" -0.0704245522899768  
"sig\_27" -0.0772483273862045  
"sig\_22" -0.0779804456040846  
"sig\_24" -0.0917841286862702  
"sig\_26" -0.100009929766389  
"sig\_28" -0.10302660841484  
"sig\_29" -0.11273512738831  
"sig\_7" -0.139579432212895  
"sig\_8" -0.165033816607569  
"sig\_2" -0.223518564656672

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"x"

"X.M." 0.0999257313876536  
"X.A." 0.0719525568889254  
"X.E." 0.0670675726211212  
"X.U." 0.0663773428590805  
"X.C." 0.0595699379699463  
"X.G." 0.0553090173486339  
"X.R." 0.0432099270423182  
"X.O." 0.0387730721041148  
"X.F." 0.0351355962557362  
"X.D." 0.00375552637924399  
"X.P." 0.0036170242868089  
"X.B." -0.080911133899033  
"X.T." -0.407239925520341

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