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    { name: 'CIN5' }, { name: 'GCR2' },
    { name: 'GLN3' }, { name: 'HAP4' },
    { name: 'HMO1' }, { name: 'MSN2' },
    { name: 'SFP1' }, { name: 'STB5' },
    { name: 'SWI4' }, { name: 'SWI5' },
    { name: 'YHP1' }, { name: 'YOX1' },
    { name: 'ZAP1' }
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      value: 1,
      type: 'arrowhead',
      stroke: 'black'
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      target: 1,
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      type: 'arrowhead',
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    {
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{  
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target: 12,
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{
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value: 1,
type: 'arrowhead',
stroke: 'black'
}
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errors: [
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errorCode: 'INVALID_GENE_TYPE',
possibleCause: "Gene 'undefined' in row 17, column A in the production_rates sheet is not a string.",
suggestedFix: 'Please make your gene name a string starting with a letter.'
},
{
errorCode: 'INVALID_GENE_TYPE',
possibleCause: "Gene 'undefined' in row 18, column A in the production_rates sheet is not a string.",
```

```
suggestedFix: 'Please make your gene name a string starting with a letter.'
},
{
  errorCode: 'INVALID_GENE_TYPE',
  possibleCause: "Gene 'undefined' in row 19, column A in the production_rates sheet is
not a string.",
  suggestedFix: 'Please make your gene name a string starting with a letter.'
},
{
  errorCode: 'INVALID_GENE_TYPE',
  possibleCause: "Gene 'undefined' in row 20, column A in the production_rates sheet is
not a string.",
  suggestedFix: 'Please make your gene name a string starting with a letter.'
},
{
  errorCode: 'INVALID_GENE_TYPE',
  possibleCause: "Gene 'undefined' in row 21, column A in the production_rates sheet is
not a string.",
  suggestedFix: 'Please make your gene name a string starting with a letter.'
},
{
  errorCode: 'INVALID_GENE_TYPE',
  possibleCause: "Gene 'undefined' in row 22, column A in the production_rates sheet is
not a string.",
  suggestedFix: 'Please make your gene name a string starting with a letter.'
},
{
  errorCode: 'INVALID_GENE_TYPE',
  possibleCause: "Gene 'undefined' in row 23, column A in the production_rates sheet is
not a string.",
  suggestedFix: 'Please make your gene name a string starting with a letter.'
},
{
  errorCode: 'INVALID_GENE_TYPE',
  possibleCause: "Gene 'undefined' in row 24, column A in the production_rates sheet is
not a string.",
  suggestedFix: 'Please make your gene name a string starting with a letter.'
},
{
  errorCode: 'INVALID_GENE_TYPE',
  possibleCause: "Gene 'undefined' in row 25, column A in the production_rates sheet is
not a string.",
  suggestedFix: 'Please make your gene name a string starting with a letter.'
},
}
```

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{
  errorCode: 'INVALID_GENE_TYPE',
  possibleCause: "Gene 'undefined' in row 26, column A in the production_rates sheet is
not a string.",
  suggestedFix: 'Please make your gene name a string starting with a letter.'
},
{
  errorCode: 'INVALID_GENE_TYPE',
  possibleCause: "Gene 'undefined' in row 27, column A in the production_rates sheet is
not a string.",
  suggestedFix: 'Please make your gene name a string starting with a letter.'
},
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  errorCode: 'INVALID_GENE_TYPE',
  possibleCause: "Gene 'undefined' in row 28, column A in the production_rates sheet is
not a string.",
  suggestedFix: 'Please make your gene name a string starting with a letter.'
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  errorCode: 'INVALID_GENE_TYPE',
  possibleCause: "Gene 'undefined' in row 29, column A in the production_rates sheet is
not a string.",
  suggestedFix: 'Please make your gene name a string starting with a letter.'
},
{
  errorCode: 'INVALID_GENE_TYPE',
  possibleCause: "Gene 'undefined' in row 30, column A in the production_rates sheet is
not a string.",
  suggestedFix: 'Please make your gene name a string starting with a letter.'
},
{
  errorCode: 'INVALID_GENE_TYPE',
  possibleCause: "Gene 'undefined' in row 31, column A in the production_rates sheet is
not a string.",
  suggestedFix: 'Please make your gene name a string starting with a letter.'
},
{
  errorCode: 'INVALID_GENE_TYPE',
  possibleCause: "Gene 'undefined' in row 32, column A in the production_rates sheet is
not a string.",
  suggestedFix: 'Please make your gene name a string starting with a letter.'
},
{
  errorCode: 'INVALID_GENE_TYPE',
```

possibleCause: "Gene 'undefined' in row 33, column A in the production_rates sheet is not a string.",

suggestedFix: 'Please make your gene name a string starting with a letter.'

},

{

errorCode: 'INVALID_GENE_TYPE',

possibleCause: "Gene 'undefined' in row 34, column A in the production_rates sheet is not a string.",

suggestedFix: 'Please make your gene name a string starting with a letter.'

},

{

errorCode: 'INVALID_GENE_TYPE',

possibleCause: "Gene 'undefined' in row 35, column A in the production_rates sheet is not a string.",

suggestedFix: 'Please make your gene name a string starting with a letter.'

},

{

errorCode: 'INVALID_GENE_TYPE',

possibleCause: "Gene 'undefined' in row 36, column A in the production_rates sheet is not a string.",

suggestedFix: 'Please make your gene name a string starting with a letter.'

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errorCode: 'ERRORS_OVERLOAD',

possibleCause: 'This workbook has over 20 errors.',

suggestedFix: 'Please check the format of your spreadsheet with the guidelines outlined on theDocumentation page and try again. If you fix these errors and try to upload again, there may be further errors detected. As a general approach for fixing the errors, consider copying and pasting just your adjacency matrix into a fresh Excel Workbook and saving it.'

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    errorCode: 'ERRORS_OVERLOAD',
    possibleCause: 'This workbook has over 20 errors.',
    suggestedFix: 'Please check the format of your spreadsheet with the guidelines outlined
on theDocumentation page and try again. If you fix these errors and try to upload again, there
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    1, 1, 1, 1, 1, 1, 1, 1, 1,
    1, 1, 1, 1
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  sheetType: 'unweighted',
  meta: {
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      MaxIter: 100000000,
      TolFun: 0.000001,
      MaxFunEval: 100000000,
      TolX: 0.000001,
      production_function: 'Sigmoid',
      L_curve: 0,
      estimate_params: 1,
      make_graphs: 1,
      fix_P: 0,
      fix_b: 0,
      expression_timepoints: [ 15, 30, 60 ],
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      simulation_timepoints: [
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        30, 35, 40, 45, 50, 55,
        60
      ],
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      taxon_id: 559292
    },
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  },
  expression: {
    wt_log2_expression: {
      errors: [],
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  30, 30, 30, 60, 60, 60,
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  'HMO1', 'MSN2', 'SFP1',
  'STB5', 'SWI4', 'SWI5',
  'YHP1', 'YOX1', 'ZAP1'
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    30, 30, 30, 60, 60, 60,
    60
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    0.1906, -0.398,
    0.5827, <1 empty item>,
    -0.3947, -0.6264,
    0.3377, 0.817,
    0.5566, -0.4357,
    -1.2497
  ],
  ASH1: [
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    -0.9904, -0.2636,
    -0.382, 0.4206,
    -0.4911, -0.1284,
    -0.7236, -1.3477,
    -1.0468, -1.0978,
    -0.9248
  ],
  CIN5: [
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    1.3909, -0.4224, 0.5461,
    1.0285, 1.2338, 2.2159,
    2.1796, 0.8447, 2.4687,
    1.4785
  ],
}
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-0.2982, -0.315,
-0.5999, -0.9447,
-0.3585
],
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-0.5133, -0.7004, -0.2467,
1.4085, 0.9733, 0.6504,
0.2025, 0.8924, 0.9007,
0.1953
],
HAP4: [
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0.138, 1.5184,
0.2794, -2.5135,
-1.1181, 0.2225,
-1.0353, -0.2074,
-1.8463
],
HMO1: [
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1.2493, -0.9525, 1.405,
1.3109, 1.2569, 1.9007,
1.4816, 0.938, 1.8391,
2.2172
],
MSN2: [
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-0.1271
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SFP1: [
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1.3828, 0.9004, 0.8888,

-1.0367
],
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0.0407, -1.3691,
-2.6627, 0.2028,
-0.2748
],
SWI4: [
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-0.4798, 0.2047,
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0.2812
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SWI5: [
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-1.0667, 0.1028,
-0.0286, 0.4798,
0.097
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-1.6964, -0.3496, 1.2371,
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-0.725
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YOX1: [
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-0.6402, -2.2532,
-0.083, -1.6117,
-0.104, -0.1487,
-0.9394, -0.5901,
0.1329, -0.7222,
-0.5117

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ZAP1: [
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]
}
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warnings: [],
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60, 60
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'GCR2', 'GLN3', 'HAP4',
'HMO1', 'MSN2', 'SFP1',
'STB5', 'SWI4', 'SWI5',
'YHP1', 'YOX1', 'ZAP1'
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data: {
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30, 30, 30, 60, 60,
60, 60
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0.5682, 0.1646,
-0.3202, -0.3888
],
ASH1: [
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-2.2704, -1.0939,
-1.3098, -1.017,
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-1.7106, -1.7777,
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CIN5: [
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0.0805, 0.4778
],
GCR2: [
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],
GLN3: [
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0.3101, -0.1589,
0.5869, 0.0341,
0.486, 0.4342,
1.0717, 0.0559,
1.1548, 0.5446
],
HAP4: [
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-1.2318, -0.1403,
-1.9814, -1.2117
],
HMO1: [
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1.5911, 1.2566,
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0.9466, 1.4665
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MSN2: [

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0.4011, 0.0603

],

SFP1: [

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0.61, 0.6721,

0.9582, 0.3127

],

STB5: [

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SWI4: [

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0.092, 0.2312

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SWI5: [

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0.0663, -0.4419,

0.9222, 0.209

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-1.3987, 0.2985
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ZAP1: [
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0.3113, -0.0906,
0.9699, -0.0441
]
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60, 60
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0.4404, -0.1933

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ASH1: [

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0.9089, -0.5136,
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],

CIN5: [

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1.3996, 1.9426, 0.2912,
0.6282, 3.2391, 2.5788

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GCR2: [

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0.7045, 0.7673

],

GLN3: [

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0.1085, -0.446,
0.8018, -0.161

],

HAP4: [

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1.2426, 1.4451,
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-0.2976, 0.2256

],

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1.3433, 0.9501,  
1.5648, 1.7134  
],  
MSN2: [  
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0.9656, 0.1669,  
0.9394, 0.6417,  
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0.7794, -0.287  
],  
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0.3564, 1.0391
],
YOX1: [
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0.9253,      1.2979
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-1.0852,      null
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'GCR2', 'GLN3', 'HAP4',
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'YHP1', 'YOX1', 'ZAP1'
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data: {
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60, 60
],
ACE2: [
-0.558, -0.313,
-0.0886, 0.5674,
-0.448, -0.4768,
-0.598, -0.1176,
-0.2783, -0.6083,
-0.6331, 0.1985
],
ASH1: [
-1.5401, -0.0523,
-0.7026, -0.4933,
-0.8167, -0.0028,
-0.6568, -1.0267,
-1.9867, -1.5253,
-1.0837, -1.5982
],
CIN5: [
-0.3943, 3.098,
-0.7818, 0.5366,
1.0477, 1.9388,
1.9985, 1.948,
2.8678, 3.26,
2.2513, 1.9187
],
GCR2: [
1.5094, 0.4057,
0.5999, 1.291,
1.5787, -0.5042,
1.659, 1.728,
0.4889, -0.2991,
0.9863, 0.9578
],
GLN3: [
-0.4169, 0.6492,
-0.1259, 0.7149,
0.0457, 0.2932,
-0.3901, 0.2321,
```

0.9238, 0.3174,
-0.0252, 1.0246
],
HAP4: [
0.4102, -0.9203,
0.3786, -0.8169,
0.0301, -1.4462,
-0.3025, -0.3727,
-0.2195, -1.1639,
0.2619, -0.5285
],
HMO1: [
2.9631, 0.0054,
1.0227, -1.8079,
2.6496, 1.8897,
1.3275, -2.4363,
1.3018, -0.2604,
2.3205, -0.2676
],
MSN2: [
0.8346, 0.5458,
-0.4035, 0.5827,
1.0075, 0.8038,
1.1451, 0.6532,
1.4213, 0.7549,
0.3324, 0.3404
],
SFP1: [
0.475, 0.8935,
0.0344, 0.9253,
-0.2822, 0.8125,
0.4466, 0.3866,
-0.1762, 0.4906,
0.4941, 0.4523
],
STB5: [
-0.1941, -0.1977,
0.3222, <1 empty item>,
0.4058, -0.84,
0.4143, <2 empty items>,
-0.1119, 0.4121,
0.1617
],
SWI4: [

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0.857, 0.3944,
-0.0101, -0.8563,
-0.1573, -0.1339,
-0.1171, <1 empty item>,
0.3775, 0.4539,
0.3331, 0.2096
],
SWI5: [
<1 empty item>, 0.1491,
-0.9615,      0.6945,
-1.177,      0.155,
-1.3155,     -0.1184,
-1.0331,     0.07,
-0.7403,     0.728
],
YHP1: [
-0.8778, -0.5421,
-1.4449, -0.6419,
-0.986, -0.0224,
-0.4459, -0.1383,
0.9324, 1.2889,
0.6571, 0.9774
],
YOX1: [
-1.7099, -1.3898,
-2.1356, -1.6842,
-0.1238, -1.0174,
0.37, -1.6723,
-0.259, -0.2008,
-1.5284, -1.0413
],
ZAP1: [
-1.903, <1 empty item>,
1.5545, -0.0849,
-0.6127, 1.2343,
-0.5888, -0.8746,
-0.8822, 0.6754,
-0.7341, -0.5958
]
}
},
dhmo1_log2_expression: {
errors: [],
warnings: [],
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timePoints: [  
  15, 15, 15, 15, 30,  
  30, 30, 30, 60, 60,  
  60, 60  
],  
columnGeneNames: [  
  'ACE2', 'ASH1', 'CIN5',  
  'GCR2', 'GLN3', 'HAP4',  
  'HMO1', 'MSN2', 'SFP1',  
  'STB5', 'SWI4', 'SWI5',  
  'YHP1', 'YOX1', 'ZAP1'  
],  
data: {  
  id: [  
    15, 15, 15, 15, 30,  
    30, 30, 30, 60, 60,  
    60, 60  
  ],  
  ACE2: [  
    0.2392, -0.3695,  
    -1.0907, 0.1755,  
    0.527, -0.1989,  
    -0.9593, -0.2329,  
    0.0175, -0.4998,  
    -0.2991, -0.2388  
  ],  
  ASH1: [  
    0.2718, 1.0969,  
    0.0825, -0.4366,  
    -2.2907, 0.5026,  
    -0.2715, -0.5741,  
    -1.5159, 0.4211,  
    1.7901, -0.8754  
  ],  
  CIN5: [  
    0.6239, 0.8184,  
    1.4916, -0.8397,  
    0.8867, 1.2387,  
    2.2606, 0.3293,  
    1.2067, 1.7983,  
    -0.7066, 1.0148  
  ],  
  GCR2: [  
    -0.5316, -0.2221,
```

1.0726, -0.9918,
0.3892, 0.3353,
-0.2957, -0.4503,
0.2892, 1.2637,
0.0502, -0.8057

],

GLN3: [

-0.3938, 0.0786,
-0.9799, 0.3603,
-0.5682, -0.0728,
-0.186, 0.6306,
0.2917, -0.1706,
0.2925, 0.8914

],

HAP4: [

0.2944, -1.0325,
-0.3442, 0.8937,
-1.578, -1.4498,
-0.7384, -0.2666,
-1.5417, -3.0545,
1.8973, -0.8844

],

HMO1: [

1.0058, -0.0317,
2.0181, 0.7888,
-0.2066, 0.3846,
0.0914, 0.1787,
0.1767, 0.4898,
0.8354, 0.4644

],

MSN2: [

-0.3229, -0.3717,
-0.8013, 0.4516,
-0.3778, -0.3248,
-0.4761, 0.9505,
-0.2303, -0.5603,
1.2227, 0.5789

],

SFP1: [

1.2329, 2.2441,
0.4948, -0.6945,
-0.8346, 1.8561,
-0.5287, -0.6066,
0.9984, 1.3966,

-0.1514, -0.5851
],
STB5: [
1.5366, 0.5574,
<2 empty items>, 0.297,
0.1843, 0.1582,
<1 empty item>, 1.7097,
0.6198, null,
null
],
SWI4: [
0.5249, 0.1762,
-0.1695, 0.3361,
1.0117, -0.5471,
-0.1491, 0.2608,
0.7408, -0.5783,
0.4557, 0.5229
],
SWI5: [
-1.5273, -0.0479,
-0.4886, -0.0472,
-0.3741, -0.8655,
-1.1639, -0.2628,
-0.6299, 0.0682,
0.3035, -0.5416
],
YHP1: [
-0.182, -1.0702,
-0.8447, -1.0068,
0.1177, -0.3511,
0.0224, -0.6165,
0.7703, -1.1442,
-0.8058, 0.1403
],
YOX1: [
-2.4929, -0.4533,
-0.2265, -1.1137,
-0.9117, -0.248,
-0.0783, -1.7543,
-0.7781, -0.3231,
0.2596, -2.0924
],
ZAP1: [
-0.2308, -0.3917,

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-1.0017, 0.1766,  
0.0117, 0.1751,  
-0.9756, -0.5304,  
0.4411, -0.709,  
-0.0099, 0.8415  
]  
}  
},  
dzap1_log2_expression: {  
errors: [],  
warnings: [],  
timePoints: [  
15, 15, 15, 15, 30,  
30, 30, 30, 60, 60,  
60, 60  
],  
columnGeneNames: [  
'ACE2', 'ASH1', 'CIN5',  
'GCR2', 'GLN3', 'HAP4',  
'HMO1', 'MSN2', 'SFP1',  
'STB5', 'SWI4', 'SWI5',  
'YHP1', 'YOX1', 'ZAP1'  
],  
data: {  
id: [  
15, 15, 15, 15, 30,  
30, 30, 30, 60, 60,  
60, 60  
],  
ACE2: [  
-0.2778, -0.804,  
-0.3835, 0.328,  
-0.6418, -0.8003,  
-3.4693, -1.458,  
0.2762, -0.7411,  
-1.2214, -0.5369  
],  
ASH1: [  
1.3934, -0.5424,  
0.2105, 2.8875,  
0.6473, -0.8143,  
0.2084, -0.8951,  
-0.0794, -1.7999,  
-0.441, -1.2416
```


],
CIN5: [
<1 empty item>, 2.4162,
1.1741, 0.7413,
1.7565, 2.5972,
0.8693, 2.4257,
1.5716, 3.7502,
2.3832, 2.675

],
GCR2: [
0.6693, 0.4593,
-0.1973, 1.153,
-0.1936, 0.3101,
0.9935, 0.3293,
0.2218, -0.2001,
0.8909, 0.6109

],
GLN3: [
0.4944, 0.6415,
-0.1257, 0.9388,
0.6684, 0.4256,
0.198, 0.5877,
0.5854, 0.178,
0.0267, 1.0084

],
HAP4: [
0.9889, 1.6616,
0.5464, 1.3427,
0.0359, -0.3139,
0.246, -1.816,
-0.1356, -0.6358,
-0.2169, -1.1214

],
HMO1: [
0.3519, 1.4939, 2.1933,
0.7561, 0.3961, 1.6777,
1.8124, 0.7252, 1.168,
2.1741, 2.2209, 2.0417

],
MSN2: [
-0.1455, 0.7077,
-0.3519, 0.9785,
1.0745, 0.5327,
0.5032, 1.0997,

1.1006, 0.4626,
-0.2581, 0.848
],
SFP1: [
0.5518, 0.6949,
0.4098, 0.5577,
0.82, 1.0041,
1.372, 1.4371,
-0.6863, 0.0001,
0.3495, 0.5506
],
STB5: [
0.3316, -3.3906,
0.8183, -0.0735,
-0.161, 0.5405,
0.5489, 0.5018,
-0.5358, -0.1065,
1.1893, 0.1914
],
SWI4: [
-0.0389, -0.9307,
0.4958, -0.0196,
0.4521, -0.6053,
-0.7988, -0.1749,
0.3006, 0.0909,
-0.7866, 0.2419
],
SWI5: [
-1.0275, -0.3405,
-1.2339, -0.6617,
1.0472, -0.2527,
-0.8267, -0.5495,
-0.217, -0.1531,
-0.3907, -0.2836
],
YHP1: [
-0.7061, -0.8436,
-2.1758, -1.6097,
-0.7422, 0.4833,
0.6116, -0.0835,
-0.4454, 0.3472,
0.7491, 0.6957
],
YOX1: [

```

-1.7194, -0.4979,
-1.2355, -1.9155,
-0.5178, 0.6255,
-0.8938, -0.5063,
-1.0352, 0.8516,
-0.3387, -1.0581
],
ZAP1: [
<1 empty item>, 0.1287,
0.7379,      0.7652,
-1.2348,     -0.2555,
-5.062,      -0.2373,
<1 empty item>, 0.6914,
-2.676,      -0.8246
]
}
}
},
test: {
  production_rates: {
    data: {
      ACE2: 0.2236,
      ASH1: 0.4332,
      CIN5: 0.2009,
      GCR2: 0.1925,
      GLN3: 0.3224,
      HAP4: 0.2718,
      HMO1: 0.099,
      MSN2: 0.4077,
      SFP1: 0.6931,
      STB5: 0.14,
      SWI4: 0.2829,
      SWI5: 0.3224,
      YHP1: 0.1733,
      YOX1: 0.7296,
      ZAP1: 0.1042
    },
    errors: [
      {
        errorCode: 'INVALID_GENE_TYPE',
        possibleCause: "Gene 'undefined' in row 17, column A in the production_rates sheet is
not a string.",
        suggestedFix: 'Please make your gene name a string starting with a letter.'
      },

```

```
{
  errorCode: 'INVALID_GENE_TYPE',
  possibleCause: "Gene 'undefined' in row 18, column A in the production_rates sheet is
not a string.",
  suggestedFix: 'Please make your gene name a string starting with a letter.'
},
{
  errorCode: 'INVALID_GENE_TYPE',
  possibleCause: "Gene 'undefined' in row 19, column A in the production_rates sheet is
not a string.",
  suggestedFix: 'Please make your gene name a string starting with a letter.'
},
{
  errorCode: 'INVALID_GENE_TYPE',
  possibleCause: "Gene 'undefined' in row 20, column A in the production_rates sheet is
not a string.",
  suggestedFix: 'Please make your gene name a string starting with a letter.'
},
{
  errorCode: 'INVALID_GENE_TYPE',
  possibleCause: "Gene 'undefined' in row 21, column A in the production_rates sheet is
not a string.",
  suggestedFix: 'Please make your gene name a string starting with a letter.'
},
{
  errorCode: 'INVALID_GENE_TYPE',
  possibleCause: "Gene 'undefined' in row 22, column A in the production_rates sheet is
not a string.",
  suggestedFix: 'Please make your gene name a string starting with a letter.'
},
{
  errorCode: 'INVALID_GENE_TYPE',
  possibleCause: "Gene 'undefined' in row 23, column A in the production_rates sheet is
not a string.",
  suggestedFix: 'Please make your gene name a string starting with a letter.'
},
{
  errorCode: 'INVALID_GENE_TYPE',
  possibleCause: "Gene 'undefined' in row 24, column A in the production_rates sheet is
not a string.",
  suggestedFix: 'Please make your gene name a string starting with a letter.'
},
{
  errorCode: 'INVALID_GENE_TYPE',
```

```
    possibleCause: "Gene 'undefined' in row 25, column A in the production_rates sheet is
not a string.",
    suggestedFix: 'Please make your gene name a string starting with a letter.'
  },
  {
    errorCode: 'INVALID_GENE_TYPE',
    possibleCause: "Gene 'undefined' in row 26, column A in the production_rates sheet is
not a string.",
    suggestedFix: 'Please make your gene name a string starting with a letter.'
  },
  {
    errorCode: 'INVALID_GENE_TYPE',
    possibleCause: "Gene 'undefined' in row 27, column A in the production_rates sheet is
not a string.",
    suggestedFix: 'Please make your gene name a string starting with a letter.'
  },
  {
    errorCode: 'INVALID_GENE_TYPE',
    possibleCause: "Gene 'undefined' in row 28, column A in the production_rates sheet is
not a string.",
    suggestedFix: 'Please make your gene name a string starting with a letter.'
  },
  {
    errorCode: 'INVALID_GENE_TYPE',
    possibleCause: "Gene 'undefined' in row 29, column A in the production_rates sheet is
not a string.",
    suggestedFix: 'Please make your gene name a string starting with a letter.'
  },
  {
    errorCode: 'INVALID_GENE_TYPE',
    possibleCause: "Gene 'undefined' in row 30, column A in the production_rates sheet is
not a string.",
    suggestedFix: 'Please make your gene name a string starting with a letter.'
  },
  {
    errorCode: 'INVALID_GENE_TYPE',
    possibleCause: "Gene 'undefined' in row 31, column A in the production_rates sheet is
not a string.",
    suggestedFix: 'Please make your gene name a string starting with a letter.'
  },
  {
    errorCode: 'INVALID_GENE_TYPE',
    possibleCause: "Gene 'undefined' in row 32, column A in the production_rates sheet is
not a string.",
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suggestedFix: 'Please make your gene name a string starting with a letter.'
},
{
  errorCode: 'INVALID_GENE_TYPE',
  possibleCause: "Gene 'undefined' in row 33, column A in the production_rates sheet is
not a string.",
  suggestedFix: 'Please make your gene name a string starting with a letter.'
},
{
  errorCode: 'INVALID_GENE_TYPE',
  possibleCause: "Gene 'undefined' in row 34, column A in the production_rates sheet is
not a string.",
  suggestedFix: 'Please make your gene name a string starting with a letter.'
},
{
  errorCode: 'INVALID_GENE_TYPE',
  possibleCause: "Gene 'undefined' in row 35, column A in the production_rates sheet is
not a string.",
  suggestedFix: 'Please make your gene name a string starting with a letter.'
},
{
  errorCode: 'INVALID_GENE_TYPE',
  possibleCause: "Gene 'undefined' in row 36, column A in the production_rates sheet is
not a string.",
  suggestedFix: 'Please make your gene name a string starting with a letter.'
},
{
  errorCode: 'ERRORS_OVERLOAD',
  possibleCause: 'This workbook has over 20 errors.',
  suggestedFix: 'Please check the format of your spreadsheet with the guidelines outlined
on theDocumentation page and try again. If you fix these errors and try to upload again, there
may be further errors detected. As a general approach for fixing the errors, consider copying
and pasting just your adjacency matrix into a fresh Excel Workbook and saving it.'
},
{
  errorCode: 'ERRORS_OVERLOAD',
  possibleCause: 'This workbook has over 20 errors.',
  suggestedFix: 'Please check the format of your spreadsheet with the guidelines outlined
on theDocumentation page and try again. If you fix these errors and try to upload again, there
may be further errors detected. As a general approach for fixing the errors, consider copying
and pasting just your adjacency matrix into a fresh Excel Workbook and saving it.'
},
{
  errorCode: 'ERRORS_OVERLOAD',
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possibleCause: 'This workbook has over 20 errors.',
suggestedFix: 'Please check the format of your spreadsheet with the guidelines outlined on theDocumentation page and try again. If you fix these errors and try to upload again, there may be further errors detected. As a general approach for fixing the errors, consider copying and pasting just your adjacency matrix into a fresh Excel Workbook and saving it.'

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},

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suggestedFix: 'Please check the format of your spreadsheet with the guidelines outlined on theDocumentation page and try again. If you fix these errors and try to upload again, there may be further errors detected. As a general approach for fixing the errors, consider copying and pasting just your adjacency matrix into a fresh Excel Workbook and saving it.'

},

{

errorCode: 'ERRORS_OVERLOAD',

possibleCause: 'This workbook has over 20 errors.',

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may be further errors detected. As a general approach for fixing the errors, consider copying and pasting just your adjacency matrix into a fresh Excel Workbook and saving it.'

},

{

errorCode: 'ERRORS_OVERLOAD',

possibleCause: 'This workbook has over 20 errors.',

suggestedFix: 'Please check the format of your spreadsheet with the guidelines outlined on theDocumentation page and try again. If you fix these errors and try to upload again, there may be further errors detected. As a general approach for fixing the errors, consider copying and pasting just your adjacency matrix into a fresh Excel Workbook and saving it.'

},

{

errorCode: 'ERRORS_OVERLOAD',

possibleCause: 'This workbook has over 20 errors.',

suggestedFix: 'Please check the format of your spreadsheet with the guidelines outlined on theDocumentation page and try again. If you fix these errors and try to upload again, there may be further errors detected. As a general approach for fixing the errors, consider copying and pasting just your adjacency matrix into a fresh Excel Workbook and saving it.'

},

{

errorCode: 'ERRORS_OVERLOAD',

possibleCause: 'This workbook has over 20 errors.',

suggestedFix: 'Please check the format of your spreadsheet with the guidelines outlined on theDocumentation page and try again. If you fix these errors and try to upload again, there may be further errors detected. As a general approach for fixing the errors, consider copying and pasting just your adjacency matrix into a fresh Excel Workbook and saving it.'

},

{

errorCode: 'ERRORS_OVERLOAD',

possibleCause: 'This workbook has over 20 errors.',

suggestedFix: 'Please check the format of your spreadsheet with the guidelines outlined on theDocumentation page and try again. If you fix these errors and try to upload again, there may be further errors detected. As a general approach for fixing the errors, consider copying and pasting just your adjacency matrix into a fresh Excel Workbook and saving it.'

},

{

errorCode: 'ERRORS_OVERLOAD',

possibleCause: 'This workbook has over 20 errors.',

suggestedFix: 'Please check the format of your spreadsheet with the guidelines outlined on theDocumentation page and try again. If you fix these errors and try to upload again, there may be further errors detected. As a general approach for fixing the errors, consider copying and pasting just your adjacency matrix into a fresh Excel Workbook and saving it.'

},

{


```
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    possibleCause: 'This workbook has over 20 errors.',
    suggestedFix: 'Please check the format of your spreadsheet with the guidelines outlined
on theDocumentation page and try again. If you fix these errors and try to upload again, there
may be further errors detected. As a general approach for fixing the errors, consider copying
and pasting just your adjacency matrix into a fresh Excel Workbook and saving it.'
  },
  {
    errorCode: 'ERRORS_OVERLOAD',
    possibleCause: 'This workbook has over 20 errors.',
    suggestedFix: 'Please check the format of your spreadsheet with the guidelines outlined
on theDocumentation page and try again. If you fix these errors and try to upload again, there
may be further errors detected. As a general approach for fixing the errors, consider copying
and pasting just your adjacency matrix into a fresh Excel Workbook and saving it.'
  },
  {
    errorCode: 'ERRORS_OVERLOAD',
    possibleCause: 'This workbook has over 20 errors.',
    suggestedFix: 'Please check the format of your spreadsheet with the guidelines outlined
on theDocumentation page and try again. If you fix these errors and try to upload again, there
may be further errors detected. As a general approach for fixing the errors, consider copying
and pasting just your adjacency matrix into a fresh Excel Workbook and saving it.'
  },
  {
    errorCode: 'ERRORS_OVERLOAD',
    possibleCause: 'This workbook has over 20 errors.',
    suggestedFix: 'Please check the format of your spreadsheet with the guidelines outlined
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may be further errors detected. As a general approach for fixing the errors, consider copying
and pasting just your adjacency matrix into a fresh Excel Workbook and saving it.'
  },
  {
    errorCode: 'ERRORS_OVERLOAD',
    possibleCause: 'This workbook has over 20 errors.',
    suggestedFix: 'Please check the format of your spreadsheet with the guidelines outlined
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and pasting just your adjacency matrix into a fresh Excel Workbook and saving it.'
```

may be further errors detected. As a general approach for fixing the errors, consider copying and pasting just your adjacency matrix into a fresh Excel Workbook and saving it.'

},

{

errorCode: 'ERRORS_OVERLOAD',

possibleCause: 'This workbook has over 20 errors.',

suggestedFix: 'Please check the format of your spreadsheet with the guidelines outlined on theDocumentation page and try again. If you fix these errors and try to upload again, there may be further errors detected. As a general approach for fixing the errors, consider copying and pasting just your adjacency matrix into a fresh Excel Workbook and saving it.'

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