

```
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```

```
(* PHTX 7778: Applied Genomics *)
```

```
(* Lab 1: SVD and Pseudoinverse Projection *)
```

```
(* General Commands *)
```

```
Clear["Global`*"]
```

```
(* SVD of Cell Cycle mRNA Expression *)
```

```
(* Read Cell_Cycle_Expression_1.txt *)
```

```
a = 1;
```

```
b = 7;
```

```
stream = "http://www.alterlab.org/teaching/PHTX7778/datasets/Cell_Cycle_Expression_1.txt";
```

```
matrix = Import[stream, "Table"];
```

```
{genes, arrays} = Dimensions[matrix] - {a, b}
```

```
Clear[stream];
```

```
{2493, 18}
```

```
arraynames = Transpose[Drop[Transpose[Drop[matrix, {a + 1, a + genes}]], {1, b}]];
```

```
matrix = Drop[matrix, 1];
```

```
matrix = Transpose[matrix];
```

```
genenames = Drop[matrix, {b + 1, b + arrays}];
```

```
matrix = Drop[matrix, {1, b}];
```

```
matrix = Transpose[matrix];
```

```
Clear[a, b];
```

```
(* Compute the SVD *)
```

```
{eigenarrays, eigenexpressions, eigengenes} = SingularValueDecomposition[matrix, arrays];
```

```
eigenexpressions = Diagonal[eigenexpressions];
```

```
eigengenes = Transpose[eigengenes];
```

```
rank = arrays - Count[eigenexpressions, 0.]
```

```
fractions = eigenexpressions^2 / Sum[eigenexpressions[[a]]^2, {a, 1, rank}];
```

```
entropy = -N[Sum[fractions[[a]] * Log[fractions[[a]]], {a, 1, rank}] / Log[rank];
```

```
entropy = N[Round[100 * entropy] / 100]
```

```
18
```

```
0.16
```

```
(* 1. What can we learn from the number of rank of freedom about the data? *)
```

```
(* 2. What can we learn from the entropy about the data? *)
```

(* Create Fractions Bar Chart Display *)

```
gridx = Table[a, {a, 0.25, 0.75, 0.25}];
framex = Table[{gridx[[a]], Rotate[gridx[[a]], Pi / 2]}, {a, 1, 3}];
gridx = Table[{gridx[[a]], RGBColor[0, 0, 0]}, {a, 1, 3}];
framey = Table[{a + 1, rank - a}, {a, 0, rank - 1}];
labelx = ColumnForm[
  {"(b) Eigenexpression Fraction", StringJoin["d = ", ToString[entropy]]},
  Center];
g2 = BarChart[
  Table[fractions[[rank - a]], {a, 0, rank - 1}],
  BarOrigin -> Left,
  PlotRange -> {{0.0001, 0.9999}, {0.5, rank + 0.5}},
  AspectRatio -> 1,
  Axes -> False,
  Frame -> True,
  FrameTicks -> {None, framey, framex, None},
  FrameLabel -> {None, None, None, labelx},
  GridLines -> {gridx, None},
  ChartStyle -> Red,
  BaseStyle -> {FontFamily -> "Courier"}];
```

(* Create Eigengenes Raster Display *)

```
contrast = 3.5;
displaying = Table[
  If[contrast * eigengenes[[i, j]] > 0,
    If[contrast * eigengenes[[i, j]] < 1, {contrast * eigengenes[[i, j]], 0}, {1, 0}],
    If[contrast * eigengenes[[i, j]] > -1, {0, -contrast * eigengenes[[i, j]]}, {0, 1}]],
  {i, 1, rank}, {j, 1, arrays}];
framex = Table[{a - 0.5, Rotate[arraynames[[1, a]], Pi / 2]}, {a, 1, arrays}];
framey = Table[{a + 1 - 0.5, rank - a}, {a, 0, rank - 1}];
labely = "Eigengenes";
labelx = "(a) Arrays";
g1 = Show[
  Graphics[
    Raster[
      Table[
        {displaying[[i, j, 1]], displaying[[i, j, 2]], 0},
        {i, rank, 1, -1}, {j, 1, arrays}]]],
  AspectRatio -> 1,
  Frame -> True,
  FrameTicks -> {None, framey, framex, None},
  FrameLabel -> {None, labely, labelx, None},
  BaseStyle -> {FontFamily -> "Courier"}];
```

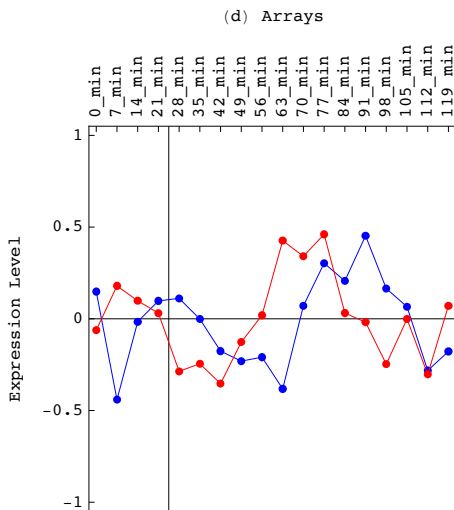
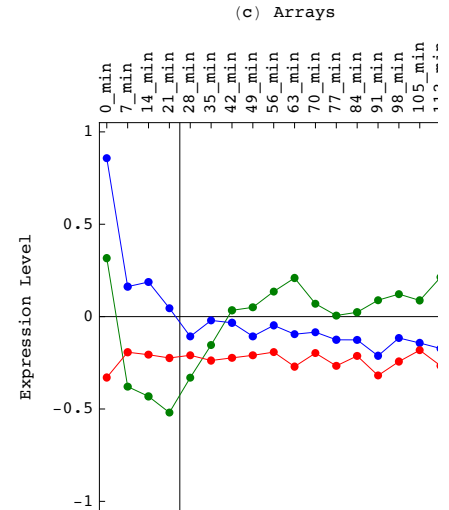
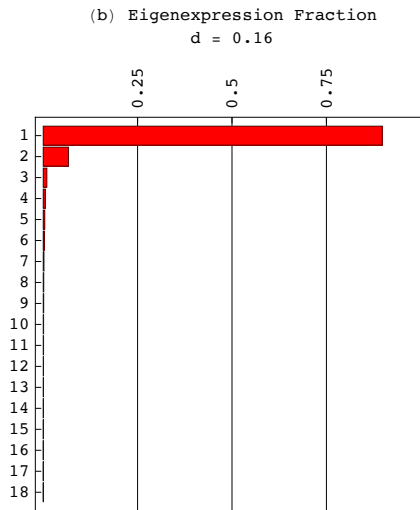
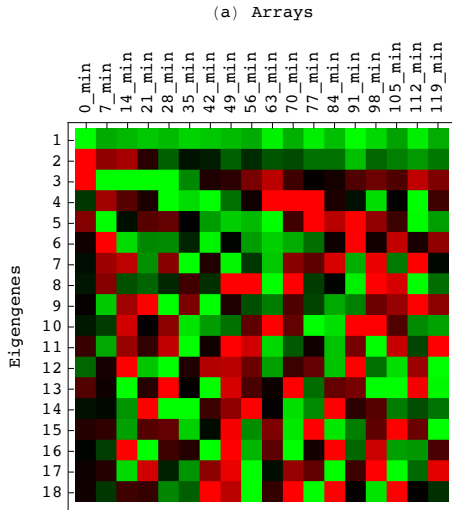
(* Create Selected Eigengenes Graph Display *)

```
p = Table[0, {n, 1, 5}];
color = {RGBColor[1, 0, 0], RGBColor[0, 0, 1],
  RGBColor[0, 0.5, 0], , RGBColor[1, 0.5, 0], RGBColor[1, 0, 0]};
labelx = "(c) Arrays";
labely = "Expression Level";
framex = Table[{a - 1, Rotate[arraynames[[1, a]], Pi / 2]}, {a, 1, arrays}];
framey = {-1, -0.5, 0, 0.5, 1};
Do[{
  coordinates = Table[{a - 1, eigengenes[[n, a]]}, {a, 1, arrays}],
  points = Table[Point[coordinates[[a]]], {a, 1, arrays}],
  line = Line[coordinates],
  g = Show[
    {Graphics[{color[[n]], PointSize[0.022], points}},
    Graphics[{color[[n]], line}]},
    Frame -> True,
    FrameLabel -> {None, labely, labelx, None},
    GridLines -> {{{3.5, RGBColor[0, 0, 0]}}, {{0, RGBColor[0, 0, 0]}},
    FrameTicks -> {None, framey, framex, None},
    BaseStyle -> {FontFamily -> "Courier"}],
  p[[n]] = Show[g,
    AspectRatio -> 1.05,
    PlotRange -> {-1.05, 1.05},
    DisplayFunction -> Identity]],
  {n, 1, 3}]
g3 = Show[{p[[3]], p[[2]], p[[1]]}];

p = Table[0, {n, 1, 2}];
color = {RGBColor[1, 0, 0], RGBColor[0, 0, 1]};
labelx = "(d) Arrays";
labely = "Expression Level";
framex = Table[{a - 1, Rotate[arraynames[[1, a]], Pi / 2]}, {a, 1, arrays}];
framey = {-1, -0.5, 0, 0.5, 1};
Do[{
  coordinates = Table[{a - 1, eigengenes[[n + 3, a]]}, {a, 1, arrays}],
  points = Table[Point[coordinates[[a]]], {a, 1, arrays}],
  line = Line[coordinates],
  g = Show[
    {Graphics[{color[[n]], PointSize[0.022], points}},
    Graphics[{color[[n]], line}]},
    Frame -> True,
    FrameLabel -> {None, labely, labelx, None},
    GridLines -> {{{3.5, RGBColor[0, 0, 0]}}, {{0, RGBColor[0, 0, 0]}},
    FrameTicks -> {None, framey, framex, None},
    BaseStyle -> {FontFamily -> "Courier"}],
  p[[n]] = Show[g,
    AspectRatio -> 1.05,
    PlotRange -> {-1.05, 1.05},
    DisplayFunction -> Identity]],
  {n, 1, 2}]
g4 = Show[{p[[2]], p[[1]]}];
```

(* Display the SVD *)

```
Show[GraphicsGrid[{{g1, g2, g3}}, Spacings -> -20],  
ImageSize -> 750]  
Show[GraphicsGrid[{{g4}}],  
ImageSize -> 250]
```



(* 3. What do the top three eigengenes look like? *)

(* 4. What biological processes might they describe? *)

(* Compute P-Value of Enrichment of Annotations Assuming Hypergeometric Distribution *)

```
headerx = {{
  ColumnForm[{" ", " ", "Eigenarray"}, Left],
  ColumnForm[{"Most Likely", "Parallel", "Association"}, Left],
  ColumnForm[{"P-Value of", "Parallel", "Association"}, Left],
  ColumnForm[{"Most Likely", "Antiparallel", "Association"}, Left],
  ColumnForm[{"P-Value of", "Antiparallel", "Association"}, Left]}};
```

(* Cell Cycle Annotations *)

```
annotations = genenames[[6]];
stages = {"M/G1", "G1", "S", "S/G2", "G2/M", "None"};

most = 150;
numbers =
  Flatten[Table[{Count[Flatten[annotations], stages[[a]]], {a, 1, Dimensions[stages][[1]]}}],
counter = Table[{a}, {a, 1, 5}];
probability = Table[{0}, {a, 1, Dimensions[counter][[1]]}];
parallelannotation = Table[{0}, {a, 1, Dimensions[counter][[1]]}];
parallelprobability = Table[{0}, {a, 1, Dimensions[counter][[1]]}];
antiannotation = Table[{0}, {a, 1, Dimensions[counter][[1]]}];
antiprobability = Table[{0}, {a, 1, Dimensions[counter][[1]]}];

{53, 117, 32, 63, 91, 2137}
```

```
Do[{{
  pattern = Transpose[Sort[Transpose[Join[{Transpose[eigenarrays][[c]], {annotations}],
    OrderedQ[{{#2}, {#1}}] &]][[2]],
  table = Table[{
    stages[[a]],
    numbers[[a]],
    Count[Flatten[Drop[pattern, {most + 1, genes}], stages[[a]]],
    {a, 1, Dimensions[stages][[1]]}],
  probability = Table[{
    Sum[N[Binomial[table[[a, 2]], b] * Binomial[genes - table[[a, 2]], most - b] /
      Binomial[genes, most]], {b, table[[a, 3]], most}],
    stages[[a]],
    {a, 1, Dimensions[stages][[1]]}],
  parallelannotation[[c]] = {Sort[probability, OrderedQ[{{#1}, {#2}}] &]][[1, 2]],
  parallelprobability[[c]] =
    {ScientificForm[Sort[probability, OrderedQ[{{#1}, {#2}}] &]][[1, 1], 2]},
  table = Table[{
    stages[[a]],
    numbers[[a]],
    Count[Flatten[Drop[pattern, {1, genes - most}], stages[[a]]],
    {a, 1, Dimensions[stages][[1]]}],
  probability = Table[{
    Sum[N[Binomial[table[[a, 2]], b] * Binomial[genes - table[[a, 2]], most - b] /
      Binomial[genes, most]], {b, table[[a, 3]], most}],
    stages[[a]],
    {a, 1, Dimensions[stages][[1]]}],
  antiannotation[[c]] = {Sort[probability, OrderedQ[{{#1}, {#2}}] &]][[1, 2]],
  antiprobability[[c]] =
    {ScientificForm[Sort[probability, OrderedQ[{{#1}, {#2}}] &]][[1, 1], 2]},
  {c, 1, Dimensions[counter][[1]]}}
```

```

table = Join[headerx, Transpose[Join[Transpose[counter],
  Transpose[parallelannotation],
  Transpose[parallelprobability],
  Transpose[antiannotation],
  Transpose[antiprobability]]]];
TableForm[table]

```

| Eigenarray | Most Likely Parallel Association | P-Value of Parallel Association | Most Likely Antiparallel Association | P-Value of Antiparallel Association |
|------------|--|---------------------------------------|--|---|
| 1 | M/G1 | 4.5×10^{-5} | G2/M | 1.8×10^{-7} |
| 2 | M/G1 | 3.6×10^{-9} | G2/M | 6.2×10^{-9} |
| 3 | G2/M | 5.2×10^{-14} | G1 | 1.9×10^{-34} |
| 4 | M/G1 | 2.2×10^{-33} | S | 4.3×10^{-19} |
| 5 | G1 | 5.9×10^{-57} | G2/M | $6. \times 10^{-19}$ |

(* Pheromone Response Annotations *)

```

annotations = genenames[[7]];
stages = {"Up", "Down", "None"};

most = 150;
numbers =
  Flatten[Table[{Count[Flatten[annotations], stages[[a]]], {a, 1, Dimensions[stages][[1]]}}]]
counter = Table[{a}, {a, 1, 5}];
probability = Table[{0}, {a, 1, Dimensions[counter][[1]]}];
parallelannotation = Table[{0}, {a, 1, Dimensions[counter][[1]]}];
parallelprobability = Table[{0}, {a, 1, Dimensions[counter][[1]]}];
antiannotation = Table[{0}, {a, 1, Dimensions[counter][[1]]}];
antiprobability = Table[{0}, {a, 1, Dimensions[counter][[1]]}];

{71, 82, 2340}

Do[{
  pattern = Transpose[Sort[Transpose[Join[{Transpose[eigenarrays][[c]], {annotations}}],
    OrderedQ[{{#2}, {#1}}] &][[2]],
  table = Table[{
    stages[[a]],
    numbers[[a]],
    Count[Flatten[Drop[pattern, {most + 1, genes}], stages[[a]]],
    {a, 1, Dimensions[stages][[1]]}],
  probability = Table[{
    Sum[N[Binomial[table[[a, 2]], b] * Binomial[genes - table[[a, 2]], most - b] /
      Binomial[genes, most]], {b, table[[a, 3]], most}],
    stages[[a]],
    {a, 1, Dimensions[stages][[1]]}],
  parallelannotation[[c]] = {Sort[probability, OrderedQ[{{#1}, {#2}}] &][[1, 2]],
  parallelprobability[[c]] =
    {ScientificForm[Sort[probability, OrderedQ[{{#1}, {#2}}] &][[1, 1], 2]],
  table = Table[{
    stages[[a]],
    numbers[[a]],
    Count[Flatten[Drop[pattern, {1, genes - most}], stages[[a]]],
    {a, 1, Dimensions[stages][[1]]}],
  probability = Table[{
    Sum[N[Binomial[table[[a, 2]], b] * Binomial[genes - table[[a, 2]], most - b] /
      Binomial[genes, most]], {b, table[[a, 3]], most}],
    stages[[a]],
    {a, 1, Dimensions[stages][[1]]}],
  antiannotation[[c]] = {Sort[probability, OrderedQ[{{#1}, {#2}}] &][[1, 2]],
  antiprobability[[c]] =
    {ScientificForm[Sort[probability, OrderedQ[{{#1}, {#2}}] &][[1, 1], 2]],
  {c, 1, Dimensions[counter][[1]]}]]

table = Join[headerx, Transpose[Join[Transpose[counter],
  Transpose[parallelannotation],
  Transpose[parallelprobability],
  Transpose[antiannotation],
  Transpose[antiprobability]]]];
TableForm[table]

```

| Eigenarray | Most Likely Parallel Association | P-Value of Parallel Association | Most Likely Antiparallel Association | P-Value of Antiparallel Association |
|------------|----------------------------------|---------------------------------|--------------------------------------|-------------------------------------|
| 1 | Up | 2.5×10^{-1} | Up | 4.1×10^{-14} |
| 2 | Up | 7.9×10^{-37} | Down | 4.1×10^{-33} |
| 3 | Up | 4.5×10^{-7} | Up | 5.4×10^{-5} |
| 4 | Up | 5.4×10^{-5} | Down | 7.1×10^{-10} |
| 5 | Down | 1.4×10^{-11} | Up | 8.4×10^{-4} |

(* 5. What annotations do the top four eigenarrays associate with? *)

(* 6. Are the eigenarray associations consistent with the eigengene patterns? *)


```
(* SVD Reconstruction of Cell Cycle mRNA Expression *)
```

```
(* Compute the SVD Reconstruction by Removing the First Eigengene and Eigenarray *)
```

```
{eigenarrays, eigenexpressions, eigengenes} = SingularValueDecomposition[matrix, arrays];  
eigenexpressions = Diagonal[eigenexpressions];  
eigengenes = Transpose[eigengenes];  
eigenexpressions[[1]] = 0;  
matrix = Dot[eigenarrays, Dot[DiagonalMatrix[eigenexpressions], eigengenes]];
```

```
(* Examine the SVD-Reconstructed Data Using SVD *)
```

```
{eigenarrays, eigenexpressions, eigengenes} = SingularValueDecomposition[matrix, arrays];  
eigenexpressions = Diagonal[eigenexpressions];  
eigengenes = Transpose[eigengenes];  
rank = arrays - Count[eigenexpressions, 0.]  
fractions = eigenexpressions^2 / Sum[eigenexpressions[[a]]^2, {a, 1, rank}];  
entropy = -N[Sum[fractions[[a]] * Log[fractions[[a]]], {a, 1, rank}] / Log[rank];  
entropy = N[Round[100 * entropy] / 100]
```

```
17
```

```
0.5
```

```
(* Create Fractions Bar Chart Display *)
```

```
gridx = Table[a, {a, 0.25, 0.75, 0.25}];  
framex = Table[{gridx[[a]], Rotate[gridx[[a]], Pi / 2]}, {a, 1, 3}];  
gridx = Table[{gridx[[a]], RGBColor[0, 0, 0]}, {a, 1, 3}];  
framey = Table[{a + 1, rank - a}, {a, 0, rank - 1}];  
labelx = ColumnForm[  
  {"(b) Eigenexpression Fraction", StringJoin["d = ", ToString[entropy]]},  
  Center];  
g2 = BarChart[  
  Table[fractions[[rank - a]], {a, 0, rank - 1}],  
  BarOrigin -> Left,  
  PlotRange -> {{0.0001, 0.9999}, {0.5, rank + 0.5}},  
  AspectRatio -> 1,  
  Axes -> False,  
  Frame -> True,  
  FrameTicks -> {None, framey, framex, None},  
  FrameLabel -> {None, None, None, labelx},  
  GridLines -> {gridx, None},  
  ChartStyle -> Red,  
  BaseStyle -> {FontFamily -> "Courier"}];
```

(* Create Eigengenes Raster Display *)

```
contrast = 3.5;
displaying = Table[
  If[contrast * eigengenes[[i, j]] > 0,
    If[contrast * eigengenes[[i, j]] < 1, {contrast * eigengenes[[i, j]], 0}, {1, 0}],
    If[contrast * eigengenes[[i, j]] > -1, {0, -contrast * eigengenes[[i, j]]}, {0, 1}]],
  {i, 1, rank}, {j, 1, arrays}];
framex = Table[{a - 0.5, Rotate[arraynames[[1, a]], Pi / 2]}, {a, 1, arrays}];
framey = Table[{a + 1 - 0.5, rank - a}, {a, 0, rank - 1}];
labely = "Eigengenes";
labelx = "(a) Arrays";
g1 = Show[
  Graphics[
    Raster[
      Table[
        {displaying[[i, j, 1]], displaying[[i, j, 2]], 0},
        {i, rank, 1, -1}, {j, 1, arrays}]]],
  AspectRatio -> 1,
  Frame -> True,
  FrameTicks -> {None, framey, framex, None},
  FrameLabel -> {None, labely, labelx, None},
  BaseStyle -> {FontFamily -> "Courier"}];
```

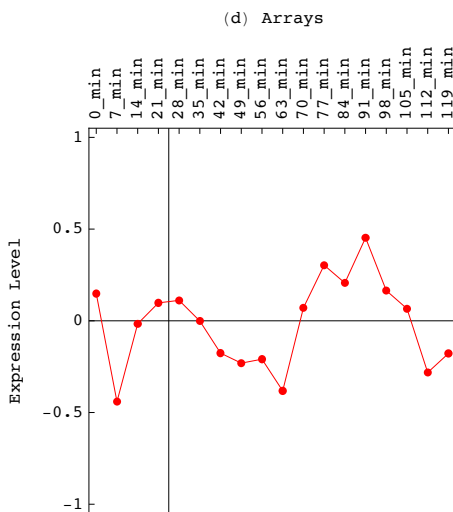
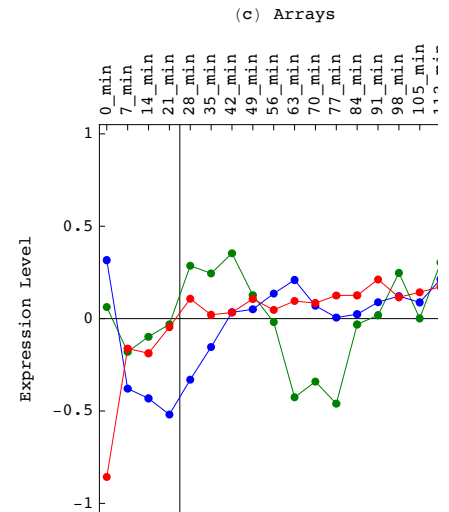
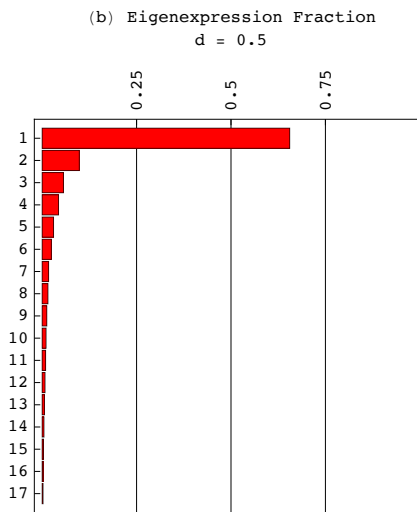
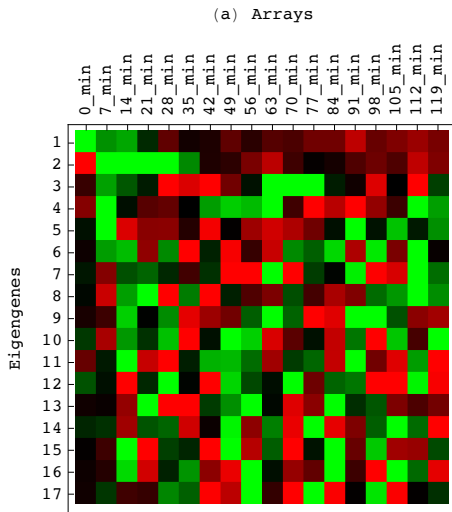
(* Create Selected Eigengenes Graph Display *)

```
p = Table[0, {n, 1, 3}];
color = {RGBColor[1, 0, 0], RGBColor[0, 0, 1], RGBColor[0, 0.5, 0]};
labelx = "(c) Arrays";
labely = "Expression Level";
framex = Table[{a - 1, Rotate[arraynames[[1, a]], Pi / 2]}, {a, 1, arrays}];
framey = {-1, -0.5, 0, 0.5, 1};
Do[{
  coordinates = Table[{a - 1, eigengenes[[n, a]]}, {a, 1, arrays}],
  points = Table[Point[coordinates[[a]]], {a, 1, arrays}],
  line = Line[coordinates],
  g = Show[
    {Graphics[{color[[n]], PointSize[0.022], points}],
    Graphics[{color[[n]], line}]},
    Frame -> True,
    FrameLabel -> {None, labely, labelx, None},
    GridLines -> {{{{3.5, RGBColor[0, 0, 0]}}, {{0, RGBColor[0, 0, 0]}},
    FrameTicks -> {None, framey, framex, None},
    BaseStyle -> {FontFamily -> "Courier"}],
  p[[n]] = Show[g,
    AspectRatio -> 1.05,
    PlotRange -> {-1.05, 1.05},
    DisplayFunction -> Identity]],
  {n, 1, 3}]
g3 = Show[{p[[3]], p[[2]], p[[1]]}];

p = Table[0, {n, 1, 2}];
color = {RGBColor[1, 0, 0], RGBColor[0, 0, 1]};
labelx = "(d) Arrays";
labely = "Expression Level";
framex = Table[{a - 1, Rotate[arraynames[[1, a]], Pi / 2]}, {a, 1, arrays}];
framey = {-1, -0.5, 0, 0.5, 1};
Do[{
  coordinates = Table[{a - 1, eigengenes[[n + 3, a]]}, {a, 1, arrays}],
  points = Table[Point[coordinates[[a]]], {a, 1, arrays}],
  line = Line[coordinates],
  g = Show[
    {Graphics[{color[[n]], PointSize[0.022], points}],
    Graphics[{color[[n]], line}]},
    Frame -> True,
    FrameLabel -> {None, labely, labelx, None},
    GridLines -> {{{{3.5, RGBColor[0, 0, 0]}}, {{0, RGBColor[0, 0, 0]}},
    FrameTicks -> {None, framey, framex, None},
    BaseStyle -> {FontFamily -> "Courier"}],
  p[[n]] = Show[g,
    AspectRatio -> 1.05,
    PlotRange -> {-1.05, 1.05},
    DisplayFunction -> Identity]],
  {n, 1, 1}]
g4 = Show[{p[[1]]}];
```

(* Display the SVD *)

```
Show[GraphicsGrid[{{g1, g2, g3}}, Spacings → -20],  
ImageSize → 750]  
Show[GraphicsGrid[{{g4}}],  
ImageSize → 250]
```



(* 7. What do the top three eigengenes look like after reconstruction? *)

(* 8. Which eigengenes in the original data do they correlate with? *)

(* 9. What biological processes might they describe? *)

(* Compute P-Value of Enrichment of Annotations Assuming Hypergeometric Distribution *)

```
headerx = {{
  ColumnForm[{" ", " ", "Eigenarray"}, Left],
  ColumnForm[{"Most Likely", "Parallel", "Association"}, Left],
  ColumnForm[{"P-Value of", "Parallel", "Association"}, Left],
  ColumnForm[{"Most Likely", "Antiparallel", "Association"}, Left],
  ColumnForm[{"P-Value of", "Antiparallel", "Association"}, Left]}};
```

(* Cell Cycle Annotations *)

```
annotations = genenames[[6]];
stages = {"M/G1", "G1", "S", "S/G2", "G2/M", "None"};

most = 150;
numbers =
  Flatten[Table[{Count[Flatten[annotations], stages[[a]]], {a, 1, Dimensions[stages][[1]]}}],
counter = Table[{a}, {a, 1, 4}];
probability = Table[{0}, {a, 1, Dimensions[counter][[1]]};
parallelannotation = Table[{0}, {a, 1, Dimensions[counter][[1]]};
parallelprobability = Table[{0}, {a, 1, Dimensions[counter][[1]]};
antiannotation = Table[{0}, {a, 1, Dimensions[counter][[1]]};
antiprobability = Table[{0}, {a, 1, Dimensions[counter][[1]]};

{53, 117, 32, 63, 91, 2137}
```

```
Do[{{
  pattern = Transpose[Sort[Transpose[Join[{Transpose[eigenarrays][[c]], {annotations}],
    OrderedQ[{{#2}, {#1}}] &]][[2]],
  table = Table[{
    stages[[a]],
    numbers[[a]],
    Count[Flatten[Drop[pattern, {most + 1, genes}], stages[[a]]],
    {a, 1, Dimensions[stages][[1]]},
  probability = Table[{
    Sum[N[Binomial[table[[a, 2]], b] * Binomial[genes - table[[a, 2]], most - b] /
      Binomial[genes, most]], {b, table[[a, 3]], most}],
    stages[[a]],
    {a, 1, Dimensions[stages][[1]]},
  parallelannotation[[c]] = {Sort[probability, OrderedQ[{{#1}, {#2}}] &][[1, 2]],
  parallelprobability[[c]] =
    {ScientificForm[Sort[probability, OrderedQ[{{#1}, {#2}}] &][[1, 1], 2]],
  table = Table[{
    stages[[a]],
    numbers[[a]],
    Count[Flatten[Drop[pattern, {1, genes - most}], stages[[a]]],
    {a, 1, Dimensions[stages][[1]]},
  probability = Table[{
    Sum[N[Binomial[table[[a, 2]], b] * Binomial[genes - table[[a, 2]], most - b] /
      Binomial[genes, most]], {b, table[[a, 3]], most}],
    stages[[a]],
    {a, 1, Dimensions[stages][[1]]},
  antiannotation[[c]] = {Sort[probability, OrderedQ[{{#1}, {#2}}] &][[1, 2]],
  antiprobability[[c]] =
    {ScientificForm[Sort[probability, OrderedQ[{{#1}, {#2}}] &][[1, 1], 2]],
  {c, 1, Dimensions[counter][[1]]}}
```

```

table = Join[headerx, Transpose[Join[Transpose[counter],
  Transpose[parallelannotation],
  Transpose[parallelprobability],
  Transpose[antiannotation],
  Transpose[antiprobability]]]];
TableForm[table]

```

| Eigenarray | Most Likely Parallel Association | P-Value of Parallel Association | Most Likely Antiparallel Association | P-Value of Antiparallel Association |
|------------|--|---------------------------------------|--|---|
| 1 | G2/M | 6.2×10^{-9} | M/G1 | 3.6×10^{-9} |
| 2 | G2/M | 5.2×10^{-14} | G1 | 1.9×10^{-34} |
| 3 | S | 4.3×10^{-19} | M/G1 | 2.2×10^{-33} |
| 4 | G1 | 5.9×10^{-57} | G2/M | $6. \times 10^{-19}$ |

(* Pheromone Response Annotations *)

```

annotations = genenames[[7]];
stages = {"Up", "Down", "None"};

most = 150;
numbers =
  Flatten[Table[{Count[Flatten[annotations], stages[[a]]], {a, 1, Dimensions[stages][[1]]}],
counter = Table[{a}, {a, 1, 4}];
probability = Table[{0}, {a, 1, Dimensions[counter][[1]]};
parallelannotation = Table[{0}, {a, 1, Dimensions[counter][[1]]};
parallelprobability = Table[{0}, {a, 1, Dimensions[counter][[1]]};
antiannotation = Table[{0}, {a, 1, Dimensions[counter][[1]]};
antiprobability = Table[{0}, {a, 1, Dimensions[counter][[1]]};

{71, 82, 2340}

Do[{
  pattern = Transpose[Sort[Transpose[Join[{Transpose[eigenarrays][[c]], {annotations}],
    OrderedQ[{{#2}, {#1}}] &][[2]],
  table = Table[{
    stages[[a]],
    numbers[[a]],
    Count[Flatten[Drop[pattern, {most + 1, genes}], stages[[a]]],
  {a, 1, Dimensions[stages][[1]]}],
  probability = Table[{
    Sum[N[Binomial[table[[a, 2]], b] * Binomial[genes - table[[a, 2]], most - b] /
      Binomial[genes, most]], {b, table[[a, 3]], most}],
    stages[[a]],
  {a, 1, Dimensions[stages][[1]]}],
  parallelannotation[[c]] = {Sort[probability, OrderedQ[{{#1}, {#2}}] &][[1, 2]],
  parallelprobability[[c]] =
  {ScientificForm[Sort[probability, OrderedQ[{{#1}, {#2}}] &][[1, 1], 2]],
  table = Table[{
    stages[[a]],
    numbers[[a]],
    Count[Flatten[Drop[pattern, {1, genes - most}], stages[[a]]],
  {a, 1, Dimensions[stages][[1]]}],
  probability = Table[{
    Sum[N[Binomial[table[[a, 2]], b] * Binomial[genes - table[[a, 2]], most - b] /
      Binomial[genes, most]], {b, table[[a, 3]], most}],
    stages[[a]],
  {a, 1, Dimensions[stages][[1]]}],
  antiannotation[[c]] = {Sort[probability, OrderedQ[{{#1}, {#2}}] &][[1, 2]],
  antiprobability[[c]] =
  {ScientificForm[Sort[probability, OrderedQ[{{#1}, {#2}}] &][[1, 1], 2]],
  {c, 1, Dimensions[counter][[1]]}]

table = Join[headerx, Transpose[Join[Transpose[counter],
  Transpose[parallelannotation],
  Transpose[parallelprobability],
  Transpose[antiannotation],
  Transpose[antiprobability]]]];
TableForm[table]

```

| Eigenarray | Most Likely Parallel Association | P-Value of Parallel Association | Most Likely Antiparallel Association | P-Value of Antiparallel Association |
|------------|--|---------------------------------------|--|---|
| 1 | Down | 4.1×10^{-33} | Up | 7.9×10^{-37} |
| 2 | Up | 4.5×10^{-7} | Up | 5.4×10^{-5} |
| 3 | Down | 7.1×10^{-10} | Up | 5.4×10^{-5} |
| 4 | Down | 1.4×10^{-11} | Up | 8.4×10^{-4} |

(* 10. What annotations do the top four eigenarrays associate with after reconstruction? *)

(* 11. Which eigenarrays in the original data do they correlate with? *)

(* 12. Are the eigenarray associations consistent with the eigene patterns? *)


```
(* Pseudoinverse Projection of the Cell Cycle mRNA Expression Data onto DNA-  
Binding of Cell Cycle Transcription Factors *)
```

```
(* Read Cell_Cycle_Binding.txt *)
```

```
a = 1;  
b = 7;
```

```
stream = "http://www.alterlab.org/teaching/PHTX7778/datasets/Cell_Cycle_Binding.txt";  
matrix = Import[stream, "Table"];  
{genes, arrays} = Dimensions[matrix] - {a, b}  
Clear[stream];
```

```
{960, 12}
```

```
arraynames = Transpose[Drop[Transpose[Drop[matrix, {a + 1, a + genes}]], {1, b}]];  
matrix = Drop[matrix, 1];
```

```
matrix = Transpose[matrix];  
genenames = Drop[matrix, {b + 1, b + arrays}];  
matrix = Drop[matrix, {1, b}];  
matrix = Transpose[matrix];  
Clear[a, b];
```

```
(* Compute the SVD Reconstruction by Removing the First Eigengene and Eigenarray *)
```

```
{eigenarrays, eigenexpressions, eigengenes} = SingularValueDecomposition[matrix, arrays];  
eigenexpressions = Diagonal[eigenexpressions];  
eigengenes = Transpose[eigengenes];  
eigenexpressions[[1]] = 0;  
matrix = Dot[eigenarrays, Dot[DiagonalMatrix[eigenexpressions], eigengenes]];
```

```
(* Save as Basis *)
```

```
basis = matrix;  
basisarrays = arrays;
```

```
(* Read Cell_Cycle_Expression_2.txt *)
```

```
a = 1;  
b = 7;
```

```
stream = "http://www.alterlab.org/teaching/PHTX7778/datasets/Cell_Cycle_Expression_2.txt";  
matrix = Import[stream, "Table"];  
{genes, arrays} = Dimensions[matrix] - {a, b}  
Clear[stream];
```

```
{960, 18}
```

```
arraynames = Transpose[Drop[Transpose[Drop[matrix, {a + 1, a + genes}]], {1, b}]];  
matrix = Drop[matrix, 1];
```

```
matrix = Transpose[matrix];  
genenames = Drop[matrix, {b + 1, b + arrays}];  
matrix = Drop[matrix, {1, b}];  
matrix = Transpose[matrix];  
Clear[a, b];
```

```
(* Compute the SVD Reconstruction by Removing the First Eigengene and Eigenarray *)
```

```
{eigenarrays, eigenexpressions, eigengenes} = SingularValueDecomposition[matrix, arrays];  
eigenexpressions = Diagonal[eigenexpressions];  
eigengenes = Transpose[eigengenes];  
eigenexpressions[[1]] = 0;  
matrix = Dot[eigenarrays, Dot[DiagonalMatrix[eigenexpressions], eigengenes]];
```

```
(* Compute Pseudoinverse Projection of Data onto Basis *)
```

```
{eigenarrays, eigenexpressions, eigengenes} =  
  SingularValueDecomposition[basis, basisarrays - 1];  
matrix = Dot[Dot[eigenarrays, Transpose[eigenarrays], matrix]];  
{genes, arrays} = Dimensions[matrix]
```

```
{960, 18}
```

```
(* Examine the Pseudoinverse-Projected Data Using SVD *)
```

```
{eigenarrays, eigenexpressions, eigengenes} = SingularValueDecomposition[matrix, arrays];  
eigenexpressions = Diagonal[eigenexpressions];  
eigengenes = Transpose[eigengenes];  
rank = arrays - Count[eigenexpressions, 0.]  
fractions = eigenexpressions^2 / Sum[eigenexpressions[[a]]^2, {a, 1, rank}];  
entropy = -N[Sum[fractions[[a]] * Log[fractions[[a]]], {a, 1, rank}] / Log[rank];  
entropy = N[Round[100 * entropy] / 100]
```

```
11
```

```
0.56
```

```
(* 13. How did the number of rank of freedom and entropy change? *)
```

```
(* 14. What can we learn from these changes about the pseudoinverse-projected data? *)
```

(* Create Fractions Bar Chart Display *)

```
gridx = Table[a, {a, 0.25, 0.75, 0.25}];
framex = Table[{gridx[[a]], Rotate[gridx[[a]], Pi / 2]}, {a, 1, 3}];
gridx = Table[{gridx[[a]], RGBColor[0, 0, 0]}, {a, 1, 3}];
framey = Table[{a + 1, rank - a}, {a, 0, rank - 1}];
labelx = ColumnForm[
  {"(b) Eigenexpression Fraction", StringJoin["d = ", ToString[entropy]]},
  Center];
g2 = BarChart[
  Table[fractions[[rank - a]], {a, 0, rank - 1}],
  BarOrigin -> Left,
  PlotRange -> {{0, 1 * 1.0001}, {0.5, rank + 0.5}},
  AspectRatio -> 1,
  Axes -> False,
  Frame -> True,
  FrameTicks -> {None, framey, framex, None},
  FrameLabel -> {None, None, None, labelx},
  GridLines -> {gridx, None},
  ChartStyle -> Red,
  BaseStyle -> {FontFamily -> "Courier"}];
```

(* Create Eigengenes Raster Display *)

```
contrast = 3.5;
displaying = Table[
  If[contrast * eigengenes[[i, j]] > 0,
    If[contrast * eigengenes[[i, j]] < 1, {contrast * eigengenes[[i, j]], 0}, {1, 0}],
    If[contrast * eigengenes[[i, j]] > -1, {0, -contrast * eigengenes[[i, j]]}, {0, 1}]],
  {i, 1, rank}, {j, 1, arrays}];
framex = Table[{a - 0.5, Rotate[arraynames[[1, a]], Pi / 2]}, {a, 1, arrays}];
framey = Table[{a + 1 - 0.5, rank - a}, {a, 0, rank - 1}];
labely = "Eigengenes";
labelx = "(a) Arrays";
g1 = Show[
  Graphics[
    Raster[
      Table[
        {displaying[[i, j, 1]], displaying[[i, j, 2]], 0},
        {i, rank, 1, -1}, {j, 1, arrays}]]],
  AspectRatio -> 1,
  Frame -> True,
  FrameTicks -> {None, framey, framex, None},
  FrameLabel -> {None, labely, labelx, None},
  BaseStyle -> {FontFamily -> "Courier"}];
```

(* Create Selected Eigengenes Graph Display *)

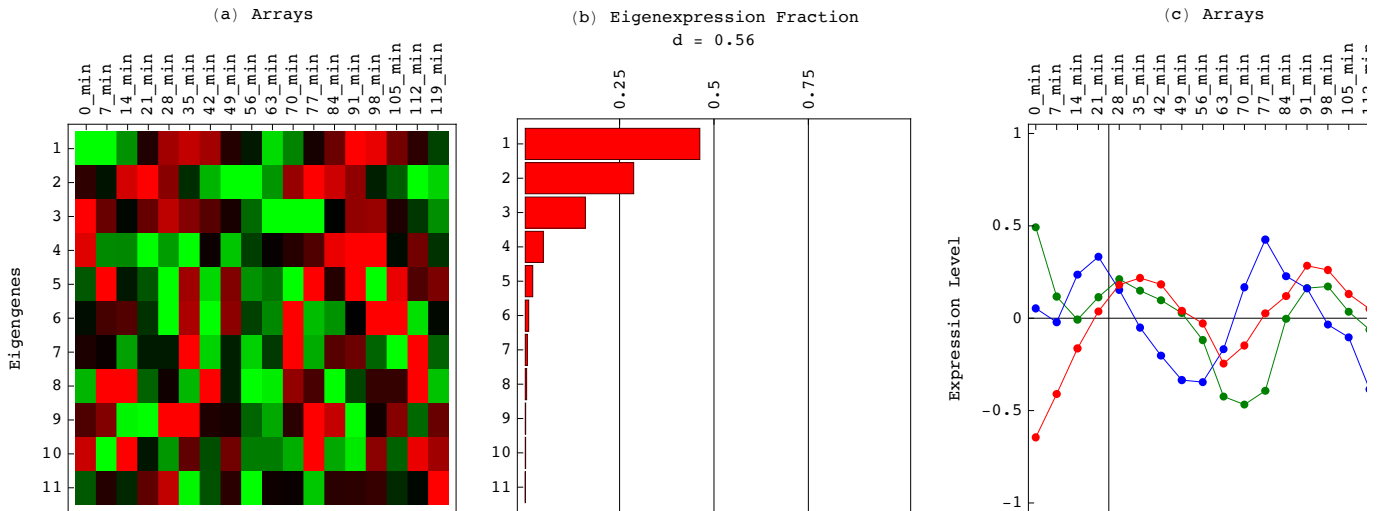
```

p = Table[0, {n, 1, 3}];
color = {RGBColor[1, 0, 0], RGBColor[0, 0, 1], RGBColor[0, 0.5, 0]};
labelx = "(c) Arrays";
labely = "Expression Level";
framex = Table[{a - 1, Rotate[arraynames[[1, a]], Pi / 2]}, {a, 1, arrays}];
framey = {-1, -0.5, 0, 0.5, 1};
Do[{
  coordinates = Table[{a - 1, eigengenes[[n, a]]}, {a, 1, arrays}],
  points = Table[Point[coordinates[[a]]], {a, 1, arrays}],
  line = Line[coordinates],
  g = Show[
    {Graphics[{color[[n]], PointSize[0.022], points}],
    Graphics[{color[[n]], line}]},
    Frame -> True,
    FrameLabel -> {None, labely, labelx, None},
    GridLines -> {{{{3.5, RGBColor[0, 0, 0]}}, {{0, RGBColor[0, 0, 0]}},},
    FrameTicks -> {None, framey, framex, None},
    BaseStyle -> {FontFamily -> "Courier"}],
  p[[n]] = Show[g,
    AspectRatio -> 1.05,
    PlotRange -> {-1.05, 1.05},
    DisplayFunction -> Identity}],
{n, 1, 3}]
g3 = Show[{p[[3]], p[[2]], p[[1]]}];

```

(* Display the SVD *)

```
Show[GraphicsGrid[{{g1, g2, g3}}, Spacings -> -20], ImageSize -> 750]
```



(* 15. What do the top three eigengenes look like after pseudoinverse projection? *)

(* 16. Which eigengenes in the original data do they correlate with? *)

(* 17. What biological processes might they describe? *)

(* Compute P-Value of Enrichment of Annotations Assuming Hypergeometric Distribution *)

```
headerx = {{
  ColumnForm[{" ", " ", "Eigenarray"}, Left],
  ColumnForm[{"Most Likely", "Parallel", "Association"}, Left],
  ColumnForm[{"P-Value of", "Parallel", "Association"}, Left],
  ColumnForm[{"Most Likely", "Antiparallel", "Association"}, Left],
  ColumnForm[{"P-Value of", "Antiparallel", "Association"}, Left]}};
```

(* Cell Cycle Annotations *)

```
annotations = genenames[[6]];
stages = {"M/G1", "G1", "S", "S/G2", "G2/M", "None"};

most = 150;
numbers =
  Flatten[Table[{Count[Flatten[annotations], stages[[a]]], {a, 1, Dimensions[stages][[1]]}],
counter = Table[{a}, {a, 1, 4}];
probability = Table[{0}, {a, 1, Dimensions[counter][[1]]};
parallelannotation = Table[{0}, {a, 1, Dimensions[counter][[1]]};
parallelprobability = Table[{0}, {a, 1, Dimensions[counter][[1]]};
antiannotation = Table[{0}, {a, 1, Dimensions[counter][[1]]};
antiprobability = Table[{0}, {a, 1, Dimensions[counter][[1]]};

{38, 66, 17, 28, 35, 776}
```

```
Do[{{
  pattern = Transpose[Sort[Transpose[Join[{Transpose[eigenarrays][[c]], {annotations}],
    OrderedQ[{{#2}, {#1}}] &]][[2]],
  table = Table[{
    stages[[a]],
    numbers[[a]],
    Count[Flatten[Drop[pattern, {most + 1, genes}], stages[[a]]],
    {a, 1, Dimensions[stages][[1]]}],
  probability = Table[{
    Sum[N[Binomial[table[[a, 2]], b] * Binomial[genes - table[[a, 2]], most - b] /
      Binomial[genes, most]], {b, table[[a, 3]], most}],
    stages[[a]],
    {a, 1, Dimensions[stages][[1]]}],
  parallelannotation[[c]] = {Sort[probability, OrderedQ[{{#1}, {#2}}] &]][[1, 2]],
  parallelprobability[[c]] =
    {ScientificForm[Sort[probability, OrderedQ[{{#1}, {#2}}] &]][[1, 1], 2]},
  table = Table[{
    stages[[a]],
    numbers[[a]],
    Count[Flatten[Drop[pattern, {1, genes - most}], stages[[a]]],
    {a, 1, Dimensions[stages][[1]]}],
  probability = Table[{
    Sum[N[Binomial[table[[a, 2]], b] * Binomial[genes - table[[a, 2]], most - b] /
      Binomial[genes, most]], {b, table[[a, 3]], most}],
    stages[[a]],
    {a, 1, Dimensions[stages][[1]]}],
  antiannotation[[c]] = {Sort[probability, OrderedQ[{{#1}, {#2}}] &]][[1, 2]],
  antiprobability[[c]] =
    {ScientificForm[Sort[probability, OrderedQ[{{#1}, {#2}}] &]][[1, 1], 2]},
  {c, 1, Dimensions[counter][[1]]}}
```

```

table = Join[headerx, Transpose[Join[Transpose[counter],
  Transpose[parallelannotation],
  Transpose[parallelprobability],
  Transpose[antiannotation],
  Transpose[antiprobability]]]];
TableForm[table]

```

| Eigenarray | Most Likely Parallel Association | P-Value of Parallel Association | Most Likely Antiparallel Association | P-Value of Antiparallel Association |
|------------|--|---------------------------------------|--|---|
| 1 | G1 | 2.3×10^{-7} | M/G1 | 2.4×10^{-6} |
| 2 | G1 | $1. \times 10^{-8}$ | G2/M | 7.9×10^{-5} |
| 3 | S | 4.8×10^{-5} | M/G1 | 5.8×10^{-5} |
| 4 | G1 | 8.5×10^{-3} | G1 | 1.6×10^{-4} |

(* Pheromone Response Annotations *)

```

annotations = genenames[[7]];
stages = {"Up", "Down", "None"};

most = 150;
numbers =
  Flatten[Table[{Count[Flatten[annotations], stages[[a]]], {a, 1, Dimensions[stages][[1]]}}]]
counter = Table[{a}, {a, 1, 4}];
probability = Table[{0}, {a, 1, Dimensions[counter][[1]]}];
parallelannotation = Table[{0}, {a, 1, Dimensions[counter][[1]]}];
parallelprobability = Table[{0}, {a, 1, Dimensions[counter][[1]]}];
antiannotation = Table[{0}, {a, 1, Dimensions[counter][[1]]}];
antiprobability = Table[{0}, {a, 1, Dimensions[counter][[1]]}];

{35, 48, 877}

Do[{{
  pattern = Transpose[Sort[Transpose[Join[{Transpose[eigenarrays][[c]], {annotations}],
    OrderedQ[{{#2}, {#1}}] &][[2]],
  table = Table[{
    stages[[a]],
    numbers[[a]],
    Count[Flatten[Drop[pattern, {most + 1, genes}], stages[[a]]],
    {a, 1, Dimensions[stages][[1]]}],
  probability = Table[{
    Sum[N[Binomial[table[[a, 2]], b] * Binomial[genes - table[[a, 2]], most - b] /
      Binomial[genes, most]], {b, table[[a, 3]], most}],
    stages[[a]],
    {a, 1, Dimensions[stages][[1]]}],
  parallelannotation[[c]] = {Sort[probability, OrderedQ[{{#1}, {#2}}] &][[1, 2]],
  parallelprobability[[c]] =
    {ScientificForm[Sort[probability, OrderedQ[{{#1}, {#2}}] &][[1, 1], 2]],
  table = Table[{
    stages[[a]],
    numbers[[a]],
    Count[Flatten[Drop[pattern, {1, genes - most}], stages[[a]]],
    {a, 1, Dimensions[stages][[1]]}],
  probability = Table[{
    Sum[N[Binomial[table[[a, 2]], b] * Binomial[genes - table[[a, 2]], most - b] /
      Binomial[genes, most]], {b, table[[a, 3]], most}],
    stages[[a]],
    {a, 1, Dimensions[stages][[1]]}],
  antiannotation[[c]] = {Sort[probability, OrderedQ[{{#1}, {#2}}] &][[1, 2]],
  antiprobability[[c]] =
    {ScientificForm[Sort[probability, OrderedQ[{{#1}, {#2}}] &][[1, 1], 2]],
  {c, 1, Dimensions[counter][[1]]}}]

table = Join[headerx, Transpose[Join[Transpose[counter],
  Transpose[parallelannotation],
  Transpose[parallelprobability],
  Transpose[antiannotation],
  Transpose[antiprobability]]]];
TableForm[table]

```

| Eigenarray | Most Likely Parallel Association | P-Value of Parallel Association | Most Likely Antiparallel Association | P-Value of Antiparallel Association |
|------------|--|---------------------------------------|--|---|
| 1 | Down | 2.6×10^{-11} | Up | 4.4×10^{-3} |
| 2 | Down | 3.2×10^{-5} | None | 2.2×10^{-1} |
| 3 | Down | 1.1×10^{-2} | None | 7.3×10^{-2} |
| 4 | Down | 1.1×10^{-2} | Down | 5.7×10^{-2} |

(* 18. What annotations do the top four eigenarrays associate with after pseudoinverse projection? *)

(* 19. Which eigenarrays in the original data do they correlate with? *)

(* 20. Are the eigenarray associations consistent with the eigene patterns? *)


```
(* Pseudoinverse Projection of the Cell Cycle mRNA Expression Data onto DNA-
Binding of Development Transcription Factors *)
```

```
(* Read Development_Binding.txt *)
```

```
a = 1;
b = 7;
```

```
stream = "http://www.alterlab.org/teaching/PHTX7778/datasets/Development_Binding.txt";
matrix = Import[stream, "Table"];
{genes, arrays} = Dimensions[matrix] - {a, b}
Clear[stream];
```

```
{1116, 12}
```

```
arraynames = Transpose[Drop[Transpose[Drop[matrix, {a + 1, a + genes}]], {1, b}]];
matrix = Drop[matrix, 1];
```

```
matrix = Transpose[matrix];
genenames = Drop[matrix, {b + 1, b + arrays}];
matrix = Drop[matrix, {1, b}];
matrix = Transpose[matrix];
Clear[a, b];
```

```
(* Compute the SVD Reconstruction by Removing the First Eigengene and Eigenarray *)
```

```
{eigenarrays, eigenexpressions, eigengenes} = SingularValueDecomposition[matrix, arrays];
eigenexpressions = Diagonal[eigenexpressions];
eigengenes = Transpose[eigengenes];
eigenexpressions[[1]] = 0;
matrix = Dot[eigenarrays, Dot[DiagonalMatrix[eigenexpressions], eigengenes]];
```

```
(* Save as Basis *)
```

```
basis = matrix;
basisarrays = arrays;
```

```
(* Read Cell_Cycle_Expression_3.txt *)
```

```
a = 1;
b = 7;
```

```
stream = "http://www.alterlab.org/teaching/PHTX7778/datasets/Cell_Cycle_Expression_3.txt";
matrix = Import[stream, "Table"];
{genes, arrays} = Dimensions[matrix] - {a, b}
Clear[stream];
```

```
{1116, 18}
```

```
arraynames = Transpose[Drop[Transpose[Drop[matrix, {a + 1, a + genes}]], {1, b}]];
matrix = Drop[matrix, 1];
```

```
matrix = Transpose[matrix];
genenames = Drop[matrix, {b + 1, b + arrays}];
matrix = Drop[matrix, {1, b}];
matrix = Transpose[matrix];
Clear[a, b];
```

```
(* Compute the SVD Reconstruction by Removing the First Eigengene and Eigenarray *)
```

```
{eigenarrays, eigenexpressions, eigengenes} = SingularValueDecomposition[matrix, arrays];  
eigenexpressions = Diagonal[eigenexpressions];  
eigengenes = Transpose[eigengenes];  
eigenexpressions[[1]] = 0;  
matrix = Dot[eigenarrays, Dot[DiagonalMatrix[eigenexpressions], eigengenes]];
```

```
(* Compute Pseudoinverse Projection of Data onto Basis *)
```

```
{eigenarrays, eigenexpressions, eigengenes} =  
  SingularValueDecomposition[basis, basisarrays - 1];  
matrix = Dot[Dot[eigenarrays, Transpose[eigenarrays], matrix]];  
{genes, arrays} = Dimensions[matrix]
```

```
{1116, 18}
```

```
(* Examine the Pseudoinverse-Projected Data Using SVD *)
```

```
{eigenarrays, eigenexpressions, eigengenes} = SingularValueDecomposition[matrix, arrays];  
eigenexpressions = Diagonal[eigenexpressions];  
eigengenes = Transpose[eigengenes];  
rank = arrays - Count[eigenexpressions, 0.]  
fractions = eigenexpressions^2 / Sum[eigenexpressions[[a]]^2, {a, 1, rank}];  
entropy = -N[Sum[fractions[[a]] * Log[fractions[[a]]], {a, 1, rank}] / Log[rank];  
entropy = N[Round[100 * entropy] / 100]
```

```
11
```

```
0.27
```

```
(* 21. How did the number of rank of freedom and entropy change? *)
```

```
(* 22. What can we learn from these changes about the pseudoinverse-projected data? *)
```

(* Create Fractions Bar Chart Display *)

```
gridx = Table[a, {a, 0.25, 0.75, 0.25}];
framex = Table[{gridx[[a]], Rotate[gridx[[a]], Pi / 2]}, {a, 1, 3}];
gridx = Table[{gridx[[a]], RGBColor[0, 0, 0]}, {a, 1, 3}];
framey = Table[{a + 1, rank - a}, {a, 0, rank - 1}];
labelx = ColumnForm[
  {"(b) Eigenexpression Fraction", StringJoin["d = ", ToString[entropy]]},
  Center];
g2 = BarChart[
  Table[fractions[[rank - a]], {a, 0, rank - 1}],
  BarOrigin -> Left,
  PlotRange -> {{0, 1 * 1.0001}, {0.5, rank + 0.5}},
  AspectRatio -> 1,
  Axes -> False,
  Frame -> True,
  FrameTicks -> {None, framey, framex, None},
  FrameLabel -> {None, None, None, labelx},
  GridLines -> {gridx, None},
  ChartStyle -> Red,
  BaseStyle -> {FontFamily -> "Courier"}];
```

(* Create Eigengenes Raster Display *)

```
contrast = 3.5;
displaying = Table[
  If[contrast * eigengenes[[i, j]] > 0,
    If[contrast * eigengenes[[i, j]] < 1, {contrast * eigengenes[[i, j]], 0}, {1, 0}],
    If[contrast * eigengenes[[i, j]] > -1, {0, -contrast * eigengenes[[i, j]]}, {0, 1}]],
  {i, 1, rank}, {j, 1, arrays}];
framex = Table[{a - 0.5, Rotate[arraynames[[1, a]], Pi / 2]}, {a, 1, arrays}];
framey = Table[{a + 1 - 0.5, rank - a}, {a, 0, rank - 1}];
labely = "Eigengenes";
labelx = "(a) Arrays";
g1 = Show[
  Graphics[
    Raster[
      Table[
        {displaying[[i, j, 1]], displaying[[i, j, 2]], 0},
        {i, rank, 1, -1}, {j, 1, arrays}]]],
  AspectRatio -> 1,
  Frame -> True,
  FrameTicks -> {None, framey, framex, None},
  FrameLabel -> {None, labely, labelx, None},
  BaseStyle -> {FontFamily -> "Courier"}];
```

(* Create Selected Eigengenes Graph Display *)

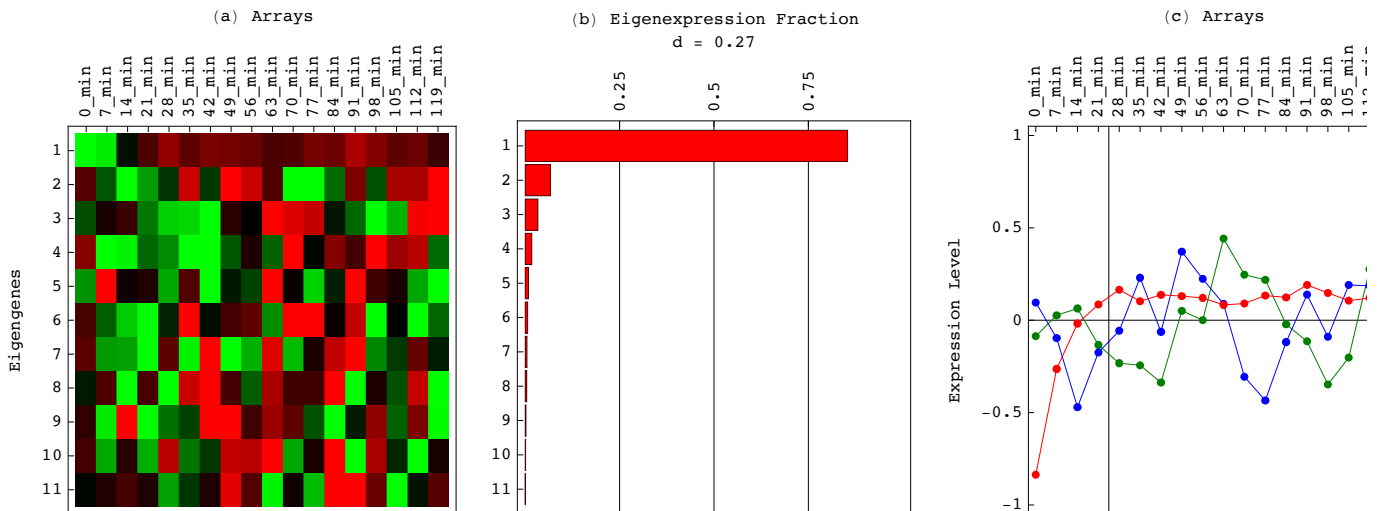
```

p = Table[0, {n, 1, 3}];
color = {RGBColor[1, 0, 0], RGBColor[0, 0, 1], RGBColor[0, 0.5, 0]};
labelx = "(c) Arrays";
labely = "Expression Level";
framex = Table[{a - 1, Rotate[arraynames[[1, a]], Pi / 2]}, {a, 1, arrays}];
framey = {-1, -0.5, 0, 0.5, 1};
Do[{
  coordinates = Table[{a - 1, eigengenes[[n, a]]}, {a, 1, arrays}],
  points = Table[Point[coordinates[[a]]], {a, 1, arrays}],
  line = Line[coordinates],
  g = Show[
    {Graphics[{color[[n]], PointSize[0.022], points}],
    Graphics[{color[[n]], line}]},
    Frame -> True,
    FrameLabel -> {None, labely, labelx, None},
    GridLines -> {{{{3.5, RGBColor[0, 0, 0]}}, {{0, RGBColor[0, 0, 0]}},},
    FrameTicks -> {None, framey, framex, None},
    BaseStyle -> {FontFamily -> "Courier"}],
  p[[n]] = Show[g,
    AspectRatio -> 1.05,
    PlotRange -> {-1.05, 1.05},
    DisplayFunction -> Identity}],
{n, 1, 3}]
g3 = Show[{p[[3]], p[[2]], p[[1]]}];

```

(* Display the SVD *)

```
Show[GraphicsGrid[{{g1, g2, g3}}, Spacings -> -20], ImageSize -> 750]
```



(* 23. What do the top three eigengenes look like after pseudoinverse projection? *)

(* 24. Which of the eigengenes are significant in terms of the fraction of the information they capture in the data? *)

(* 25. Which eigengenes in the original data do they correlate with? *)

(* 26. What biological processes might they describe? *)

(* Compute P-Value of Enrichment of Annotations Assuming Hypergeometric Distribution *)

```
headerx = {{  
  ColumnForm[{" ", " ", "Eigenarray"}, Left],  
  ColumnForm[{"Most Likely", "Parallel", "Association"}, Left],  
  ColumnForm[{"P-Value of", "Parallel", "Association"}, Left],  
  ColumnForm[{"Most Likely", "Antiparallel", "Association"}, Left],  
  ColumnForm[{"P-Value of", "Antiparallel", "Association"}, Left]}};
```

(* Cell Cycle Annotations *)

```
annotations = genenames[[6]];
stages = {"M/G1", "G1", "S", "S/G2", "G2/M", "None"};

most = 150;
numbers =
  Flatten[Table[{Count[Flatten[annotations], stages[[a]]], {a, 1, Dimensions[stages][[1]]}}]]
counter = Table[{a}, {a, 1, 4}];
probability = Table[{0}, {a, 1, Dimensions[counter][[1]]}];
parallelannotation = Table[{0}, {a, 1, Dimensions[counter][[1]]}];
parallelprobability = Table[{0}, {a, 1, Dimensions[counter][[1]]}];
antiannotation = Table[{0}, {a, 1, Dimensions[counter][[1]]}];
antiprobability = Table[{0}, {a, 1, Dimensions[counter][[1]]}];

{37, 71, 18, 30, 50, 910}

Do[{
  pattern = Transpose[Sort[Transpose[Join[{Transpose[eigenarrays][[c]], {annotations}}],
    OrderedQ[{{#2}, {#1}}] &][[2]],
  table = Table[{
    stages[[a]],
    numbers[[a]],
    Count[Flatten[Drop[pattern, {most + 1, genes}], stages[[a]]],
    {a, 1, Dimensions[stages][[1]]}],
  probability = Table[{
    Sum[N[Binomial[table[[a, 2]], b] * Binomial[genes - table[[a, 2]], most - b] /
      Binomial[genes, most]], {b, table[[a, 3]], most}],
    stages[[a]],
    {a, 1, Dimensions[stages][[1]]}],
  parallelannotation[[c]] = {Sort[probability, OrderedQ[{{#1}, {#2}}] &][[1, 2]],
  parallelprobability[[c]] =
    {ScientificForm[Sort[probability, OrderedQ[{{#1}, {#2}}] &][[1, 1], 2]],
  table = Table[{
    stages[[a]],
    numbers[[a]],
    Count[Flatten[Drop[pattern, {1, genes - most}], stages[[a]]],
    {a, 1, Dimensions[stages][[1]]}],
  probability = Table[{
    Sum[N[Binomial[table[[a, 2]], b] * Binomial[genes - table[[a, 2]], most - b] /
      Binomial[genes, most]], {b, table[[a, 3]], most}],
    stages[[a]],
    {a, 1, Dimensions[stages][[1]]}],
  antiannotation[[c]] = {Sort[probability, OrderedQ[{{#1}, {#2}}] &][[1, 2]],
  antiprobability[[c]] =
    {ScientificForm[Sort[probability, OrderedQ[{{#1}, {#2}}] &][[1, 1], 2]],
  {c, 1, Dimensions[counter][[1]]}]

table = Join[headerx, Transpose[Join[Transpose[counter],
  Transpose[parallelannotation],
  Transpose[parallelprobability],
  Transpose[antiannotation],
  Transpose[antiprobability]]]];
TableForm[table]
```

| Eigenarray | Most Likely Parallel Association | P-Value of Parallel Association | Most Likely Antiparallel Association | P-Value of Antiparallel Association |
|------------|--|---------------------------------------|--|---|
| 1 | G2/M | 2.2×10^{-1} | M/G1 | 6.7×10^{-3} |
| 2 | None | 1.8×10^{-3} | M/G1 | 1.4×10^{-7} |
| 3 | M/G1 | 6.7×10^{-3} | S | 8.2×10^{-2} |
| 4 | G1 | 1.4×10^{-1} | None | 1.2×10^{-1} |

(* Pheromone Response Annotations *)

```

annotations = genenames[[7]];
stages = {"Up", "Down", "None"};

most = 150;
numbers =
  Flatten[Table[{Count[Flatten[annotations], stages[[a]]], {a, 1, Dimensions[stages][[1]]}],
counter = Table[{a}, {a, 1, 4}];
probability = Table[{0}, {a, 1, Dimensions[counter][[1]]};
parallelannotation = Table[{0}, {a, 1, Dimensions[counter][[1]]};
parallelprobability = Table[{0}, {a, 1, Dimensions[counter][[1]]};
antiannotation = Table[{0}, {a, 1, Dimensions[counter][[1]]};
antiprobability = Table[{0}, {a, 1, Dimensions[counter][[1]]};

{44, 48, 1024}

Do[{
  pattern = Transpose[Sort[Transpose[Join[{Transpose[eigenarrays][[c]], {annotations}],
    OrderedQ[{{#2}, {#1}}] &][[2]],
  table = Table[{
    stages[[a]],
    numbers[[a]],
    Count[Flatten[Drop[pattern, {most + 1, genes}], stages[[a]]],
  {a, 1, Dimensions[stages][[1]]}],
  probability = Table[{
    Sum[N[Binomial[table[[a, 2]], b] * Binomial[genes - table[[a, 2]], most - b] /
      Binomial[genes, most]], {b, table[[a, 3]], most}],
    stages[[a]],
  {a, 1, Dimensions[stages][[1]]}],
  parallelannotation[[c]] = {Sort[probability, OrderedQ[{{#1}, {#2}}] &][[1, 2]],
  parallelprobability[[c]] =
  {ScientificForm[Sort[probability, OrderedQ[{{#1}, {#2}}] &][[1, 1], 2]],
  table = Table[{
    stages[[a]],
    numbers[[a]],
    Count[Flatten[Drop[pattern, {1, genes - most}], stages[[a]]],
  {a, 1, Dimensions[stages][[1]]}],
  probability = Table[{
    Sum[N[Binomial[table[[a, 2]], b] * Binomial[genes - table[[a, 2]], most - b] /
      Binomial[genes, most]], {b, table[[a, 3]], most}],
    stages[[a]],
  {a, 1, Dimensions[stages][[1]]}],
  antiannotation[[c]] = {Sort[probability, OrderedQ[{{#1}, {#2}}] &][[1, 2]],
  antiprobability[[c]] =
  {ScientificForm[Sort[probability, OrderedQ[{{#1}, {#2}}] &][[1, 1], 2]],
  {c, 1, Dimensions[counter][[1]]}]

table = Join[headerx, Transpose[Join[Transpose[counter],
  Transpose[parallelannotation],
  Transpose[parallelprobability],
  Transpose[antiannotation],
  Transpose[antiprobability]]]];
TableForm[table]

```


| Eigenarray | Most Likely Parallel Association | P-Value of Parallel Association | Most Likely Antiparallel Association | P-Value of Antiparallel Association |
|------------|--|---------------------------------------|--|---|
| 1 | Down | 3.1×10^{-1} | Up | 3.5×10^{-6} |
| 2 | None | 1.8×10^{-1} | Down | 7.8×10^{-3} |
| 3 | Up | 1.2×10^{-1} | Down | 1.8×10^{-1} |
| 4 | None | $4. \times 10^{-1}$ | Down | 4.7×10^{-1} |

(* 27. What annotations do the top four eigenarrays associate with after pseudoinverse projection? *)