

clusterbio.m

```
%  
% Script file: clusterbio.m - Drawing 2d dendrogram  
%  
d=16; N=55;  
fin=fopen('biodata.txt');  
fgetl(fin); fgetl(fin); fgetl(fin); % skip 3 headlines  
A=fscanf(fin,'%f',[1+N d]);  
%  
% Select only 38 patients for testing clusterbio  
%  
X=A(2:39,1:d); % 38 patients of NVI, 17 patients of HCC VI  
R={'Pat101','Pat103','Pat105','Pat107','Pat109','Pat110',...  
  'Pat201','Pat203','Pat205','Pat207','Pat209','Pat211',...  
  'Pat301','Pat303','Pat305','Pat307','Pat309','Pat311',...  
  'Pat401','Pat403','Pat405','Pat407','Pat409','Pat411',...  
  'Pat501','Pat503','Pat505','Pat507','Pat509','Pat511',...  
  'Pat601','Pat603','Pat605','Pat607','Pat609','Pat611',...  
  'Pat99005','Pat99007'};  
C={'Gene01','Gene02','Gene03','Gene04','Gene05','Gene06','Gene07','Gene08',...  
  'Gene09','Gene10','Gene11','Gene12','Gene13','Gene14','Gene15','Gene16'};  
clustergram(X,'Pdist','euclidean','Linkage','complete','Dimension',2,...  
  'ROWLABELS',R,'COLUMNLABELS',C,'Dendrogram',{'color',5})
```

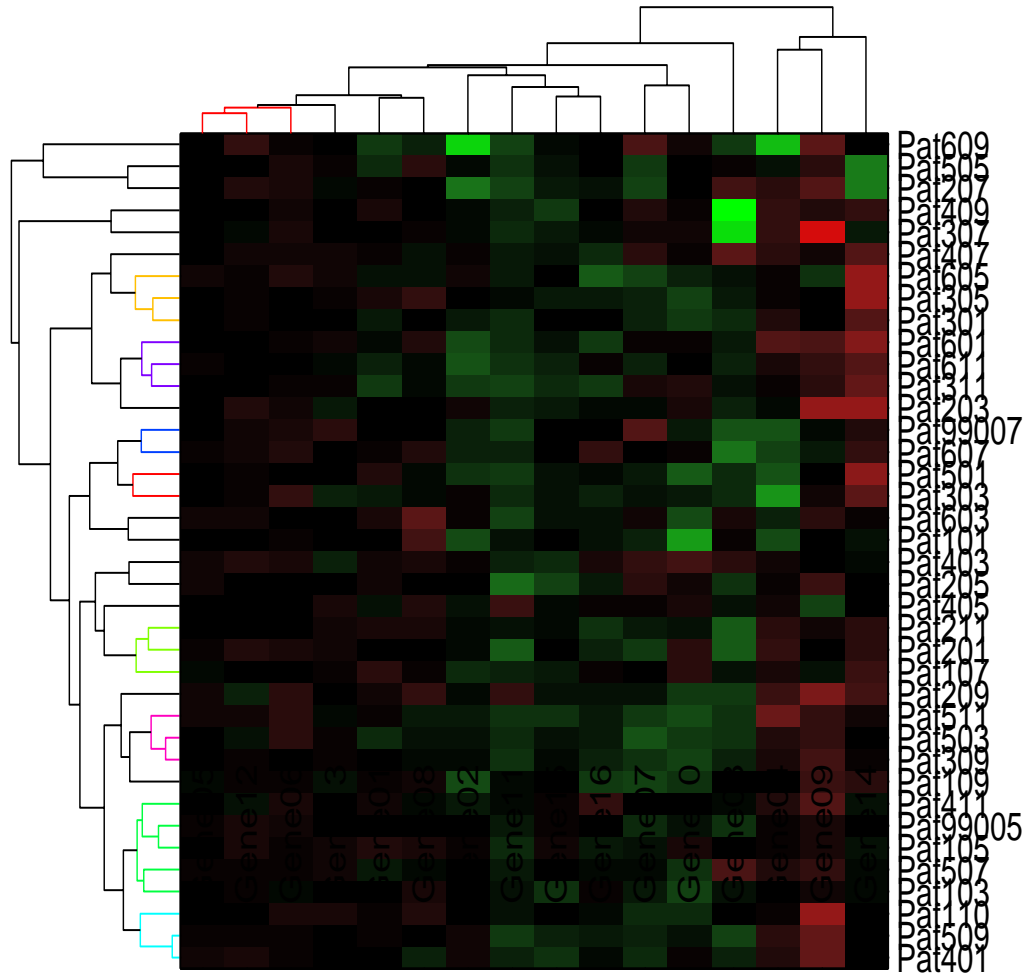


Figure 1: 2D Dendrogram for biodata.txt