

- Construct an FDR program using the basic approach
- Input :
 - Vector of P values
 - Q value (desired false discovery rate)
 - Are the data independent or not? (T,F input)
- Output
 - Graph like that in slide 14
 - The Tests that are considered discoveries (“interesting”) from the original order of the p values
 - Whether you assumed independence or not
- Comment your code
- Test your code with the vectors psmall.renal,plarge.renal
- Submit your code with results of your test

Commented Code:

```
fdrmyv<-function(p_values, Q, independent = TRUE) {
  #Sort P values
  sorted_p <- sort(p_values)
  #count tests
  m <- length(sorted_p)
  #Plot sorted Pvalues(smallest to largest) vs 1:m
  plot(1:m, sorted_p, xlab = "Test Index", ylab = "P Value",
       main = "Sorted P Values vs Test Index")
  #conditional statement to modify the threshold line calculation
  if (independent) {
    threshold_line <- Q * (1:m) / m
  } else {
    threshold_line <- Q * (1:m) / (m * sum(1 / (1:m)))
  }
  #draw line Q*c(1:m)/m vs 1:m
  lines(1:m, threshold_line)
  #find p*
  p_star <- max(sorted_p[sorted_p <= threshold_line])
  #find interesting pvalues
  interesting <- p_values <= p_star
  #find pvalues and their indecies below the q line
  below_threshold_indices <- which(sorted_p <= threshold_line)
  #plots the pval points in the color blue
  points(below_threshold_indices, sorted_p[below_threshold_indices], col = "blue", pch = 20)
  #outputs the list of hypotheses which are interesting by number in the original unsorted list of
  p values.
  result <- list(
    ind = independent,
```

```

    p_values = p_values[interesting]
)

return(result)
}

```

Command:

```
> fdrmyv(plarge.renal,0.05,T)
```

```
$ind
```

```
[1] TRUE
```

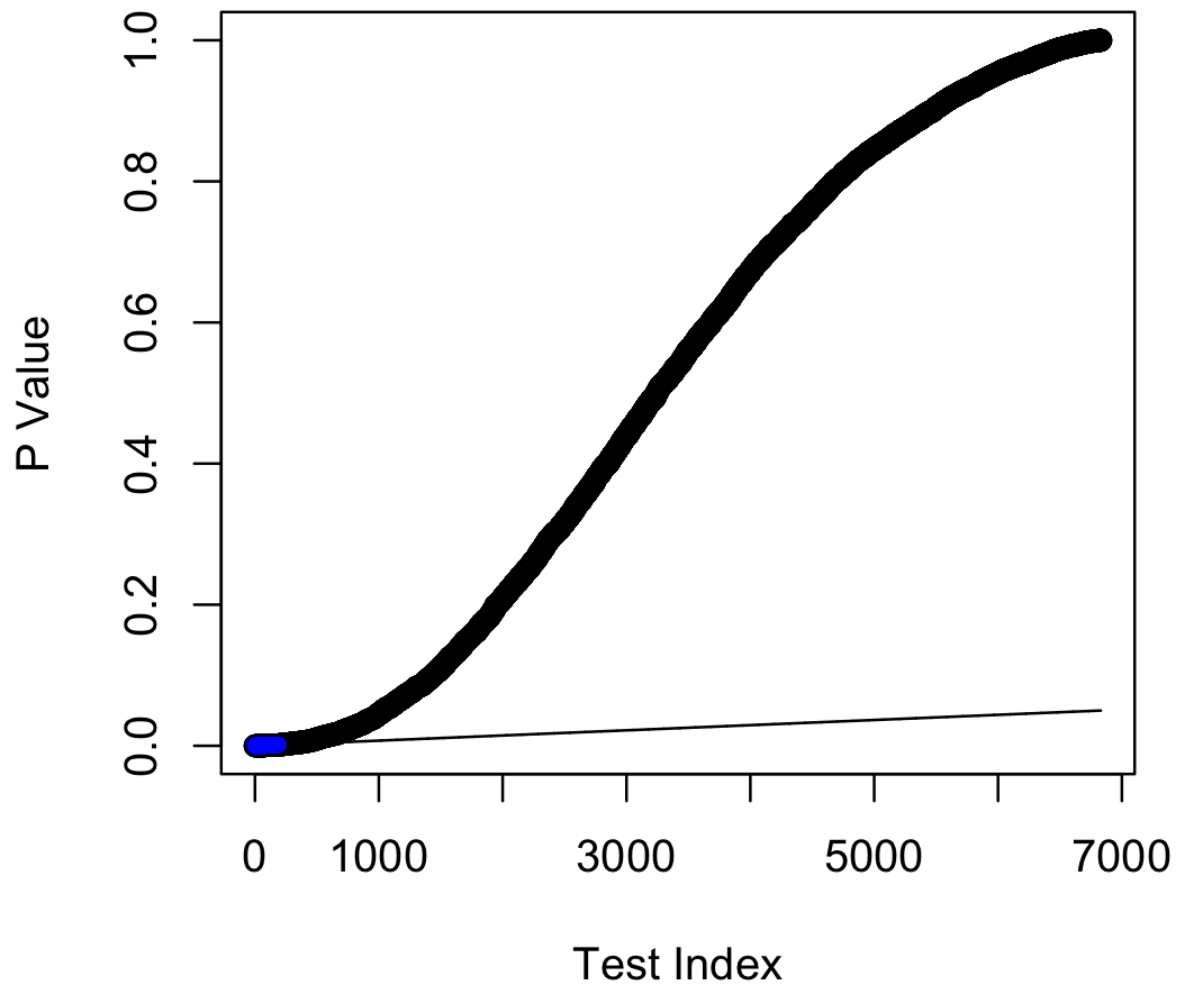
```
$p_values
```

31	98	192	282
2.959879e-04	7.642524e-04	2.871781e-04	1.152815e-04
287	371	2944	3273
4.511068e-04	1.076571e-04	6.526256e-04	1.205582e-04
3480	3921	3944	3945
1.239189e-03	7.400137e-04	2.225394e-04	2.363462e-04
4352	4698	4889	4974
5.073217e-04	5.549103e-04	7.053085e-05	1.315523e-03
4985	5308	5332	5335
7.374827e-04	1.099037e-03	7.906926e-04	5.480408e-04
5343	5351	5373	5377
7.562665e-04	6.264279e-04	4.736922e-04	2.855105e-04
5378	5380	5422	5424
5.869518e-04	9.000759e-04	8.739628e-04	8.097469e-04
5436	5463	5484	5488
9.178630e-04	1.039181e-03	5.438401e-04	1.007565e-03
5512	5513	5514	5521
2.741131e-04	8.056634e-04	2.458763e-04	8.174293e-04
5522	5528	5529	5530
4.416560e-04	6.325155e-04	8.674428e-04	4.529063e-04
5545	5549	5585	5587
1.186079e-03	4.799969e-04	2.229922e-04	1.346991e-03
5589	5590	5608	5617
7.284643e-05	1.491713e-04	9.327992e-05	4.290037e-04
5620	5623	5628	5632
5.624074e-04	1.237428e-03	2.459207e-04	1.886811e-04
5635	5636	5637	5641
6.818866e-04	2.123553e-04	3.813318e-04	1.115732e-03
5651	5652	5670	5680
3.979354e-05	9.514090e-04	5.142784e-04	3.795537e-04
5759	5761	5762	5763
1.307103e-03	1.782726e-04	5.077594e-04	6.655769e-04

5795	5796	5797	5803
5.851834e-04	3.460966e-04	1.362555e-04	8.732202e-04
5804	5805	5807	5812
2.123486e-04	2.683372e-04	6.868115e-04	2.593974e-05
5813	5816	5820	5821
8.568311e-05	1.097744e-03	9.447324e-04	5.109434e-04
5822	5823	5828	5830
3.483273e-04	1.112049e-04	1.132543e-05	1.566907e-04
5832	5833	5836	5837
6.700364e-05	2.720452e-04	1.296398e-03	1.277771e-03
5841	5842	5847	5848
4.250192e-04	8.450116e-04	1.233250e-03	2.213332e-04
5849	5850	5853	5854
6.384393e-04	5.631613e-04	4.764993e-04	5.972159e-04
5855	5856	5862	5865
2.958955e-04	9.829917e-04	8.556281e-04	6.647926e-04
5875	5884	5886	5887
5.598866e-04	3.201951e-04	5.037025e-04	8.461922e-04
5889	5897	5898	5899
5.157007e-04	8.791929e-04	4.761664e-06	1.977438e-05
5900	5901	5902	5913
3.330095e-04	1.498965e-05	1.061645e-05	1.038983e-03
5921	5922	5923	5924
5.709334e-05	4.227788e-05	7.438005e-04	8.006230e-04
5933	5934	5936	5937
1.311121e-05	7.221992e-05	1.535013e-04	1.478501e-05
5938	5939	5940	5941
6.657444e-05	2.700294e-05	9.824466e-04	1.398805e-05
5942	5944	5945	5946
1.281628e-07	7.649251e-04	1.136976e-03	2.212664e-04
5947	5949	5950	5958
4.971904e-04	3.328199e-04	4.514374e-04	1.728395e-04
5960	5962	5964	5966
1.063450e-03	2.720865e-04	1.146331e-04	4.656714e-04
5967	5968	5970	5971
5.802970e-04	7.908351e-04	9.600935e-04	7.635310e-04
5972	5974	5975	5977
1.002950e-03	2.558267e-04	2.754016e-04	8.308493e-05
5978	5979	5980	5981
4.649841e-05	8.389548e-05	4.517211e-05	2.608405e-04
5984	5988	5989	6006
8.739562e-04	1.626714e-04	8.194811e-05	5.953713e-04
6046	6048	6049	6072
1.047143e-03	2.340885e-04	1.180876e-03	2.042677e-04

6073	6081	6082	6084
1.049499e-03	7.859878e-04	1.290564e-03	9.859505e-06
6085	6086	6087	6091
1.011994e-04	1.873110e-04	7.331746e-04	1.999285e-05
6094	6095	6096	6097
2.781741e-04	9.749322e-05	9.235397e-04	4.929365e-05
6099	6113	6117	6147
2.493569e-04	9.703096e-04	5.828510e-04	8.985490e-04
6153	6167	6188	6244
1.010780e-03	1.037534e-03	8.691471e-05	8.005049e-04
6245	6246	6257	6258
5.563732e-04	7.341839e-04	5.878467e-04	8.574240e-04
6259	6262	6277	6305
1.664674e-04	2.078417e-04	1.375651e-03	6.041662e-04
6306	6339	6383	6391
1.015877e-04	1.654805e-04	6.393138e-04	1.008077e-03
6392	6393	6431	6553
8.881405e-04	3.242900e-04	2.678556e-04	2.555699e-04

Sorted P Values vs Test Index



```
> fdrmyv(psmall.renal,0.1,T)
```

```
$ind
```

```
[1] TRUE
```

```
$p_values
```

28	691	814	1088
3.209616e-04	4.262325e-04	7.953098e-05	1.426557e-04
1818	1964	2183	2245
6.960019e-05	3.317904e-04	1.616803e-04	1.698585e-04
2250	2255	2256	2258
2.150155e-04	4.255775e-04	2.513404e-04	2.161570e-04

2471	2551	2723	2724
3.459943e-04	3.070802e-04	2.452732e-04	1.824076e-04
2738	2820	2828	2836
2.421681e-04	3.681149e-04	4.142306e-04	8.449396e-05
3108	3175	4059	4062
9.466860e-05	2.551468e-04	3.570159e-04	8.559170e-06
4195	4216	4504	4505
1.624721e-04	4.049933e-04	1.469877e-04	4.282842e-04
4893	6423		
3.618564e-05	3.538998e-04		

Sorted P Values vs Test Index

