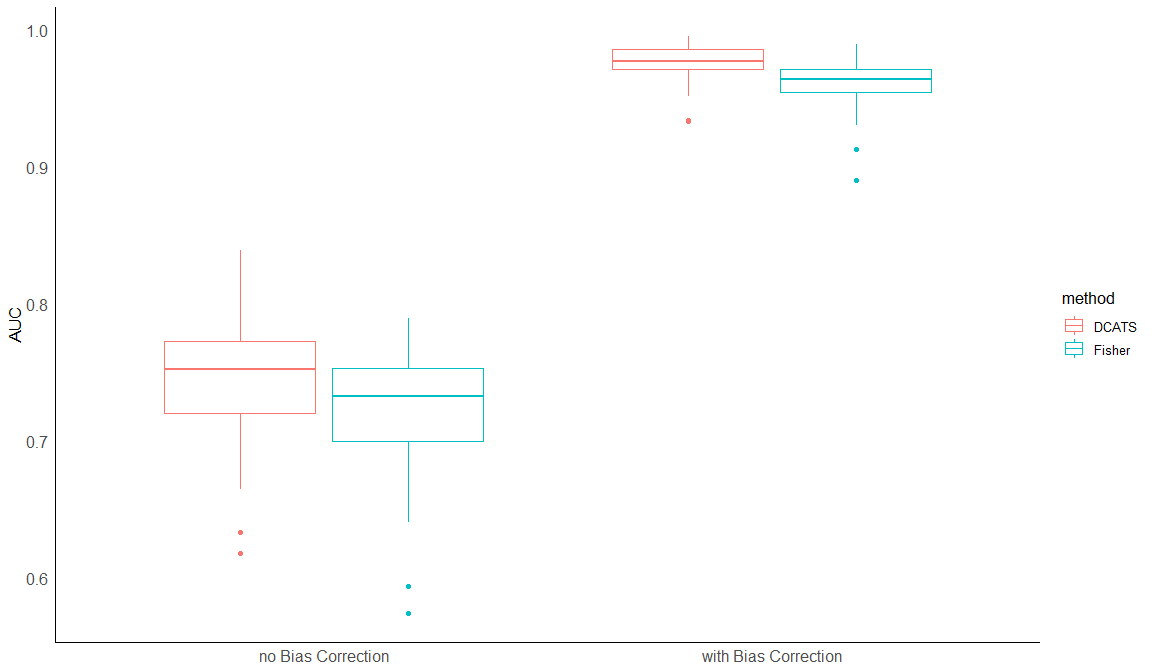
Figure Draft - Three plots version

Xinyi Lin

1/7/2022

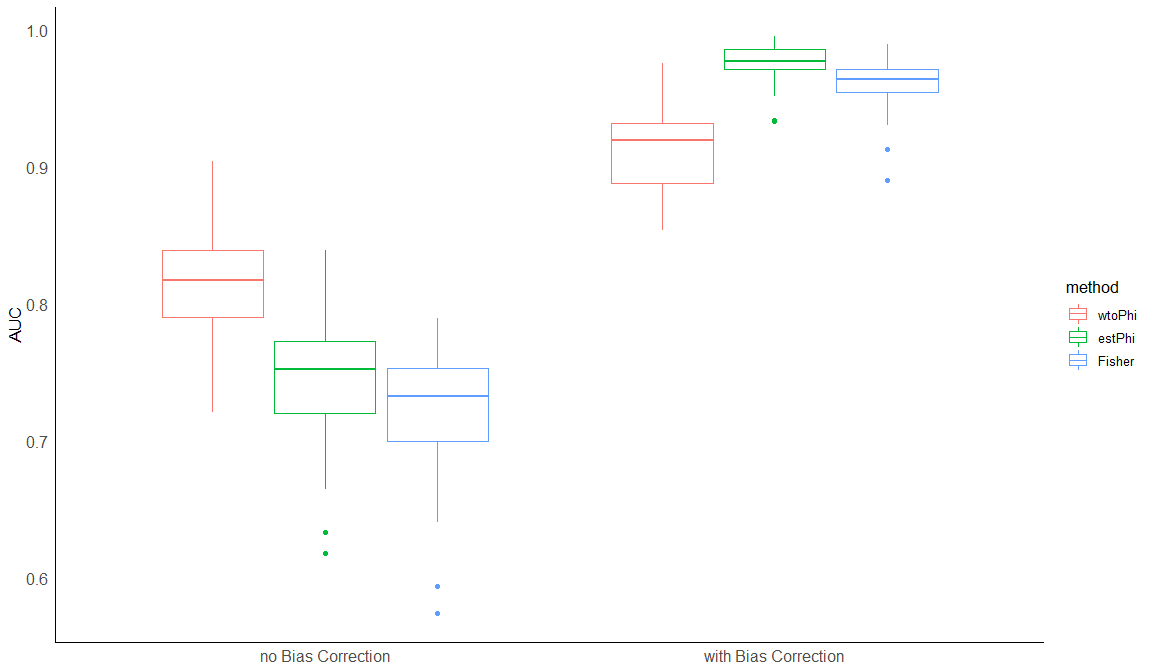
## Figure 1

### Figure 1 - B

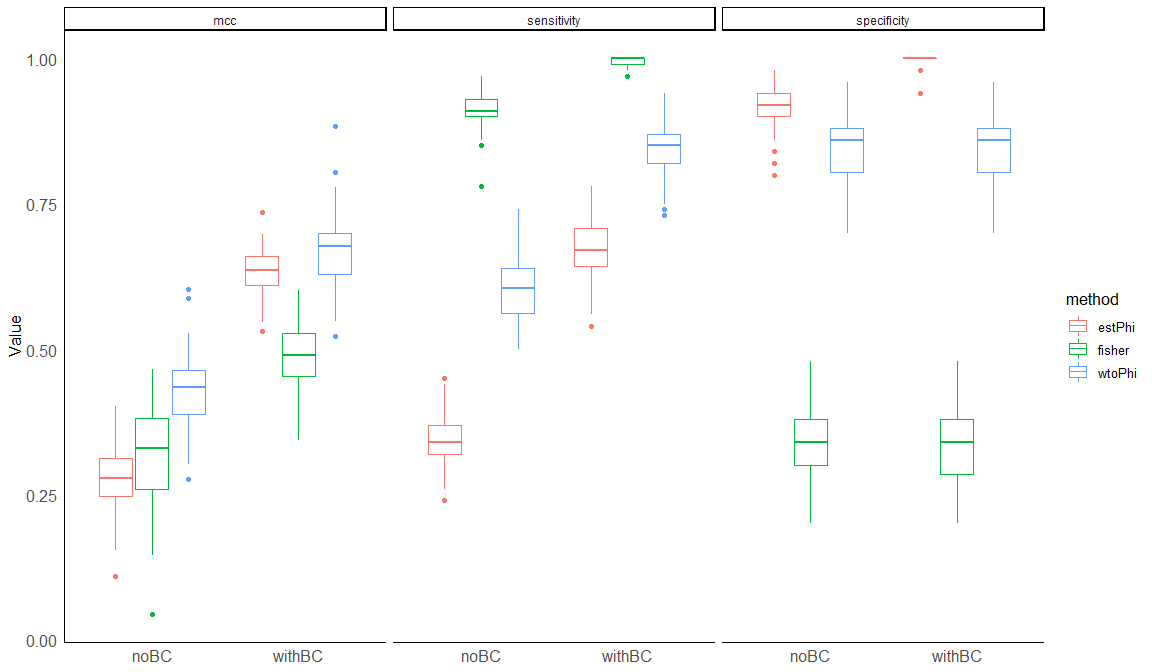


## Saving 12 x 7 in image

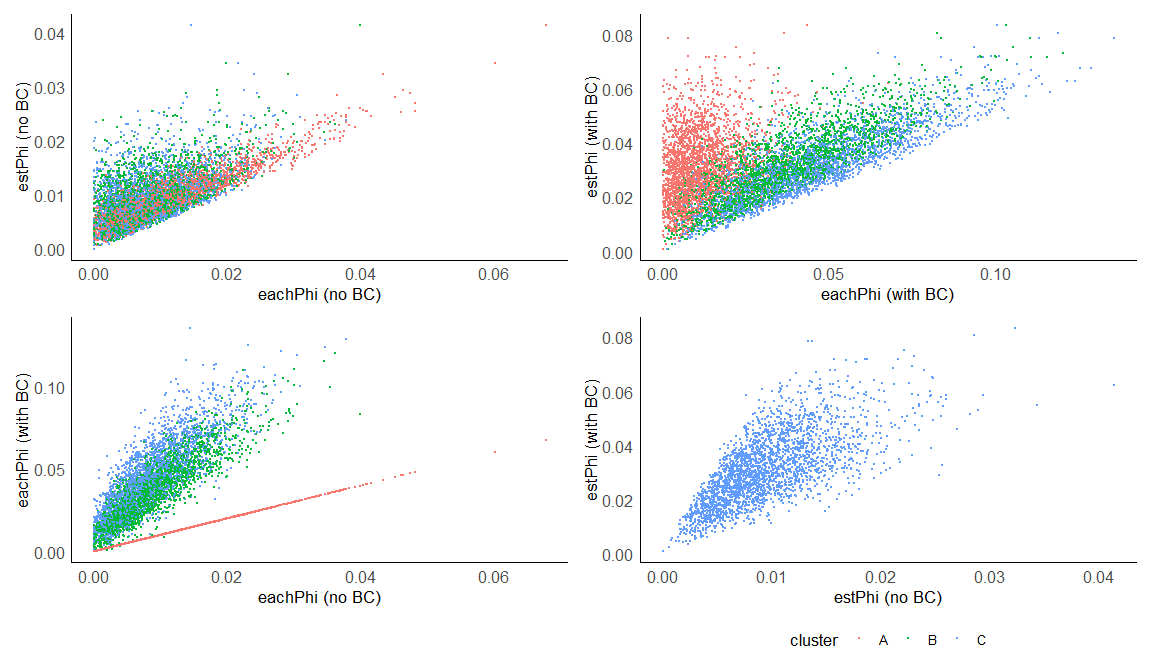
Simulation 1: Supplementary Plots

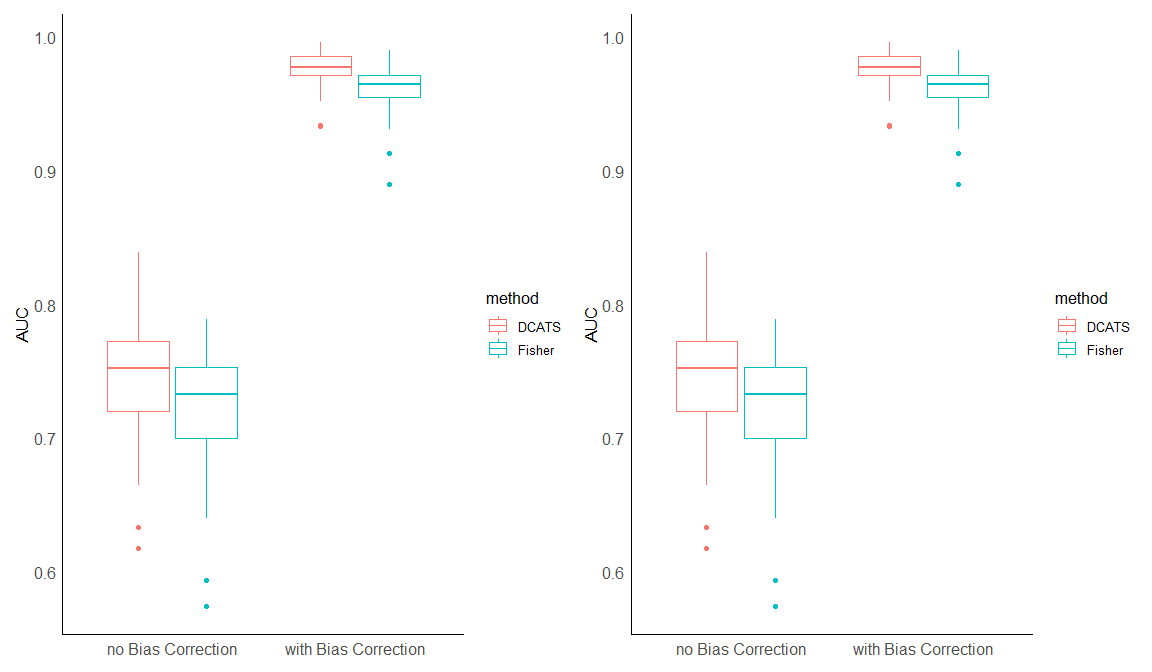


## Saving 12 x 7 in image



## Saving 12 x 7 in image





## Figure 2

### Figure 2-A

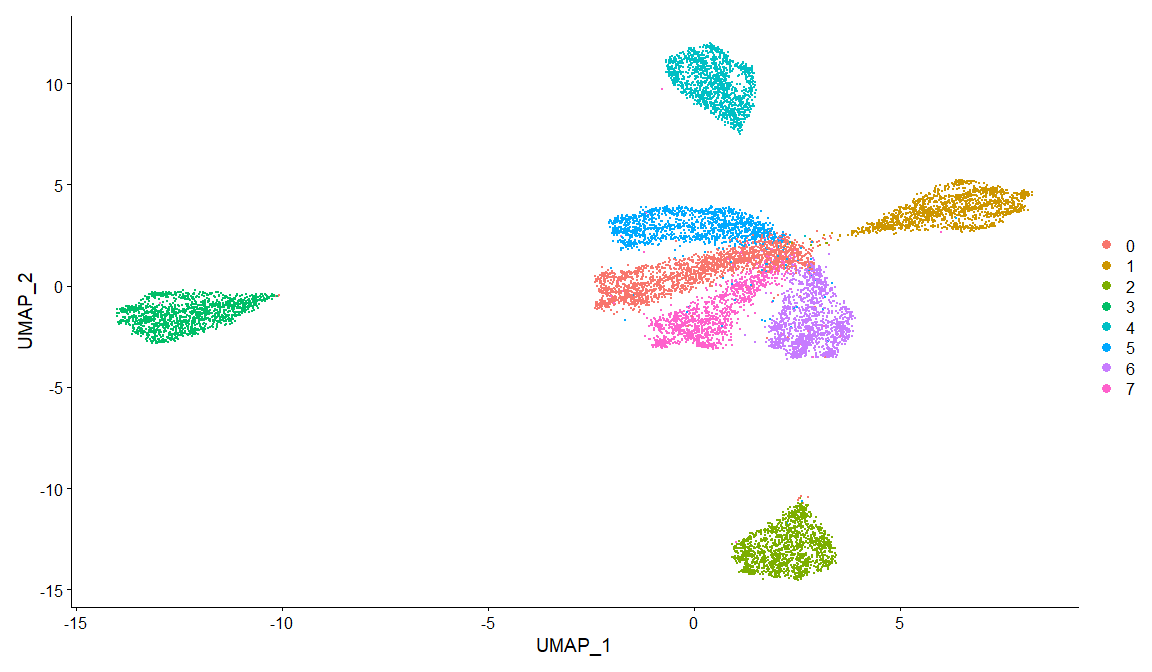
The Distribution of cell pool

## Warning: The following arguments are not used: row.names

## Centering and scaling data matrix

## PC\_ 1   
## Positive: Gene862, Gene593, Gene473, Gene94, Gene511, Gene508, Gene724, Gene830, Gene623, Gene584   
## Gene662, Gene396, Gene439, Gene214, Gene524, Gene714, Gene285, Gene485, Gene395, Gene19   
## Gene840, Gene191, Gene676, Gene88, Gene418, Gene111, Gene569, Gene713, Gene179, Gene434   
## Negative: Gene754, Gene241, Gene650, Gene117, Gene705, Gene244, Gene665, Gene971, Gene864, Gene443   
## Gene734, Gene540, Gene908, Gene280, Gene378, Gene369, Gene456, Gene136, Gene26, Gene401   
## Gene159, Gene267, Gene594, Gene965, Gene559, Gene174, Gene322, Gene703, Gene148, Gene935   
## PC\_ 2   
## Positive: Gene273, Gene88, Gene327, Gene713, Gene173, Gene981, Gene397, Gene60, Gene349, Gene724   
## Gene356, Gene511, Gene24, Gene150, Gene14, Gene624, Gene373, Gene418, Gene161, Gene819   
## Gene57, Gene126, Gene817, Gene142, Gene214, Gene763, Gene485, Gene191, Gene46, Gene345   
## Negative: Gene171, Gene260, Gene138, Gene36, Gene189, Gene444, Gene68, Gene743, Gene93, Gene145   
## Gene806, Gene883, Gene809, Gene799, Gene726, Gene507, Gene170, Gene672, Gene896, Gene83   
## Gene147, Gene117, Gene53, Gene715, Gene867, Gene184, Gene673, Gene778, Gene125, Gene810   
## PC\_ 3   
## Positive: Gene655, Gene94, Gene171, Gene3, Gene241, Gene479, Gene624, Gene179, Gene833, Gene521   
## Gene883, Gene362, Gene513, Gene862, Gene951, Gene593, Gene830, Gene524, Gene391, Gene714   
## Gene797, Gene402, Gene419, Gene902, Gene600, Gene118, Gene584, Gene569, Gene865, Gene235   
## Negative: Gene754, Gene679, Gene458, Gene155, Gene27, Gene531, Gene220, Gene309, Gene208, Gene731   
## Gene298, Gene300, Gene614, Gene953, Gene782, Gene819, Gene428, Gene510, Gene566, Gene420   
## Gene765, Gene791, Gene730, Gene810, Gene255, Gene565, Gene393, Gene170, Gene68, Gene715   
## PC\_ 4   
## Positive: Gene521, Gene475, Gene525, Gene877, Gene888, Gene397, Gene431, Gene655, Gene651, Gene219   
## Gene85, Gene171, Gene235, Gene575, Gene970, Gene34, Gene860, Gene552, Gene201, Gene402   
## Gene780, Gene236, Gene839, Gene557, Gene301, Gene955, Gene36, Gene736, Gene349, Gene638   
## Negative: Gene214, Gene593, Gene862, Gene623, Gene662, Gene27, Gene569, Gene138, Gene473, Gene99   
## Gene511, Gene666, Gene395, Gene560, Gene676, Gene444, Gene809, Gene743, Gene510, Gene713   
## Gene425, Gene132, Gene398, Gene19, Gene723, Gene798, Gene787, Gene439, Gene94, Gene640   
## PC\_ 5   
## Positive: Gene166, Gene624, Gene179, Gene557, Gene970, Gene552, Gene993, Gene909, Gene663, Gene301   
## Gene623, Gene575, Gene799, Gene586, Gene797, Gene508, Gene548, Gene402, Gene877, Gene754   
## Gene830, Gene521, Gene235, Gene234, Gene213, Gene374, Gene404, Gene633, Gene19, Gene736   
## Negative: Gene14, Gene425, Gene362, Gene619, Gene444, Gene713, Gene439, Gene511, Gene70, Gene241   
## Gene6, Gene546, Gene184, Gene31, Gene946, Gene216, Gene781, Gene169, Gene593, Gene676   
## Gene651, Gene142, Gene775, Gene914, Gene67, Gene273, Gene351, Gene714, Gene640, Gene340

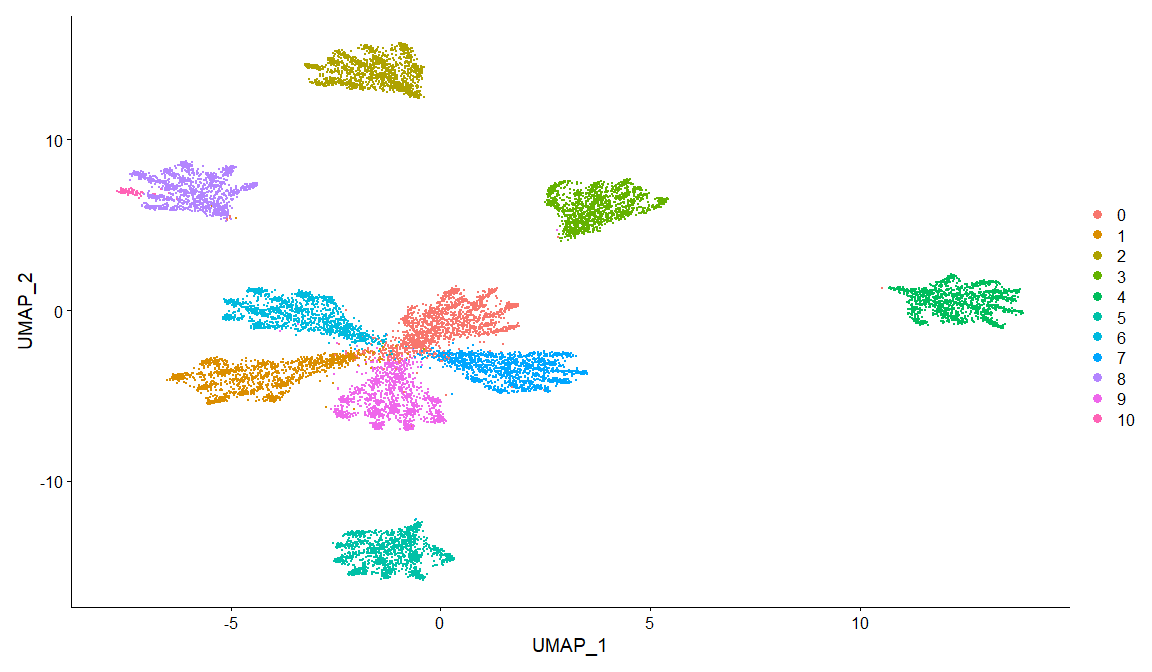
## Warning: The default method for RunUMAP has changed from calling Python UMAP via reticulate to the R-native UWOT using the cosine metric  
## To use Python UMAP via reticulate, set umap.method to 'umap-learn' and metric to 'correlation'  
## This message will be shown once per session



## Warning: The following arguments are not used: row.names

## Centering and scaling data matrix

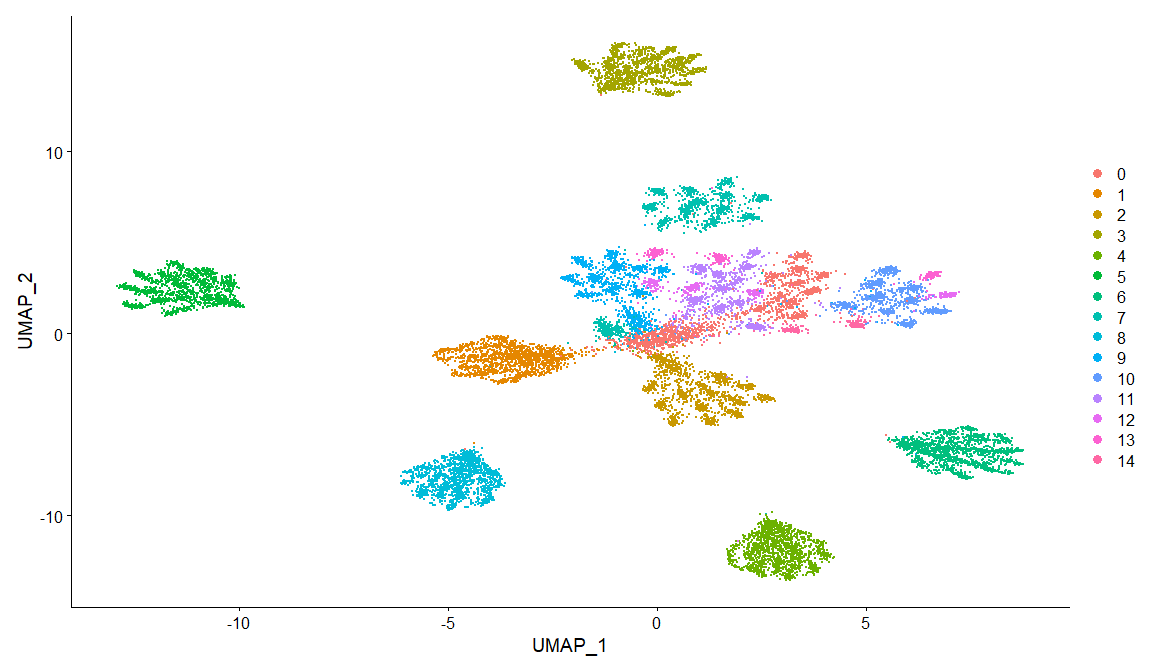
## PC\_ 1   
## Positive: Gene623, Gene412, Gene469, Gene313, Gene433, Gene400, Gene198, Gene589, Gene464, Gene973   
## Gene151, Gene251, Gene654, Gene340, Gene317, Gene56, Gene102, Gene524, Gene392, Gene872   
## Gene344, Gene766, Gene748, Gene980, Gene303, Gene873, Gene811, Gene652, Gene155, Gene485   
## Negative: Gene605, Gene650, Gene746, Gene143, Gene110, Gene153, Gene409, Gene620, Gene714, Gene460   
## Gene755, Gene615, Gene475, Gene370, Gene936, Gene65, Gene950, Gene335, Gene3, Gene921   
## Gene164, Gene328, Gene195, Gene985, Gene821, Gene818, Gene849, Gene793, Gene859, Gene140   
## PC\_ 2   
## Positive: Gene413, Gene418, Gene579, Gene479, Gene373, Gene605, Gene513, Gene190, Gene559, Gene388   
## Gene601, Gene560, Gene660, Gene816, Gene522, Gene24, Gene203, Gene542, Gene746, Gene912   
## Gene566, Gene98, Gene5, Gene438, Gene241, Gene186, Gene914, Gene672, Gene270, Gene322   
## Negative: Gene258, Gene339, Gene735, Gene469, Gene503, Gene384, Gene820, Gene595, Gene833, Gene556   
## Gene675, Gene617, Gene168, Gene259, Gene96, Gene470, Gene491, Gene84, Gene42, Gene589   
## Gene607, Gene488, Gene321, Gene649, Gene313, Gene552, Gene276, Gene608, Gene347, Gene919   
## PC\_ 3   
## Positive: Gene746, Gene820, Gene842, Gene373, Gene215, Gene96, Gene927, Gene800, Gene648, Gene739   
## Gene20, Gene46, Gene773, Gene913, Gene402, Gene74, Gene86, Gene349, Gene672, Gene347   
## Gene42, Gene203, Gene99, Gene689, Gene291, Gene605, Gene844, Gene237, Gene932, Gene14   
## Negative: Gene524, Gene627, Gene544, Gene464, Gene23, Gene510, Gene384, Gene251, Gene623, Gene400   
## Gene155, Gene872, Gene313, Gene781, Gene875, Gene809, Gene38, Gene340, Gene366, Gene56   
## Gene642, Gene595, Gene469, Gene315, Gene344, Gene992, Gene973, Gene490, Gene589, Gene127   
## PC\_ 4   
## Positive: Gene731, Gene807, Gene608, Gene811, Gene385, Gene274, Gene402, Gene513, Gene356, Gene12   
## Gene234, Gene809, Gene158, Gene510, Gene508, Gene315, Gene362, Gene118, Gene616, Gene11   
## Gene958, Gene339, Gene544, Gene443, Gene605, Gene961, Gene266, Gene938, Gene276, Gene384   
## Negative: Gene689, Gene866, Gene67, Gene533, Gene746, Gene219, Gene552, Gene584, Gene564, Gene941   
## Gene267, Gene350, Gene595, Gene695, Gene503, Gene777, Gene148, Gene326, Gene934, Gene854   
## Gene613, Gene59, Gene617, Gene290, Gene883, Gene344, Gene711, Gene488, Gene352, Gene56   
## PC\_ 5   
## Positive: Gene464, Gene158, Gene927, Gene265, Gene64, Gene173, Gene362, Gene230, Gene690, Gene739   
## Gene258, Gene424, Gene412, Gene508, Gene668, Gene902, Gene259, Gene349, Gene672, Gene954   
## Gene664, Gene236, Gene99, Gene938, Gene653, Gene523, Gene597, Gene400, Gene560, Gene695   
## Negative: Gene627, Gene148, Gene42, Gene267, Gene438, Gene644, Gene270, Gene103, Gene912, Gene347   
## Gene777, Gene126, Gene800, Gene957, Gene813, Gene911, Gene131, Gene809, Gene384, Gene839   
## Gene987, Gene59, Gene84, Gene1, Gene276, Gene607, Gene262, Gene434, Gene658, Gene117

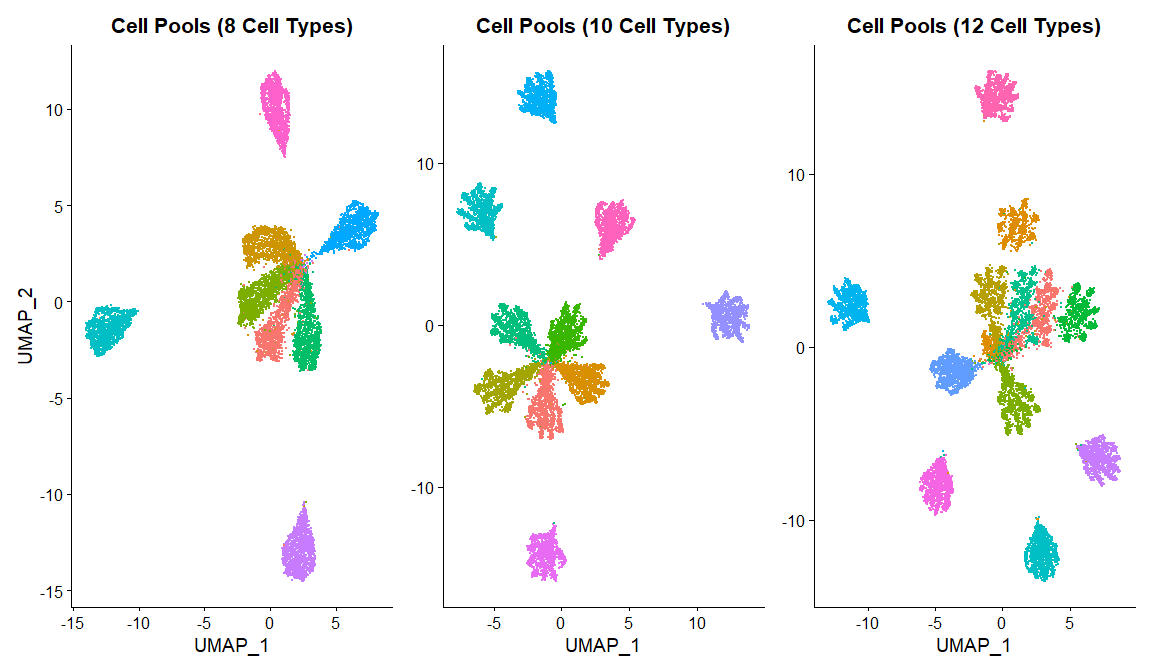


## Warning: The following arguments are not used: row.names

## Centering and scaling data matrix

## PC\_ 1   
## Positive: Gene422, Gene948, Gene338, Gene23, Gene233, Gene837, Gene895, Gene131, Gene387, Gene552   
## Gene209, Gene428, Gene740, Gene396, Gene366, Gene835, Gene554, Gene149, Gene269, Gene516   
## Gene488, Gene522, Gene670, Gene571, Gene560, Gene189, Gene65, Gene700, Gene937, Gene866   
## Negative: Gene958, Gene216, Gene810, Gene868, Gene452, Gene870, Gene563, Gene44, Gene820, Gene925   
## Gene329, Gene848, Gene767, Gene972, Gene660, Gene311, Gene377, Gene156, Gene207, Gene323   
## Gene721, Gene507, Gene161, Gene604, Gene953, Gene126, Gene712, Gene673, Gene626, Gene580   
## PC\_ 2   
## Positive: Gene675, Gene736, Gene393, Gene777, Gene255, Gene799, Gene66, Gene925, Gene441, Gene661   
## Gene966, Gene881, Gene665, Gene847, Gene15, Gene580, Gene360, Gene44, Gene180, Gene502   
## Gene600, Gene685, Gene712, Gene208, Gene867, Gene819, Gene26, Gene869, Gene519, Gene323   
## Negative: Gene21, Gene972, Gene197, Gene500, Gene95, Gene56, Gene821, Gene745, Gene725, Gene642   
## Gene127, Gene813, Gene784, Gene362, Gene790, Gene960, Gene43, Gene341, Gene927, Gene911   
## Gene493, Gene126, Gene602, Gene803, Gene588, Gene673, Gene351, Gene576, Gene399, Gene344   
## PC\_ 3   
## Positive: Gene222, Gene56, Gene989, Gene957, Gene639, Gene526, Gene311, Gene143, Gene799, Gene215   
## Gene671, Gene238, Gene74, Gene328, Gene966, Gene815, Gene917, Gene409, Gene1000, Gene932   
## Gene165, Gene860, Gene347, Gene704, Gene717, Gene275, Gene707, Gene721, Gene9, Gene290   
## Negative: Gene339, Gene216, Gene608, Gene870, Gene287, Gene728, Gene803, Gene952, Gene995, Gene436   
## Gene227, Gene745, Gene137, Gene797, Gene360, Gene911, Gene661, Gene810, Gene859, Gene443   
## Gene407, Gene766, Gene993, Gene252, Gene887, Gene505, Gene434, Gene316, Gene566, Gene820   
## PC\_ 4   
## Positive: Gene632, Gene573, Gene874, Gene809, Gene381, Gene762, Gene526, Gene191, Gene804, Gene213   
## Gene790, Gene174, Gene593, Gene3, Gene838, Gene248, Gene783, Gene382, Gene881, Gene991   
## Gene889, Gene813, Gene333, Gene7, Gene328, Gene193, Gene394, Gene710, Gene237, Gene857   
## Negative: Gene215, Gene584, Gene887, Gene284, Gene681, Gene310, Gene409, Gene777, Gene74, Gene350   
## Gene230, Gene239, Gene406, Gene21, Gene956, Gene377, Gene80, Gene252, Gene664, Gene338   
## Gene391, Gene110, Gene534, Gene363, Gene495, Gene900, Gene407, Gene316, Gene810, Gene431   
## PC\_ 5   
## Positive: Gene790, Gene733, Gene1000, Gene948, Gene328, Gene534, Gene495, Gene143, Gene848, Gene953   
## Gene884, Gene56, Gene7, Gene476, Gene275, Gene791, Gene341, Gene717, Gene844, Gene878   
## Gene641, Gene347, Gene839, Gene689, Gene870, Gene206, Gene424, Gene287, Gene116, Gene314   
## Negative: Gene129, Gene582, Gene207, Gene744, Gene246, Gene707, Gene858, Gene137, Gene125, Gene665   
## Gene778, Gene682, Gene350, Gene538, Gene711, Gene905, Gene952, Gene200, Gene960, Gene322   
## Gene580, Gene979, Gene321, Gene21, Gene589, Gene987, Gene838, Gene83, Gene503, Gene851





### Figure 2-B

#### Different numbers of replicates

## [1] "D:/Data/DCATS/simulation/replicates/replicates2&2\_K8\_con100\_splatter3000&3000para.RData"  
## [2] "D:/Data/DCATS/simulation/replicates/replicates3&3\_K8\_con100\_splatter3000&3000para.RData"  
## [3] "D:/Data/DCATS/simulation/replicates/replicates4&4\_K8\_con100\_splatter3000&3000para.RData"

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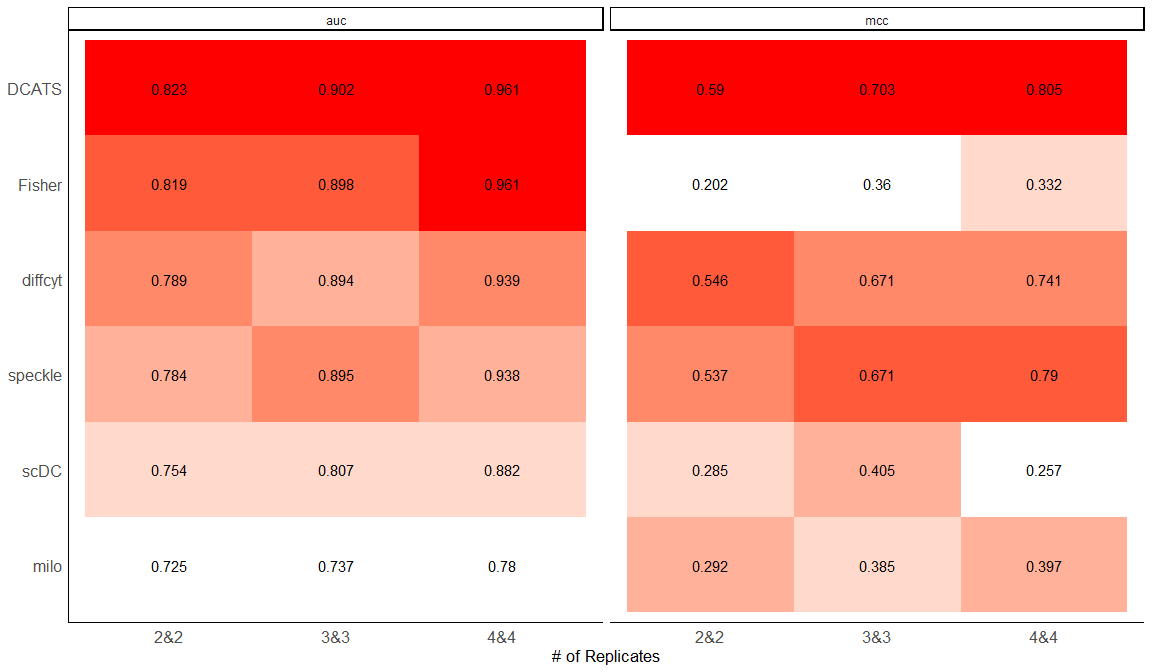
## Warning in if (!is.na(oper[[idx]])) {: the condition has length > 1 and only the  
## first element will be used

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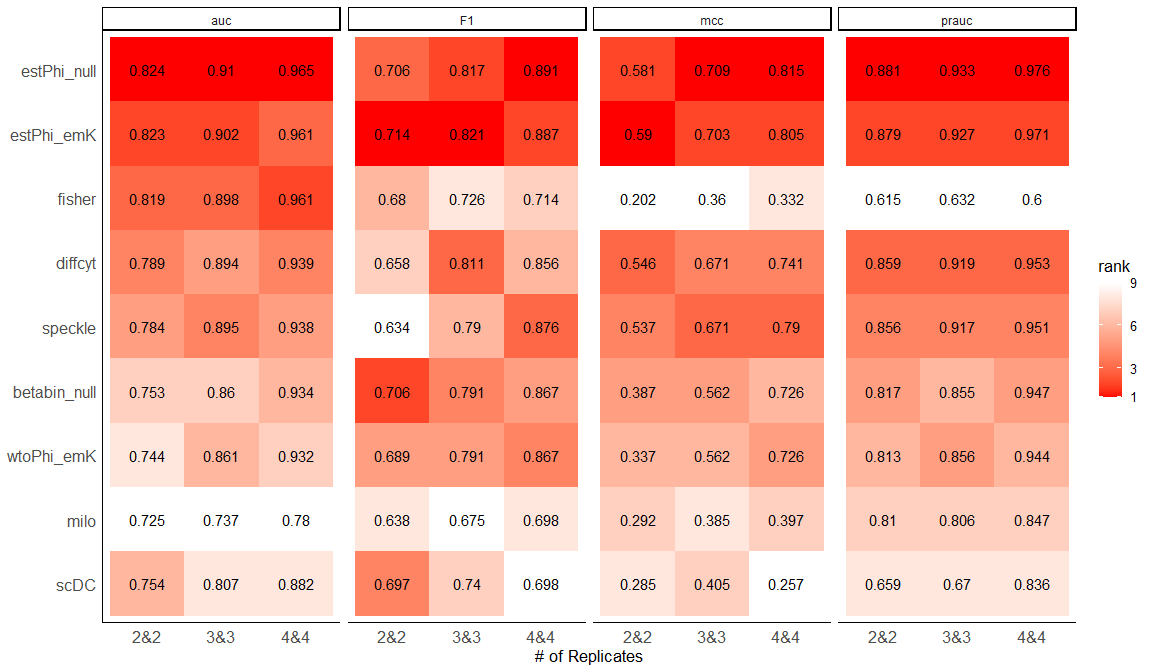
## Warning in if (!is.na(oper[[idx]])) {: the condition has length > 1 and only the  
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## method mcc auc sensitivity specificity F1 replicates  
## 1 estPhi\_emU 0.649 0.833 0.646 0.969 0.770 2&2  
## 2 estPhi\_null 0.581 0.824 0.562 0.969 0.706 2&2  
## 3 estPhi\_emK 0.590 0.823 0.573 0.969 0.714 2&2  
## 4 diffcyt 0.546 0.789 0.500 0.979 0.658 2&2  
## 5 speckle 0.537 0.784 0.469 0.990 0.634 2&2  
## 6 betabin\_null 0.387 0.753 0.740 0.646 0.706 2&2  
## 7 wtoPhi\_emK 0.337 0.744 0.740 0.594 0.689 2&2  
## 8 milo 0.292 0.725 0.625 0.667 0.638 2&2  
## 9 scDC 0.285 0.754 0.865 0.385 0.697 2&2  
## 10 fisher 0.202 0.819 0.896 0.260 0.680 2&2  
## 11 estPhi\_emU 0.732 0.910 0.792 0.933 0.852 3&3  
## 12 estPhi\_null 0.709 0.910 0.708 0.975 0.817 3&3  
## 13 estPhi\_emK 0.703 0.902 0.725 0.958 0.821 3&3  
## 14 diffcyt 0.671 0.894 0.733 0.925 0.811 3&3  
## 15 speckle 0.671 0.895 0.675 0.967 0.790 3&3  
## 16 wtoPhi\_emK 0.562 0.861 0.833 0.725 0.791 3&3  
## 17 betabin\_null 0.562 0.860 0.833 0.725 0.791 3&3  
## 18 milo 0.385 0.737 0.642 0.742 0.675 3&3  
## 19 scDC 0.405 0.807 0.950 0.383 0.740 3&3  
## 20 fisher 0.360 0.898 0.950 0.333 0.726 3&3  
## 21 estPhi\_emU 0.839 0.966 0.879 0.957 0.915 4&4  
## 22 estPhi\_null 0.815 0.965 0.810 0.991 0.891 4&4  
## 23 estPhi\_emK 0.805 0.961 0.810 0.983 0.887 4&4  
## 24 diffcyt 0.741 0.939 0.793 0.940 0.856 4&4  
## 25 speckle 0.790 0.938 0.793 0.983 0.876 4&4  
## 26 betabin\_null 0.726 0.934 0.897 0.828 0.867 4&4  
## 27 wtoPhi\_emK 0.726 0.932 0.897 0.828 0.867 4&4  
## 28 milo 0.397 0.780 0.698 0.698 0.698 4&4  
## 29 scDC 0.257 0.882 0.957 0.216 0.698 4&4  
## 30 fisher 0.332 0.961 1.000 0.198 0.714 4&4



Simulation 2: Supplementary Plots

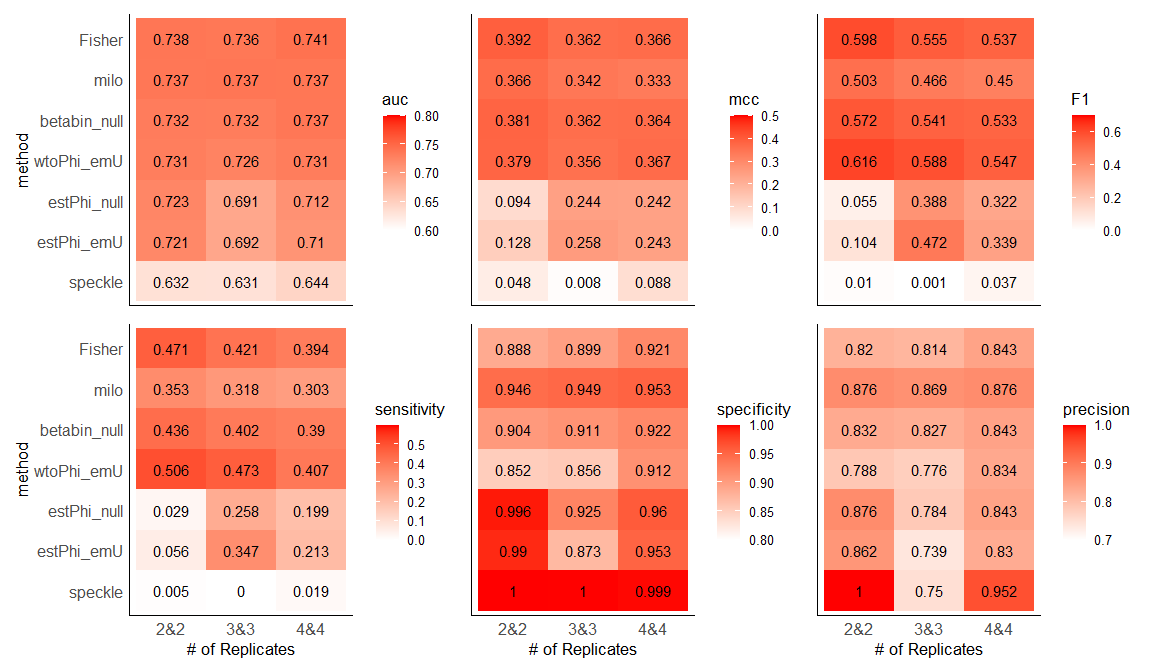


Details of statistics value

| method | mcc | auc | prauc | sensitivity | specificity | precision | F1 | replicates |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| estPhi\_null | 0.581 | 0.824 | 0.881 | 0.562 | 0.969 | 0.947 | 0.706 | 2&2 |
| estPhi\_emK | 0.590 | 0.823 | 0.879 | 0.573 | 0.969 | 0.948 | 0.714 | 2&2 |
| Fisher | 0.202 | 0.819 | 0.615 | 0.896 | 0.260 | 0.548 | 0.680 | 2&2 |
| diffcyt | 0.546 | 0.789 | 0.859 | 0.500 | 0.979 | 0.960 | 0.658 | 2&2 |
| speckle | 0.537 | 0.784 | 0.856 | 0.469 | 0.990 | 0.978 | 0.634 | 2&2 |
| scDC | 0.285 | 0.754 | 0.659 | 0.865 | 0.385 | 0.585 | 0.697 | 2&2 |
| betabin\_null | 0.387 | 0.753 | 0.817 | 0.740 | 0.646 | 0.676 | 0.706 | 2&2 |
| wtoPhi\_emK | 0.337 | 0.744 | 0.813 | 0.740 | 0.594 | 0.645 | 0.689 | 2&2 |
| milo | 0.292 | 0.725 | 0.810 | 0.625 | 0.667 | 0.652 | 0.638 | 2&2 |
| estPhi\_null | 0.709 | 0.910 | 0.933 | 0.708 | 0.975 | 0.966 | 0.817 | 3&3 |
| estPhi\_emK | 0.703 | 0.902 | 0.927 | 0.725 | 0.958 | 0.946 | 0.821 | 3&3 |
| Fisher | 0.360 | 0.898 | 0.632 | 0.950 | 0.333 | 0.588 | 0.726 | 3&3 |
| speckle | 0.671 | 0.895 | 0.917 | 0.675 | 0.967 | 0.953 | 0.790 | 3&3 |
| diffcyt | 0.671 | 0.894 | 0.919 | 0.733 | 0.925 | 0.907 | 0.811 | 3&3 |
| wtoPhi\_emK | 0.562 | 0.861 | 0.856 | 0.833 | 0.725 | 0.752 | 0.791 | 3&3 |
| betabin\_null | 0.562 | 0.860 | 0.855 | 0.833 | 0.725 | 0.752 | 0.791 | 3&3 |
| scDC | 0.405 | 0.807 | 0.670 | 0.950 | 0.383 | 0.606 | 0.740 | 3&3 |
| milo | 0.385 | 0.737 | 0.806 | 0.642 | 0.742 | 0.713 | 0.675 | 3&3 |
| estPhi\_null | 0.815 | 0.965 | 0.976 | 0.810 | 0.991 | 0.989 | 0.891 | 4&4 |
| estPhi\_emK | 0.805 | 0.961 | 0.971 | 0.810 | 0.983 | 0.979 | 0.887 | 4&4 |
| Fisher | 0.332 | 0.961 | 0.600 | 1.000 | 0.198 | 0.555 | 0.714 | 4&4 |
| diffcyt | 0.741 | 0.939 | 0.953 | 0.793 | 0.940 | 0.929 | 0.856 | 4&4 |
| speckle | 0.790 | 0.938 | 0.951 | 0.793 | 0.983 | 0.979 | 0.876 | 4&4 |
| betabin\_null | 0.726 | 0.934 | 0.947 | 0.897 | 0.828 | 0.839 | 0.867 | 4&4 |
| wtoPhi\_emK | 0.726 | 0.932 | 0.944 | 0.897 | 0.828 | 0.839 | 0.867 | 4&4 |
| scDC | 0.257 | 0.882 | 0.836 | 0.957 | 0.216 | 0.550 | 0.698 | 4&4 |
| milo | 0.397 | 0.780 | 0.847 | 0.698 | 0.698 | 0.698 | 0.698 | 4&4 |

nhoods level

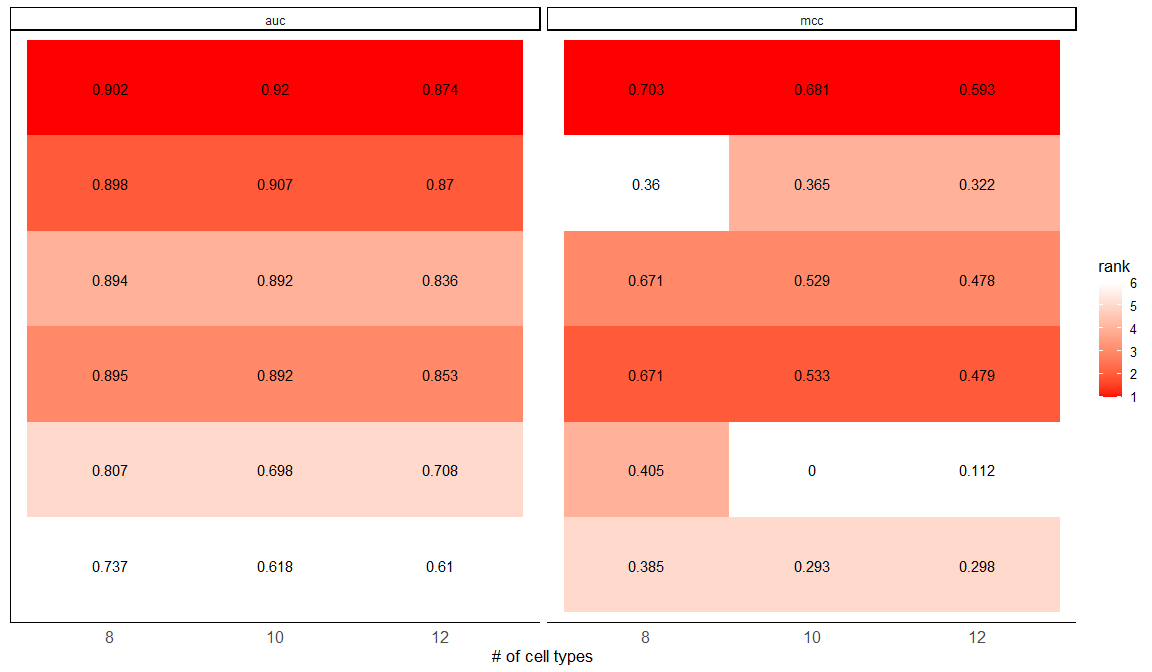
## method mcc auc sensitivity specificity F1 replicates prauc  
## 1 fisher 0.392 0.7377099 0.471 0.888 0.598 2&2 0.738  
## 2 milo 0.366 0.7366896 0.353 0.946 0.503 2&2 0.737  
## 3 betabin\_null 0.381 0.7318045 0.436 0.904 0.572 2&2 0.732  
## 4 wtoPhi\_emU 0.379 0.7306293 0.506 0.852 0.616 2&2 0.731  
## 5 estPhi\_null 0.094 0.7226221 0.029 0.996 0.055 2&2 0.723  
## 6 estPhi\_emU 0.128 0.7208475 0.056 0.990 0.104 2&2 0.721  
## 7 speckle 0.048 0.6315081 0.005 1.000 0.010 2&2 0.632  
## 8 milo 0.342 0.7373016 0.318 0.949 0.466 3&3 0.737  
## 9 fisher 0.362 0.7362261 0.421 0.899 0.555 3&3 0.736  
## 10 betabin\_null 0.362 0.7316439 0.402 0.911 0.541 3&3 0.732  
## 11 wtoPhi\_emU 0.356 0.7261082 0.473 0.856 0.588 3&3 0.726  
## 12 estPhi\_emU 0.258 0.6919914 0.347 0.873 0.472 3&3 0.692  
## 13 estPhi\_null 0.244 0.6912699 0.258 0.925 0.388 3&3 0.691  
## 14 speckle 0.008 0.6311336 0.000 1.000 0.001 3&3 0.631  
## 15 fisher 0.366 0.7414264 0.394 0.921 0.537 4&4 0.741  
## 16 milo 0.333 0.7371261 0.303 0.953 0.450 4&4 0.737  
## 17 betabin\_null 0.364 0.7366463 0.390 0.922 0.533 4&4 0.737  
## 18 wtoPhi\_emU 0.367 0.7310928 0.407 0.912 0.547 4&4 0.731  
## 19 estPhi\_null 0.242 0.7122683 0.199 0.960 0.322 4&4 0.712  
## 20 estPhi\_emU 0.243 0.7099651 0.213 0.953 0.339 4&4 0.710  
## 21 speckle 0.088 0.6440106 0.019 0.999 0.037 4&4 0.644



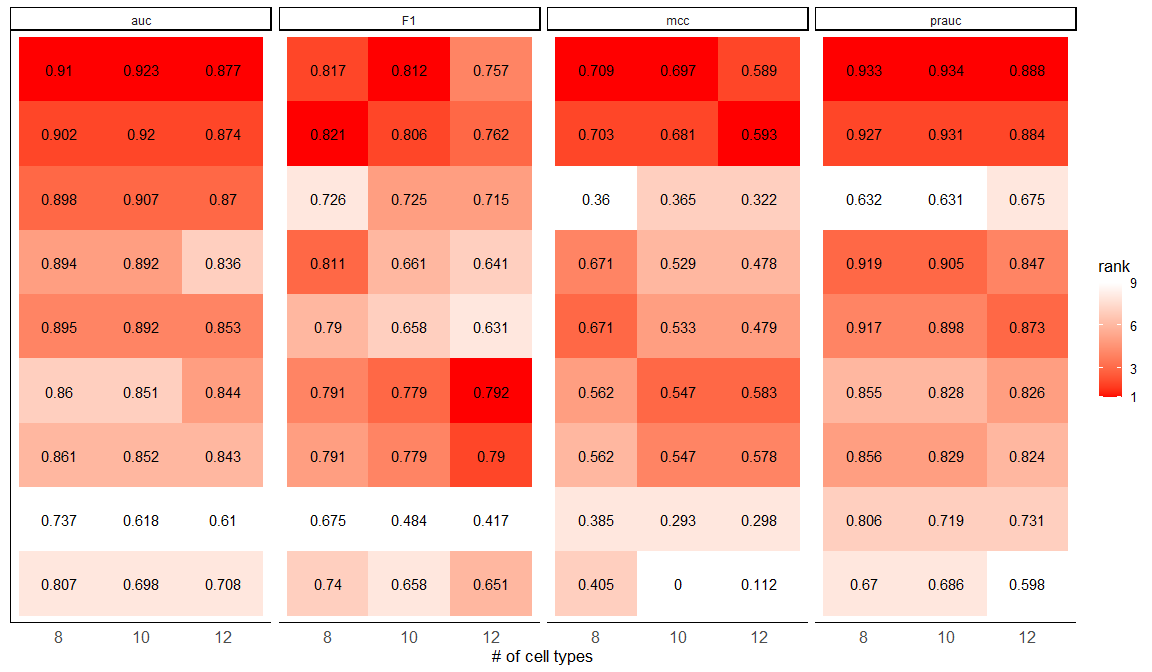
#### Different numbers of clusters

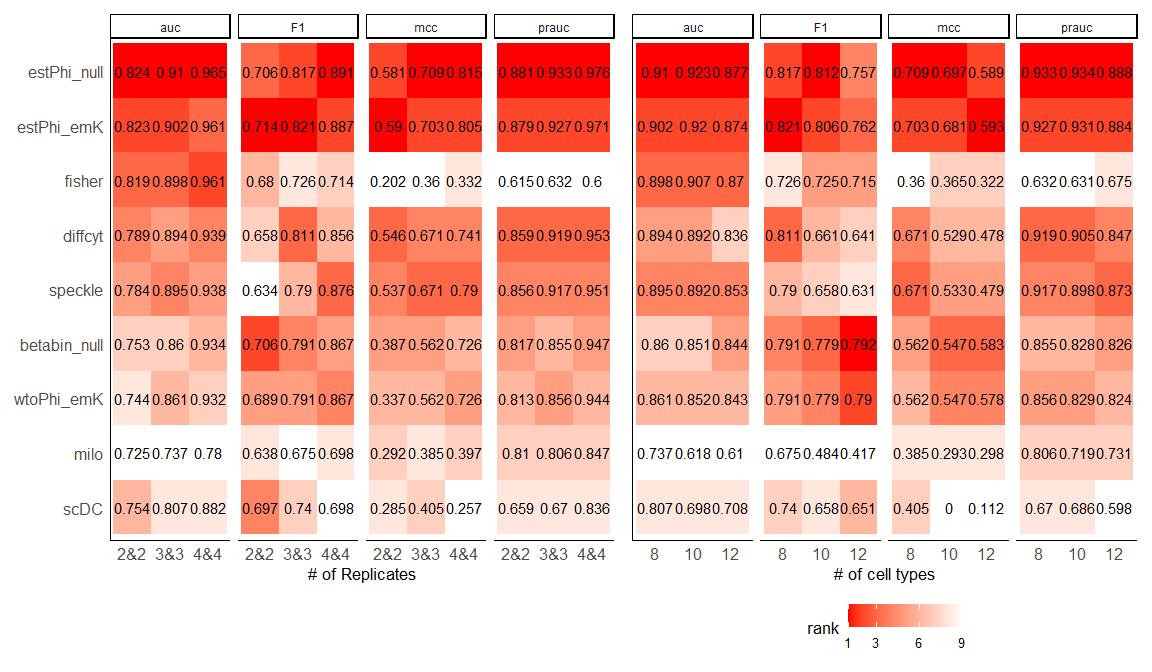
## [1] "D:/Data/DCATS/simulation/clusterN/replicates3&3\_K10\_con100\_splatter3000&3000para.RData"  
## [2] "D:/Data/DCATS/simulation/clusterN/replicates3&3\_K12\_con100\_splatter1500&2500para.RData"  
## [3] "D:/Data/DCATS/simulation/clusterN/replicates3&3\_K8\_con100\_splatter3000&3000para.RData"

## method mcc auc sensitivity specificity F1 clustersN  
## 1 estPhi\_null 0.709 0.910 0.708 0.975 0.817 8  
## 2 estPhi\_emK 0.703 0.902 0.725 0.958 0.821 8  
## 3 fisher 0.360 0.898 0.950 0.333 0.726 8  
## 4 speckle 0.671 0.895 0.675 0.967 0.790 8  
## 5 diffcyt 0.671 0.894 0.733 0.925 0.811 8  
## 6 wtoPhi\_emK 0.562 0.861 0.833 0.725 0.791 8  
## 7 betabin\_null 0.562 0.860 0.833 0.725 0.791 8  
## 8 scDC 0.405 0.807 0.950 0.383 0.740 8  
## 9 milo 0.385 0.737 0.642 0.742 0.675 8  
## 10 estPhi\_null 0.697 0.923 0.707 0.967 0.812 10  
## 11 estPhi\_emK 0.681 0.920 0.707 0.953 0.806 10  
## 12 fisher 0.365 0.907 0.987 0.267 0.725 10  
## 13 speckle 0.533 0.892 0.507 0.967 0.658 10  
## 14 diffcyt 0.529 0.892 0.513 0.960 0.661 10  
## 15 wtoPhi\_emK 0.547 0.852 0.800 0.747 0.779 10  
## 16 betabin\_null 0.547 0.851 0.800 0.747 0.779 10  
## 17 scDC 0.000 0.698 0.960 0.040 0.658 10  
## 18 milo 0.293 0.618 0.353 0.893 0.484 10  
## 19 estPhi\_null 0.589 0.877 0.667 0.906 0.757 12  
## 20 estPhi\_emK 0.593 0.874 0.678 0.900 0.762 12  
## 21 fisher 0.322 0.870 0.961 0.272 0.715 12  
## 22 speckle 0.479 0.853 0.489 0.939 0.631 12  
## 23 betabin\_null 0.583 0.844 0.794 0.789 0.792 12  
## 24 wtoPhi\_emK 0.578 0.843 0.794 0.783 0.790 12  
## 25 diffcyt 0.478 0.836 0.506 0.928 0.641 12  
## 26 scDC 0.112 0.708 0.850 0.239 0.651 12  
## 27 milo 0.298 0.610 0.278 0.944 0.417 12



Simulation 2: Supplementary Plot



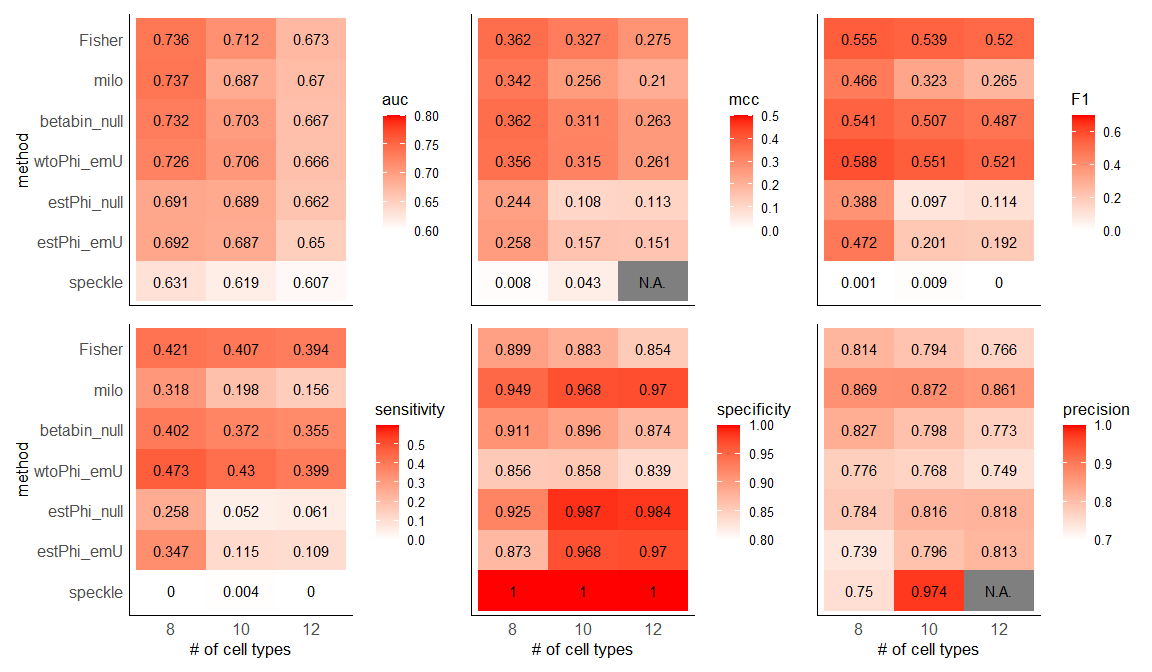


Details of statistics value

| method | mcc | auc | prauc | sensitivity | specificity | precision | F1 | clustersN |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| estPhi\_null | 0.709 | 0.910 | 0.933 | 0.708 | 0.975 | 0.966 | 0.817 | 8 |
| estPhi\_emK | 0.703 | 0.902 | 0.927 | 0.725 | 0.958 | 0.946 | 0.821 | 8 |
| Fisher | 0.360 | 0.898 | 0.632 | 0.950 | 0.333 | 0.588 | 0.726 | 8 |
| speckle | 0.671 | 0.895 | 0.917 | 0.675 | 0.967 | 0.953 | 0.790 | 8 |
| diffcyt | 0.671 | 0.894 | 0.919 | 0.733 | 0.925 | 0.907 | 0.811 | 8 |
| wtoPhi\_emK | 0.562 | 0.861 | 0.856 | 0.833 | 0.725 | 0.752 | 0.791 | 8 |
| betabin\_null | 0.562 | 0.860 | 0.855 | 0.833 | 0.725 | 0.752 | 0.791 | 8 |
| scDC | 0.405 | 0.807 | 0.670 | 0.950 | 0.383 | 0.606 | 0.740 | 8 |
| milo | 0.385 | 0.737 | 0.806 | 0.642 | 0.742 | 0.713 | 0.675 | 8 |
| estPhi\_null | 0.697 | 0.923 | 0.934 | 0.707 | 0.967 | 0.955 | 0.812 | 10 |
| estPhi\_emK | 0.681 | 0.920 | 0.931 | 0.707 | 0.953 | 0.938 | 0.806 | 10 |
| Fisher | 0.365 | 0.907 | 0.631 | 0.987 | 0.267 | 0.574 | 0.725 | 10 |
| speckle | 0.533 | 0.892 | 0.898 | 0.507 | 0.967 | 0.938 | 0.658 | 10 |
| diffcyt | 0.529 | 0.892 | 0.905 | 0.513 | 0.960 | 0.928 | 0.661 | 10 |
| wtoPhi\_emK | 0.547 | 0.852 | 0.829 | 0.800 | 0.747 | 0.759 | 0.779 | 10 |
| betabin\_null | 0.547 | 0.851 | 0.828 | 0.800 | 0.747 | 0.759 | 0.779 | 10 |
| scDC | 0.000 | 0.698 | 0.686 | 0.960 | 0.040 | 0.500 | 0.658 | 10 |
| milo | 0.293 | 0.618 | 0.719 | 0.353 | 0.893 | 0.768 | 0.484 | 10 |
| estPhi\_null | 0.589 | 0.877 | 0.888 | 0.667 | 0.906 | 0.876 | 0.757 | 12 |
| estPhi\_emK | 0.593 | 0.874 | 0.884 | 0.678 | 0.900 | 0.871 | 0.762 | 12 |
| Fisher | 0.322 | 0.870 | 0.675 | 0.961 | 0.272 | 0.569 | 0.715 | 12 |
| speckle | 0.479 | 0.853 | 0.873 | 0.489 | 0.939 | 0.889 | 0.631 | 12 |
| betabin\_null | 0.583 | 0.844 | 0.826 | 0.794 | 0.789 | 0.790 | 0.792 | 12 |
| wtoPhi\_emK | 0.578 | 0.843 | 0.824 | 0.794 | 0.783 | 0.786 | 0.790 | 12 |
| diffcyt | 0.478 | 0.836 | 0.847 | 0.506 | 0.928 | 0.875 | 0.641 | 12 |
| scDC | 0.112 | 0.708 | 0.598 | 0.850 | 0.239 | 0.528 | 0.651 | 12 |
| milo | 0.298 | 0.610 | 0.731 | 0.278 | 0.944 | 0.833 | 0.417 | 12 |

nhoods level

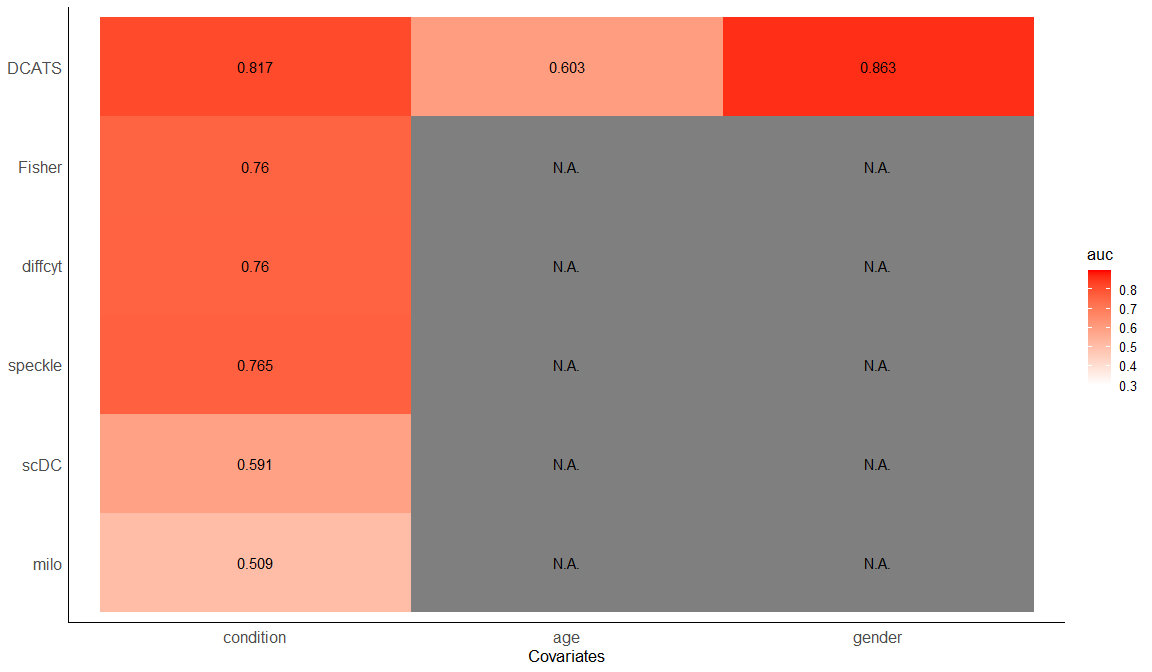
## method mcc auc sensitivity specificity F1 clustersN prauc  
## 1 milo 0.342 0.7373016 0.318 0.949 0.466 8 0.737  
## 2 fisher 0.362 0.7362261 0.421 0.899 0.555 8 0.736  
## 3 betabin\_null 0.362 0.7316439 0.402 0.911 0.541 8 0.732  
## 4 wtoPhi\_emU 0.356 0.7261082 0.473 0.856 0.588 8 0.726  
## 5 estPhi\_emU 0.258 0.6919914 0.347 0.873 0.472 8 0.692  
## 6 estPhi\_null 0.244 0.6912699 0.258 0.925 0.388 8 0.691  
## 7 speckle 0.008 0.6311336 0.000 1.000 0.001 8 0.631  
## 8 fisher 0.327 0.7123539 0.407 0.883 0.539 10 0.712  
## 9 wtoPhi\_emU 0.315 0.7055823 0.430 0.858 0.551 10 0.706  
## 10 betabin\_null 0.311 0.7025420 0.372 0.896 0.507 10 0.703  
## 11 estPhi\_null 0.108 0.6887386 0.052 0.987 0.097 10 0.689  
## 12 milo 0.256 0.6870602 0.198 0.968 0.323 10 0.687  
## 13 estPhi\_emU 0.157 0.6867209 0.115 0.968 0.201 10 0.687  
## 14 speckle 0.043 0.6186797 0.004 1.000 0.009 10 0.619  
## 15 fisher 0.275 0.6732405 0.394 0.854 0.520 12 0.673  
## 16 milo 0.210 0.6698016 0.156 0.970 0.265 12 0.670  
## 17 betabin\_null 0.263 0.6669149 0.355 0.874 0.487 12 0.667  
## 18 wtoPhi\_emU 0.261 0.6656266 0.399 0.839 0.521 12 0.666  
## 19 estPhi\_null 0.113 0.6620511 0.061 0.984 0.114 12 0.662  
## 20 estPhi\_emU 0.151 0.6504172 0.109 0.970 0.192 12 0.650  
## 21 speckle NaN 0.6071733 0.000 1.000 0.000 12 0.607



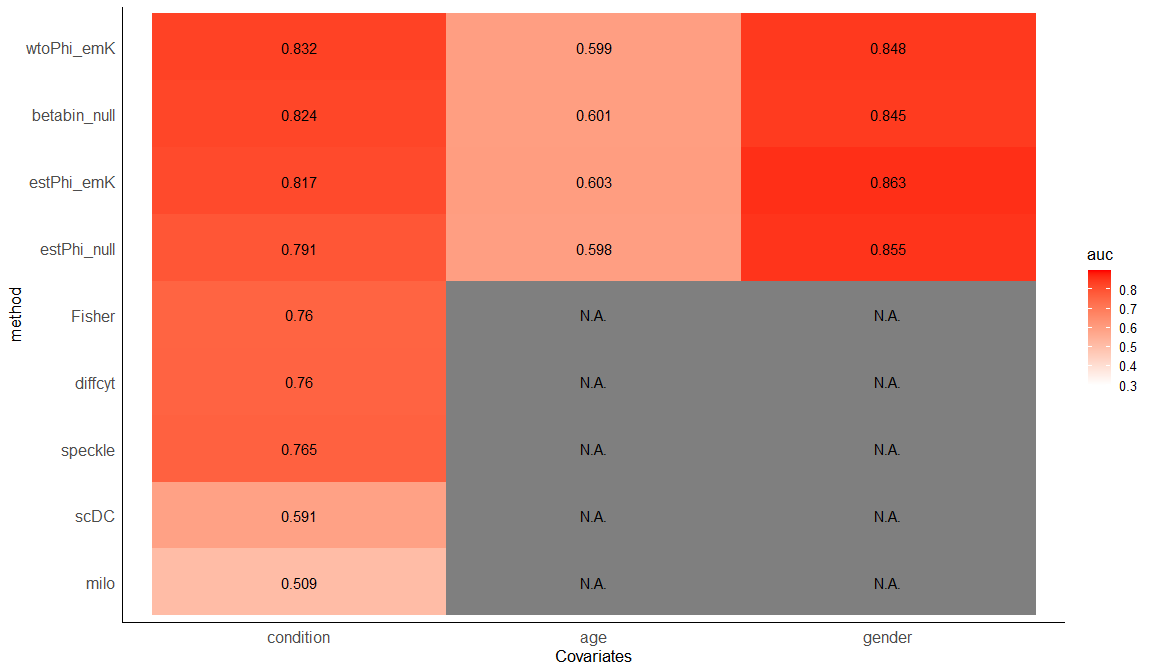
### Figure 2 - C

## Warning in if (!is.na(oper[[idx]])) {: the condition has length > 1 and only the  
## first element will be used  
  
## Warning in if (!is.na(oper[[idx]])) {: the condition has length > 1 and only the  
## first element will be used  
  
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## first element will be used  
  
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## first element will be used

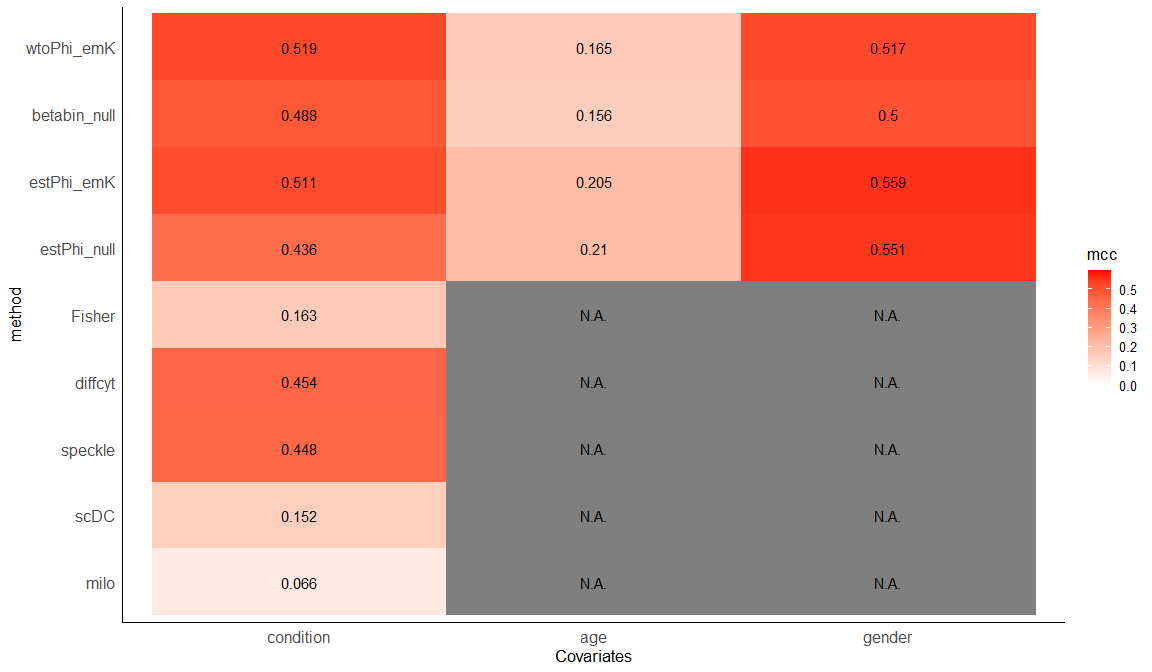
## method mcc auc prauc sensitivity specificity  
## 1 estPhi\_emK 0.51050817 0.8165502 0.8419367 0.55172414 0.9224138  
## 2 wtoPhi\_emK 0.51892326 0.8320452 0.8408372 0.65517241 0.8534483  
## 3 wtoPhi\_emSVM 0.50320460 0.8265458 0.8384214 0.63793103 0.8534483  
## 4 estPhi\_emSVM 0.50311529 0.8084869 0.8370024 0.54310345 0.9224138  
## 5 betabin\_null 0.48752812 0.8241305 0.8350238 0.62068966 0.8534483  
## 6 wtoPhi\_emU 0.49536190 0.8237961 0.8336510 0.62931034 0.8534483  
## 7 estPhi\_emU 0.50493500 0.7943297 0.8192986 0.59482759 0.8879310  
## 8 estPhi\_null 0.43611285 0.7910226 0.8148534 0.46551724 0.9224138  
## 9 wtoPhi\_emT 0.46406380 0.8004608 0.8104003 0.59482759 0.8534483  
## 10 speckle 0.44777366 0.7649376 0.8028349 0.35344828 0.9913793  
## 11 diffcyt 0.45409307 0.7600327 0.8019207 0.39655172 0.9741379  
## 12 estPhi\_emT 0.39626708 0.7646775 0.7555120 0.50862069 0.8620690  
## 13 milo 0.06622662 0.5087322 0.6336207 0.02586207 0.9913793  
## 14 fisher 0.16305547 0.7596240 0.5819575 0.89655172 0.2241379  
## 15 scDC 0.15151080 0.5905916 0.4460766 0.77586207 0.3620690  
## 16 estPhi\_emU 0.17591980 0.6096537 0.6483777 0.25862069 0.8793103  
## 17 wtoPhi\_emT 0.16319735 0.6015904 0.6407866 0.30172414 0.8362069  
## 18 estPhi\_emSVM 0.19500598 0.6044144 0.6399630 0.21551724 0.9224138  
## 19 estPhi\_emK 0.20473014 0.6028166 0.6384089 0.22413793 0.9224138  
## 20 estPhi\_null 0.20978064 0.5983948 0.6381711 0.21551724 0.9310345  
## 21 wtoPhi\_emU 0.15612300 0.6040428 0.6331490 0.28448276 0.8448276  
## 22 wtoPhi\_emK 0.16537965 0.5990265 0.6321348 0.29310345 0.8448276  
## 23 wtoPhi\_emSVM 0.14675988 0.6018133 0.6306124 0.27586207 0.8448276  
## 24 betabin\_null 0.15612300 0.6006243 0.6296939 0.28448276 0.8448276  
## 25 estPhi\_emT 0.20149815 0.5714551 0.6115173 0.25862069 0.8965517  
## 26 estPhi\_emK 0.55903517 0.8631466 0.8859377 0.62068966 0.9137931  
## 27 estPhi\_emSVM 0.56651103 0.8634810 0.8845681 0.62931034 0.9137931  
## 28 estPhi\_emU 0.56011203 0.8611400 0.8831924 0.68965517 0.8620690  
## 29 estPhi\_null 0.55103877 0.8553805 0.8752108 0.58620690 0.9310345  
## 30 wtoPhi\_emK 0.51716595 0.8478002 0.8612641 0.66379310 0.8448276  
## 31 wtoPhi\_emU 0.49963490 0.8449391 0.8584946 0.65517241 0.8362069  
## 32 wtoPhi\_emSVM 0.51558380 0.8462768 0.8579211 0.67241379 0.8362069  
## 33 betabin\_null 0.49963490 0.8446418 0.8577380 0.65517241 0.8362069  
## 34 estPhi\_emT 0.57115544 0.8428954 0.8560983 0.64655172 0.9051724  
## 35 wtoPhi\_emT 0.47412220 0.8311905 0.8499814 0.63793103 0.8275862  
## precision F1 factor  
## 1 0.8767123 0.6772487 condition  
## 2 0.8172043 0.7272727 condition  
## 3 0.8131868 0.7149758 condition  
## 4 0.8750000 0.6702128 condition  
## 5 0.8089888 0.7024390 condition  
## 6 0.8111111 0.7087379 condition  
## 7 0.8414634 0.6969697 condition  
## 8 0.8571429 0.6033520 condition  
## 9 0.8023256 0.6831683 condition  
## 10 0.9761905 0.5189873 condition  
## 11 0.9387755 0.5575758 condition  
## 12 0.7866667 0.6178010 condition  
## 13 0.7500000 0.0500000 condition  
## 14 0.5360825 0.6709677 condition  
## 15 0.5487805 0.6428571 condition  
## 16 0.6818182 0.3750000 age  
## 17 0.6481481 0.4117647 age  
## 18 0.7352941 0.3333333 age  
## 19 0.7428571 0.3443709 age  
## 20 0.7575758 0.3355705 age  
## 21 0.6470588 0.3952096 age  
## 22 0.6538462 0.4047619 age  
## 23 0.6400000 0.3855422 age  
## 24 0.6470588 0.3952096 age  
## 25 0.7142857 0.3797468 age  
## 26 0.8780488 0.7272727 gender  
## 27 0.8795181 0.7336683 gender  
## 28 0.8333333 0.7547170 gender  
## 29 0.8947368 0.7083333 gender  
## 30 0.8105263 0.7298578 gender  
## 31 0.8000000 0.7203791 gender  
## 32 0.8041237 0.7323944 gender  
## 33 0.8000000 0.7203791 gender  
## 34 0.8720930 0.7425743 gender  
## 35 0.7872340 0.7047619 gender



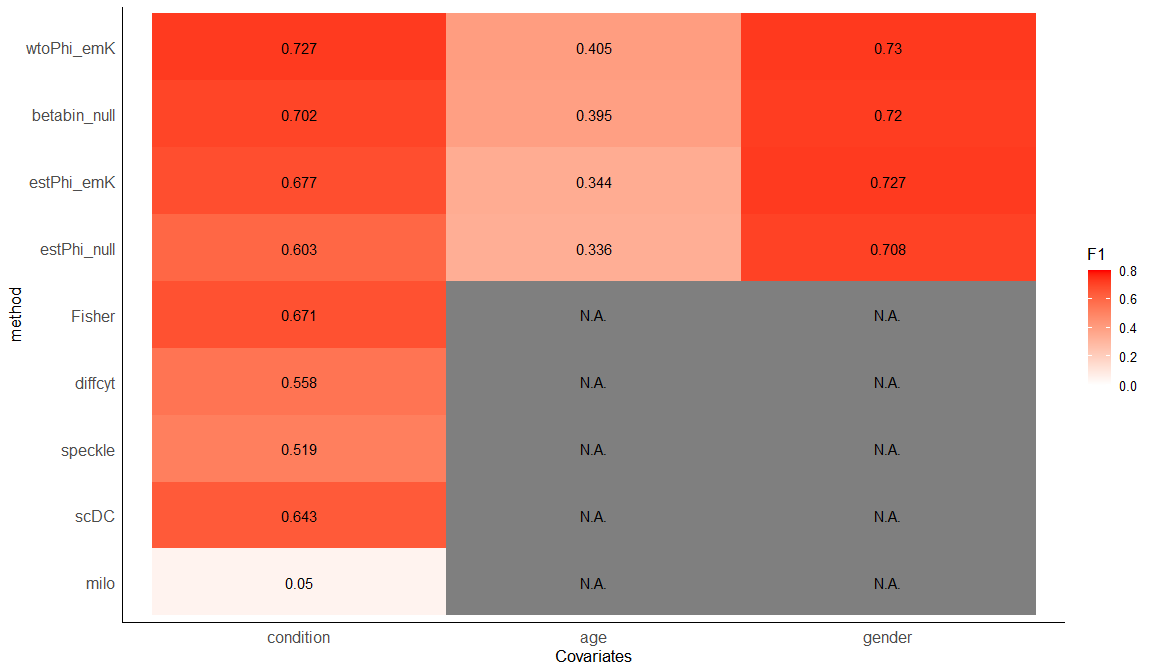
## Saving 12 x 7 in image



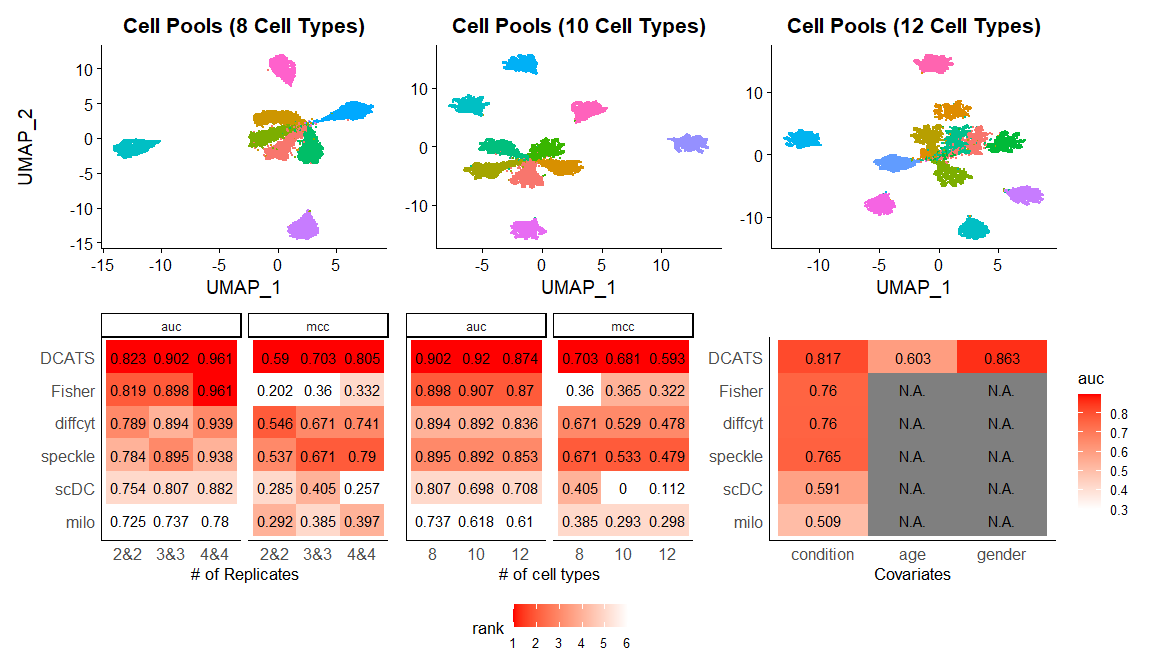
## Saving 12 x 7 in image



## Saving 12 x 7 in image



## Saving 12 x 7 in image



## Figure 3

### real-world data 1 - Experiment 7

The ‘group’ column started with ‘B’ is the indicators of replicates

## `summarise()` has grouped output by 'batch', 'condition'. You can override using the `.groups` argument.

## `summarise()` has grouped output by 'condition'. You can override using the `.groups` argument.

| cluster | truth | betabin\_null | wtoPhi\_emSVM | estPhi\_null | estPhi\_emSVM | fisher | scDC | speckle | milo\_pct | treatment |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Endocrine | N | 0.130 | 0.130 | 0.288 | 0.273 | 0.000 | 0.360 | 0.714 | 0.000 | Hpoly.Day3 |
| Enterocyte | N | 0.641 | 0.641 | 0.448 | 0.410 | 0.000 | 0.002 | 0.748 | 0.071 | Hpoly.Day3 |
| Enterocyte.Progenitor | N | 0.103 | 0.103 | 0.315 | 0.278 | 0.000 | 0.341 | 0.714 | 0.067 | Hpoly.Day3 |
| Goblet | N | 0.437 | 0.437 | 0.589 | 0.571 | 0.002 | 0.003 | 0.748 | 0.000 | Hpoly.Day3 |
| Stem | N | 0.254 | 0.254 | 0.222 | 0.164 | 0.032 | 0.010 | 0.714 | 0.000 | Hpoly.Day3 |
| TA | N | 0.883 | 0.883 | 0.883 | 0.975 | 0.205 | 0.099 | 0.993 | 0.000 | Hpoly.Day3 |
| TA.Early | N | 0.288 | 0.288 | 0.640 | 0.612 | 0.002 | 0.006 | 0.781 | 0.088 | Hpoly.Day3 |
| Tuft | P | 0.040 | 0.040 | 0.070 | 0.061 | 0.000 | 0.069 | 0.714 | 0.000 | Hpoly.Day3 |

| cluster | truth | betabin\_null | wtoPhi\_emSVM | estPhi\_null | estPhi\_emSVM | fisher | scDC | speckle | milo\_pct | treatment |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Endocrine | N | 0.390 | 0.390 | 0.925 | 0.867 | 0.379 | 0.035 | 0.923 | 0.000 | Hpoly.Day10 |
| Enterocyte | P | 0.091 | 0.091 | 0.009 | 0.006 | 0.000 | 0.002 | 0.149 | 0.472 | Hpoly.Day10 |
| Enterocyte.Progenitor | N | 0.132 | 0.132 | 0.285 | 0.233 | 0.000 | 0.103 | 0.349 | 0.162 | Hpoly.Day10 |
| Goblet | P | 0.051 | 0.051 | 0.116 | 0.105 | 0.000 | 0.009 | 0.235 | 0.217 | Hpoly.Day10 |
| Stem | N | 0.824 | 0.824 | 0.865 | 0.830 | 0.279 | 0.406 | 0.923 | 0.096 | Hpoly.Day10 |
| TA | N | 0.852 | 0.852 | 0.836 | 0.592 | 1.000 | 0.572 | 0.923 | 0.647 | Hpoly.Day10 |
| TA.Early | P | 0.015 | 0.015 | 0.132 | 0.083 | 0.000 | 0.224 | 0.235 | 0.266 | Hpoly.Day10 |
| Tuft | P | 0.020 | 0.020 | 0.013 | 0.010 | 0.000 | 0.000 | 0.112 | 0.500 | Hpoly.Day10 |

| cluster | truth | betabin\_null | wtoPhi\_emSVM | estPhi\_null | estPhi\_emSVM | fisher | scDC | speckle | milo\_pct | treatment |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Endocrine | N | 0.426 | 0.426 | 0.798 | 0.784 | 0.429 | 0.840 | 0.761 | 0.308 | Salmonella |
| Enterocyte | P | 0.008 | 0.008 | 0.000 | 0.000 | 0.000 | 0.022 | 0.008 | 0.457 | Salmonella |
| Enterocyte.Progenitor | N | 0.146 | 0.146 | 0.561 | 0.495 | 0.000 | 0.357 | 0.647 | 0.019 | Salmonella |
| Goblet | N | 0.681 | 0.681 | 0.821 | 0.802 | 0.558 | 0.253 | 0.864 | 0.100 | Salmonella |
| Stem | P | 0.031 | 0.031 | 0.059 | 0.046 | 0.000 | 0.080 | 0.094 | 0.320 | Salmonella |
| TA | P | 0.026 | 0.026 | 0.192 | 0.318 | 0.000 | 0.801 | 0.216 | 0.538 | Salmonella |
| TA.Early | P | 0.030 | 0.030 | 0.261 | 0.268 | 0.000 | 0.390 | 0.216 | 0.015 | Salmonella |
| Tuft | N | 0.587 | 0.587 | 0.833 | 0.844 | 0.129 | 0.059 | 0.761 | 0.000 | Salmonella |

|  | Tuft | Endocrine | Enterocyte.Progenitor | Stem | Goblet | TA.Early | Enterocyte | TA |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| origin | P | N | N | N | N | N | N | N |
| DCATS | \* | n.s. | n.s. | n.s. | n.s. | n.s. | n.s. | n.s. |
| fisher | \*\*\* | \*\*\* | \*\*\* | \*\* | \*\*\* | \*\*\* | \*\*\* | n.s. |
| scDC | \* | n.s. | n.s. | \*\*\* | \*\*\* | \*\*\* | \*\*\* | \* |
| speckle | n.s. | n.s. | n.s. | n.s. | n.s. | n.s. | n.s. | n.s. |
| milo | N | N | N | N | N | N | N | N |

|  | Tuft | TA.Early | Goblet | Enterocyte | Enterocyte.Progenitor | Endocrine | Stem | TA |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| origin | P | P | P | P | N | N | N | N |
| DCATS | \*\* | \* | n.s. | \*\*\* | n.s. | n.s. | n.s. | n.s. |
| fisher | \*\*\* | \*\*\* | \*\*\* | \*\*\* | \*\*\* | n.s. | n.s. | n.s. |
| scDC | \*\*\* | n.s. | \*\*\* | \*\*\* | n.s. | \*\* | n.s. | n.s. |
| speckle | n.s. | n.s. | n.s. | n.s. | n.s. | n.s. | n.s. | n.s. |
| milo | P | P | P | P | N | N | N | P |

|  | Enterocyte | Stem | TA | TA.Early | Enterocyte.Progenitor | Tuft | Goblet | Endocrine |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| origin | P | P | P | P | N | N | N | N |
| DCATS | \*\*\* | \*\* | n.s. | n.s. | n.s. | n.s. | n.s. | n.s. |
| fisher | \*\*\* | \*\*\* | \*\*\* | \*\*\* | \*\*\* | n.s. | n.s. | n.s. |
| scDC | \*\* | \* | n.s. | n.s. | n.s. | \* | n.s. | n.s. |
| speckle | \*\*\* | \* | n.s. | n.s. | n.s. | n.s. | n.s. | n.s. |
| milo | P | P | P | N | N | N | N | P |

|  | Endocrine | Enterocyte | Enterocyte.Progenitor | Goblet | Stem | TA | TA.Early | Tuft |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Endocrine | 0.9785933 | 0.0006868 | 0.0005495 | 0.0093209 | 0.0102934 | 0.0114537 | 0.0087549 | 0 |
| Enterocyte | 0.0000000 | 0.9800824 | 0.0170330 | 0.0000000 | 0.0000000 | 0.0000000 | 0.0000000 | 0 |
| Enterocyte.Progenitor | 0.0000000 | 0.0185440 | 0.9401099 | 0.0000000 | 0.0005147 | 0.0572687 | 0.0087549 | 0 |
| Goblet | 0.0091743 | 0.0000000 | 0.0000000 | 0.9826897 | 0.0056613 | 0.0017621 | 0.0019455 | 0 |
| Stem | 0.0030581 | 0.0006868 | 0.0000000 | 0.0026631 | 0.8625836 | 0.0933921 | 0.0345331 | 0 |
| TA | 0.0000000 | 0.0000000 | 0.0335165 | 0.0000000 | 0.0761709 | 0.7506608 | 0.0617704 | 0 |
| TA.Early | 0.0000000 | 0.0000000 | 0.0082418 | 0.0039947 | 0.0303654 | 0.0748899 | 0.8793774 | 0 |
| Tuft | 0.0091743 | 0.0000000 | 0.0005495 | 0.0013316 | 0.0144107 | 0.0105727 | 0.0048638 | 1 |

## real-world data2

## cell tsne1 tsne2 ind condition cluster clusterRes  
## 1 AAACATACAATGCC-1 -4.277833 -19.294709 107 ctrl 5 CD4 T cells  
## 2 AAACATACATTTCC-1 -27.640373 14.966629 1016 ctrl 9 CD14+ Monocytes  
## 3 AAACATACCAGAAA-1 -27.493646 28.924885 1256 ctrl 9 CD14+ Monocytes  
## 4 AAACATACCAGCTA-1 -28.132584 24.925484 1256 ctrl 9 CD14+ Monocytes  
## 5 AAACATACCATGCA-1 -10.468194 -5.984389 1488 ctrl 3 CD4 T cells  
## 6 AAACATACCTCGCT-1 -24.367997 20.429285 1256 ctrl 9 CD14+ Monocytes  
## multiplets  
## 1 doublet  
## 2 singlet  
## 3 singlet  
## 4 doublet  
## 5 singlet  
## 6 singlet

## `summarise()` has grouped output by 'condition'. You can override using the `.groups` argument.

## # A tibble: 16 x 3  
## # Groups: condition [2]  
## condition clusterRes n  
## <chr> <chr> <int>  
## 1 ctrl B cells 1488  
## 2 ctrl CD14+ Monocytes 3365  
## 3 ctrl CD4 T cells 6005  
## 4 ctrl CD8 T cells 1409  
## 5 ctrl Dendritic cells 227  
## 6 ctrl FCGR3A+ Monocytes 906  
## 7 ctrl Megakaryocytes 166  
## 8 ctrl NK cells 1051  
## 9 stim B cells 1392  
## 10 stim CD14+ Monocytes 3082  
## 11 stim CD4 T cells 6028  
## 12 stim CD8 T cells 1225  
## 13 stim Dendritic cells 245  
## 14 stim FCGR3A+ Monocytes 1008  
## 15 stim Megakaryocytes 180  
## 16 stim NK cells 1279

## # A tibble: 0 x 2  
## # ... with 2 variables: cell <chr>, n <int>

## BARCODE RD.TOTL RD.PASS RD.UNIQ N.SNP BEST SNG.1ST  
## 1 AAACATACAATGCC-1 5799 280 269 185 DBL-107-1244-0.500 107  
## 2 AAACATACATTTCC-1 5466 592 501 236 SNG-1016 1016  
## 3 AAACATACCAGAAA-1 4337 330 300 154 SNG-1256 1256  
## 4 AAACATACCAGCTA-1 7120 418 338 179 DBL-1256-1244-0.500 1256  
## 5 AAACATACCATGCA-1 2422 86 76 54 SNG-1488 1488  
## 6 AAACATACCTCGCT-1 5312 561 497 207 SNG-1256 1256  
## SNG.LLK1 SNG.2ND SNG.LLK2 SNG.LLK0 DBL.1ST DBL.2ND ALPHA LLK12  
## 1 -78.5388 1244 -92.3864 -75.9878 107 1244 0.5 -62.8745  
## 2 -61.8525 1256 -193.3940 -135.9317 1016 1256 0.5 -93.0213  
## 3 -50.6213 1015 -100.6965 -67.2587 101 1256 0.5 -64.5022  
## 4 -70.2734 1244 -110.3962 -82.1916 1256 1244 0.5 -67.3787  
## 5 -16.1294 1015 -31.7146 -27.0167 1015 1488 0.5 -18.5646  
## 6 -66.3586 1015 -180.3066 -115.0556 1256 101 0.5 -101.4645  
## LLK1 LLK2 LLK10 LLK20 LLK00 PRB.DBL PRB.SNG1  
## 1 -78.5388 -92.3864 -88.6649 -94.1498 -77.4107 1.00e+00 1  
## 2 -61.8525 -193.3940 -103.2284 -168.3927 -132.6010 4.15e-15 1  
## 3 -107.8190 -50.6213 -111.3319 -64.5022 -72.4244 1.95e-07 1  
## 4 -70.2734 -110.3962 -80.3745 -103.1706 -85.1143 7.21e-01 1  
## 5 -31.7146 -16.1294 -30.2045 -22.5295 -28.2980 1.28e-02 1  
## 6 -66.3586 -190.9367 -101.4645 -194.9529 -124.2197 8.42e-17 1

## BARCODE RD.TOTL RD.PASS RD.UNIQ N.SNP BEST SNG.1ST SNG.LLK1  
## 1 AAACATACCAAGCT-1 2491 239 228 141 SNG-101 101 -31.2822  
## 2 AAACATACCCCTAC-1 3747 282 274 173 SNG-1488 1488 -37.4261  
## 3 AAACATACCCGTAA-1 2844 144 133 108 SNG-1244 1244 -35.0043  
## 4 AAACATACCCTCGT-1 3575 199 189 115 SNG-1488 1488 -31.5489  
## 5 AAACATACGAGGTG-1 2649 170 158 99 SNG-1488 1488 -33.2782  
## 6 AAACATACGCGAAG-1 9874 880 822 345 SNG-101 101 -139.7810  
## SNG.2ND SNG.LLK2 SNG.LLK0 DBL.1ST DBL.2ND ALPHA LLK12 LLK1  
## 1 1015 -81.3393 -59.5871 101 1015 0.5 -47.8026 -31.2822  
## 2 1256 -104.7874 -74.9247 1256 1488 0.5 -53.8991 -104.7874  
## 3 1488 -61.5604 -51.6974 1488 1244 0.5 -36.9775 -61.5604  
## 4 1244 -79.8040 -57.9696 1256 1488 0.5 -42.8116 -83.5802  
## 5 1244 -66.4966 -48.9522 101 1488 0.5 -36.4330 -75.8228  
## 6 1256 -266.4763 -170.1924 101 1488 0.5 -154.9333 -139.7810  
## LLK2 LLK10 LLK20 LLK00 PRB.DBL PRB.SNG1  
## 1 -81.3393 -32.1591 -47.8026 -64.9647 1.07e-08 1  
## 2 -37.4261 -101.7666 -64.5707 -79.2115 1.00e-08 1  
## 3 -35.0043 -72.6479 -50.8297 -52.6835 2.03e-02 1  
## 4 -31.5489 -80.4661 -49.8506 -58.0733 2.38e-06 1  
## 5 -33.2782 -72.2344 -36.4330 -48.3017 8.06e-03 1  
## 6 -273.8806 -136.9040 -154.9333 -175.5614 3.82e-08 1

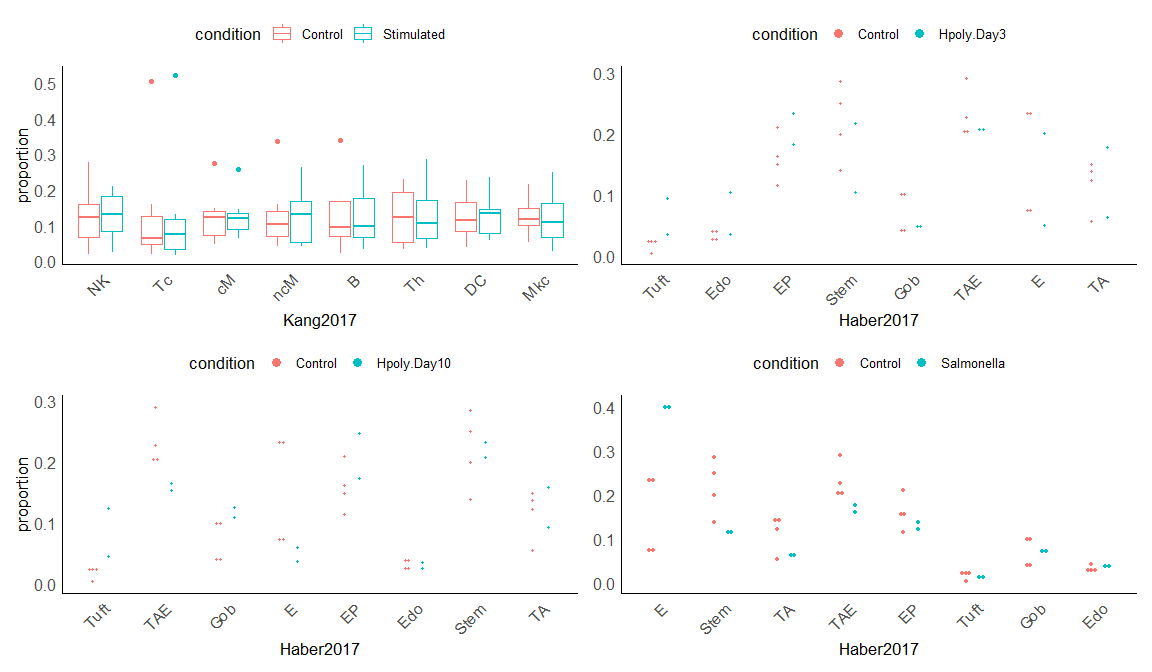
## cell batch  
## 1 AAACATACATTTCC-1 SNG-1016  
## 2 AAACATACCAGAAA-1 SNG-1256  
## 3 AAACATACCATGCA-1 SNG-1488  
## 4 AAACATACCTCGCT-1 SNG-1256  
## 5 AAACATACCTGGTA-1 SNG-1039  
## 6 AAACATACGATGAA-1 SNG-1488

## `summarise()` has grouped output by 'condition', 'clusterRes'. You can override using the `.groups` argument.

| cluster | truth | betabin\_null | wtoPhi\_emSVM | estPhi\_null | estPhi\_emSVM | fisher | scDC | speckle | milo\_pct |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| B cells | N | 0.997 | 0.997 | 0.995 | 0.995 | 0.338 | 0.000 | 0.989 | 0.032 |
| CD14+ Monocytes | N | 0.510 | 0.510 | 0.537 | 0.527 | 0.001 | 0.480 | 0.989 | 0.186 |
| CD4 T cells | N | 0.953 | 0.953 | 0.926 | 0.921 | 0.252 | 0.408 | 0.989 | 0.058 |
| CD8 T cells | N | 0.734 | 0.734 | 0.581 | 0.566 | 0.008 | 0.348 | 0.989 | 0.187 |
| Dendritic cells | N | 0.496 | 0.496 | 0.815 | 0.960 | 0.252 | 0.333 | 0.989 | 0.000 |
| FCGR3A+ Monocytes | N | 0.603 | 0.603 | 0.729 | 0.335 | 0.008 | 0.077 | 0.989 | 0.101 |
| Megakaryocytes | N | 0.738 | 0.738 | 0.820 | 0.364 | 0.862 | 0.761 | 0.989 | 0.167 |
| NK cells | N | 0.244 | 0.244 | 0.514 | 0.508 | 0.000 | 0.018 | 0.989 | 0.071 |

|  | NK | Tc | cM | ncM | B | Th | DC | Mkc |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| origin | N | N | N | N | N | N | N | N |
| DCATS | n.s. | n.s. | n.s. | n.s. | n.s. | n.s. | n.s. | n.s. |
| fisher | \*\*\* | \*\*\* | \*\*\* | \*\*\* | n.s. | n.s. | n.s. | n.s. |
| scDC | \*\* | n.s. | n.s. | \* | \*\*\* | n.s. | n.s. | n.s. |
| speckle | n.s. | n.s. | n.s. | n.s. | n.s. | n.s. | n.s. | n.s. |
| milo | N | N | N | N | N | N | N | N |

## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.  
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## Figure 4

### real-world data 3

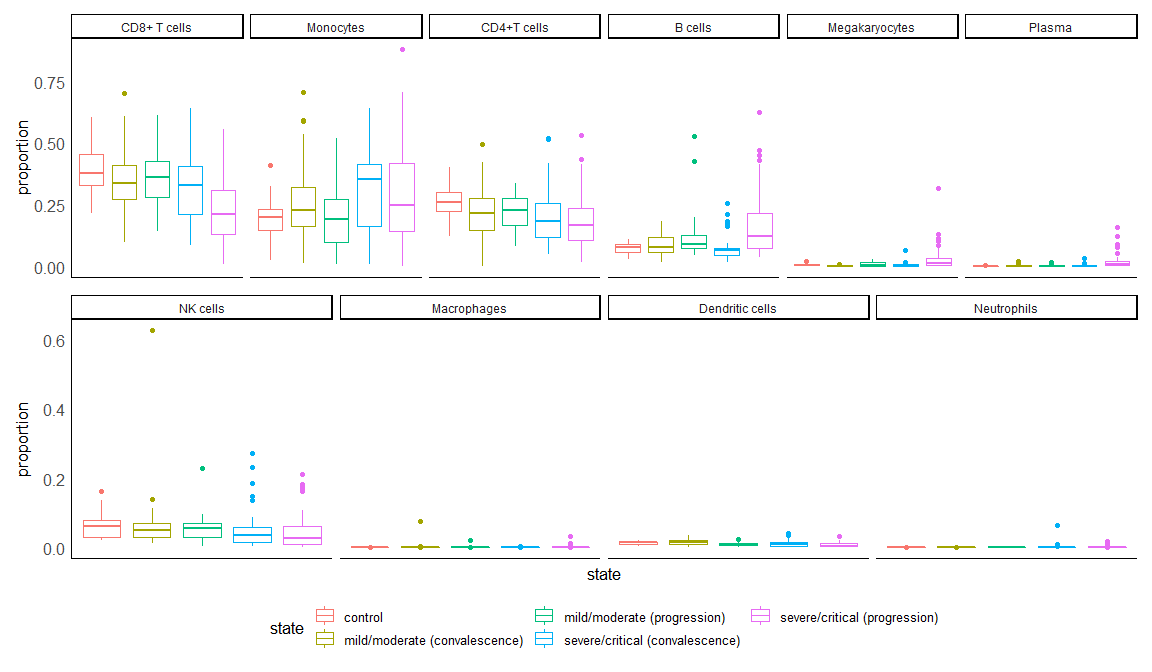
Test between different groups

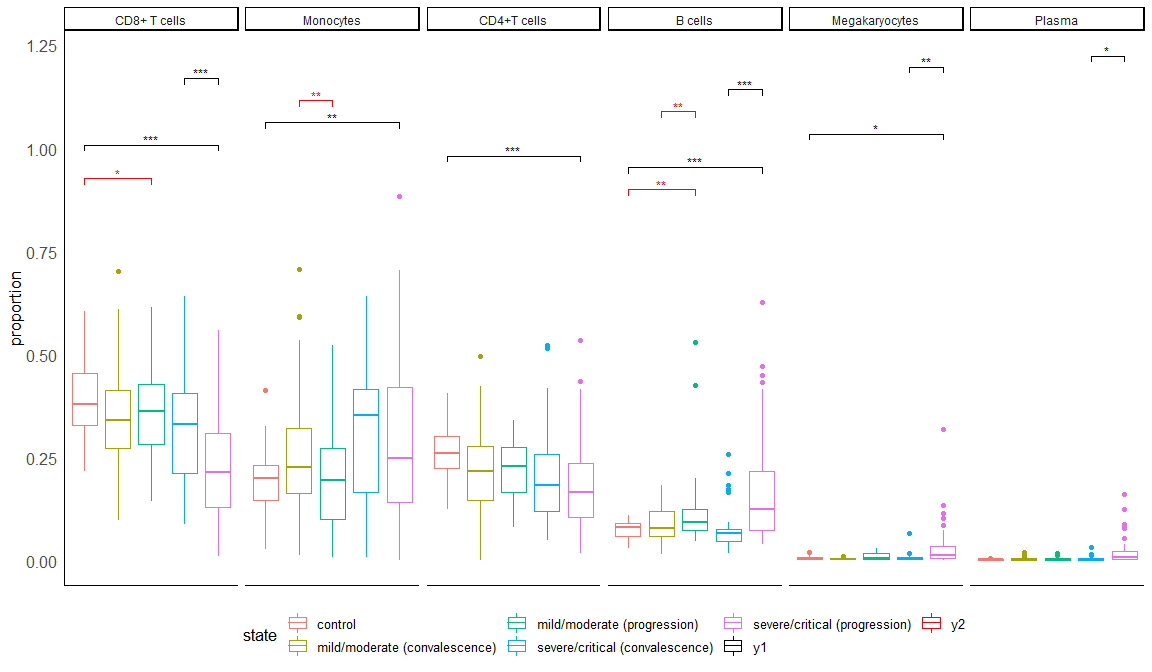
control vs mild/moderate\_progression

control vs severe/critical\_progression

mild/moderate\_convalescence vs mild/moderate\_progression

severe/critical\_convalescence vs severe/critical\_progression





### UMAP plot