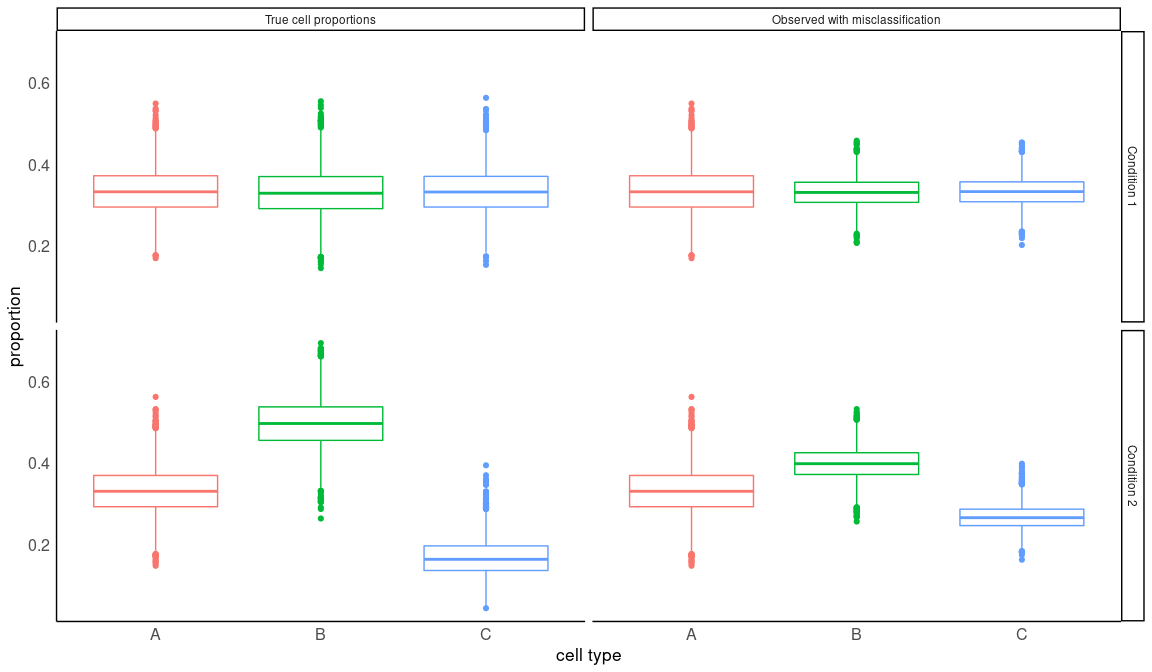
Figure Draft - Three plots version

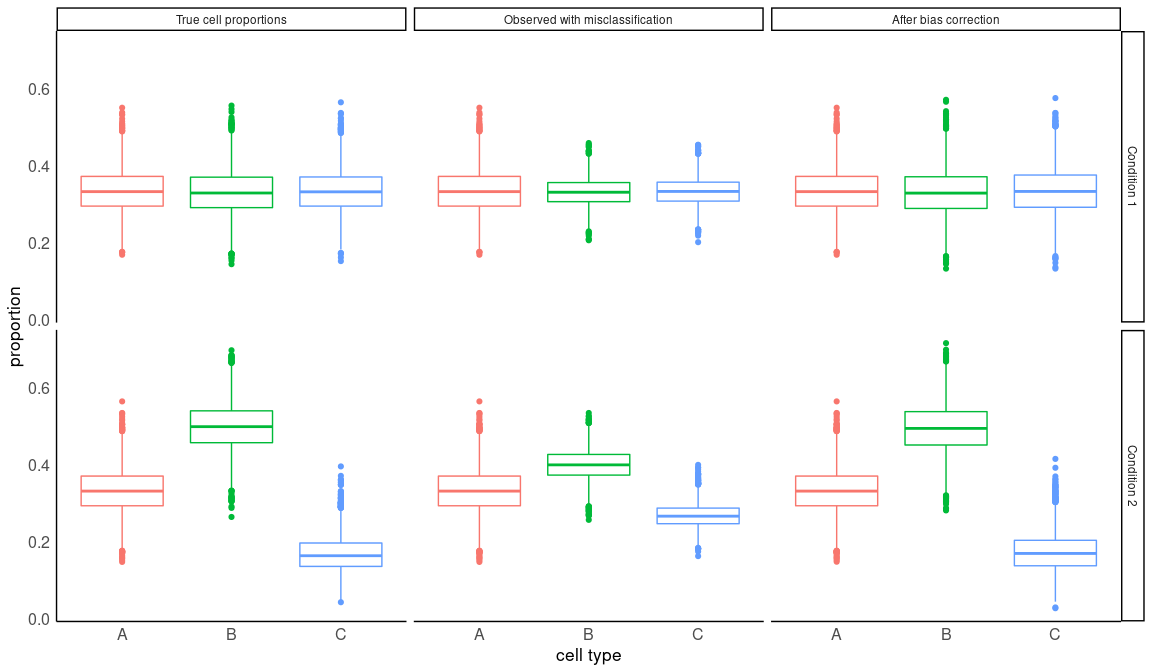
Xinyi Lin

1/7/2022

## Figure 1

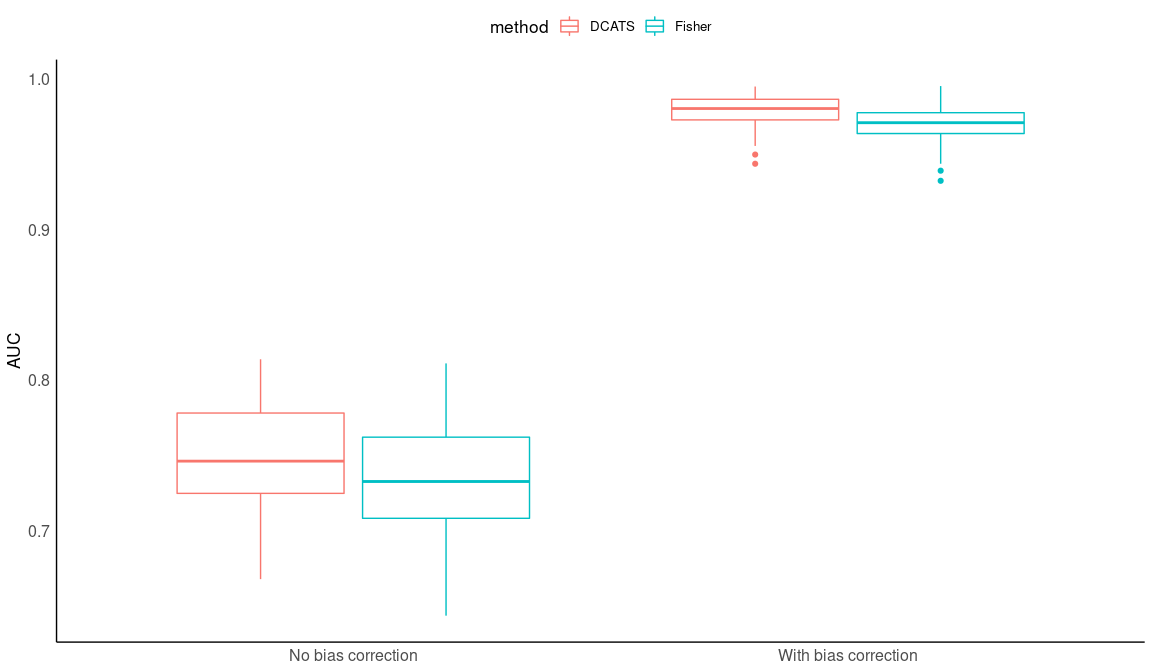
### Figure 1 - B





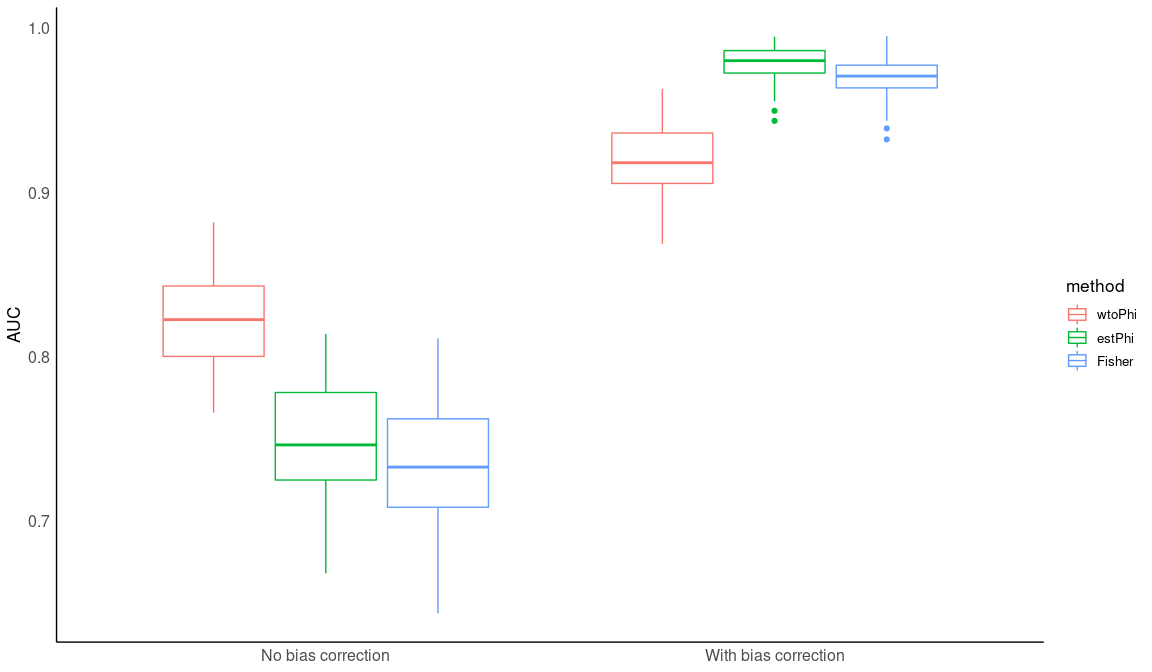
## Saving 12 x 7 in image

### Figure 1 - C

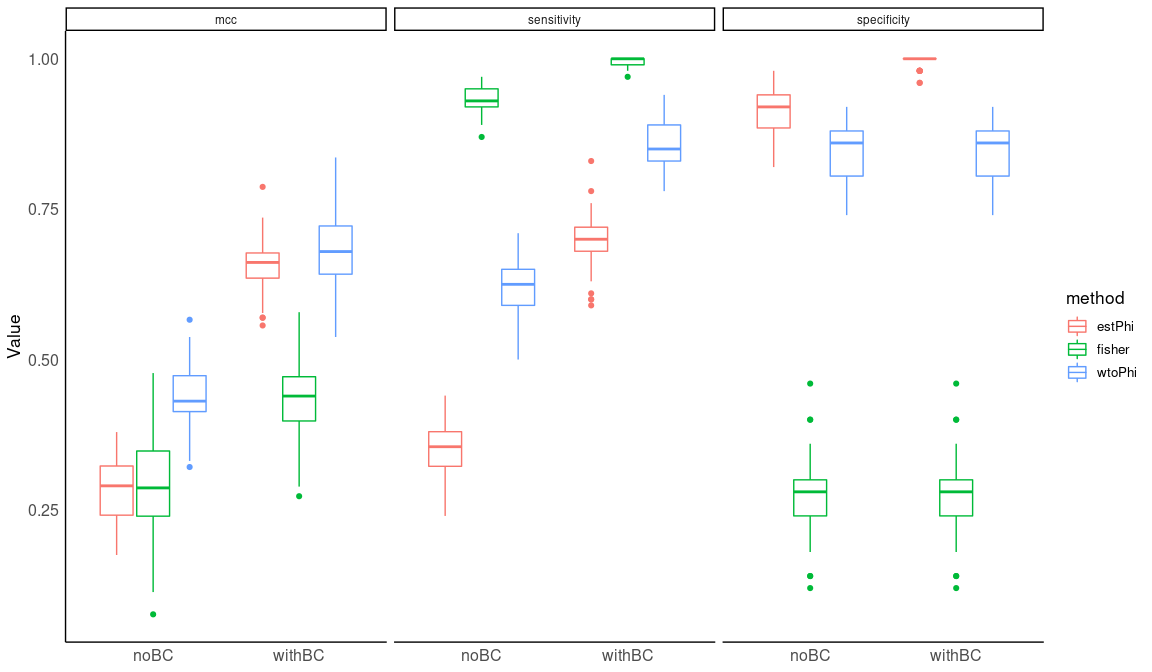


## Saving 12 x 7 in image

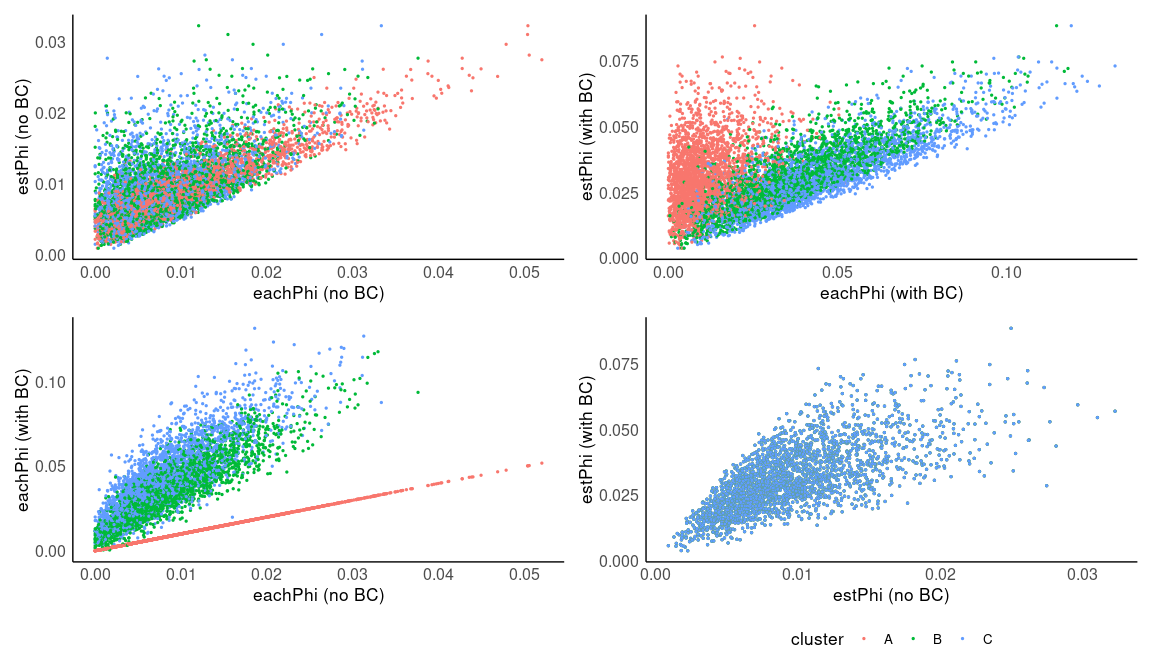
Simulation 1: Supplementary Plots

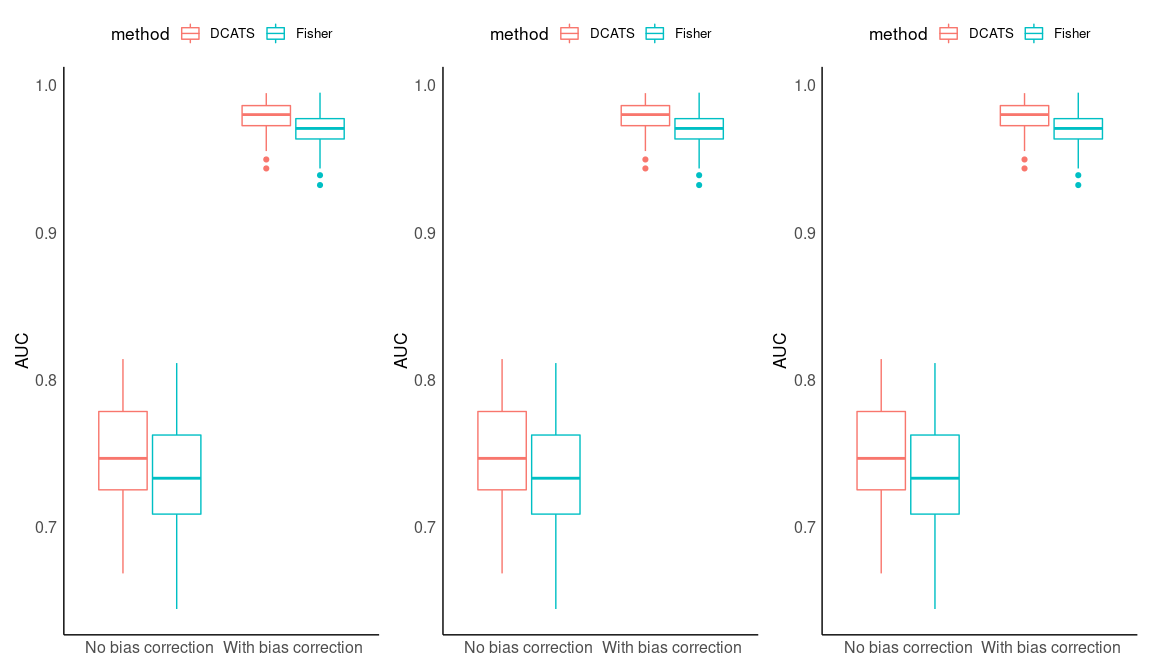
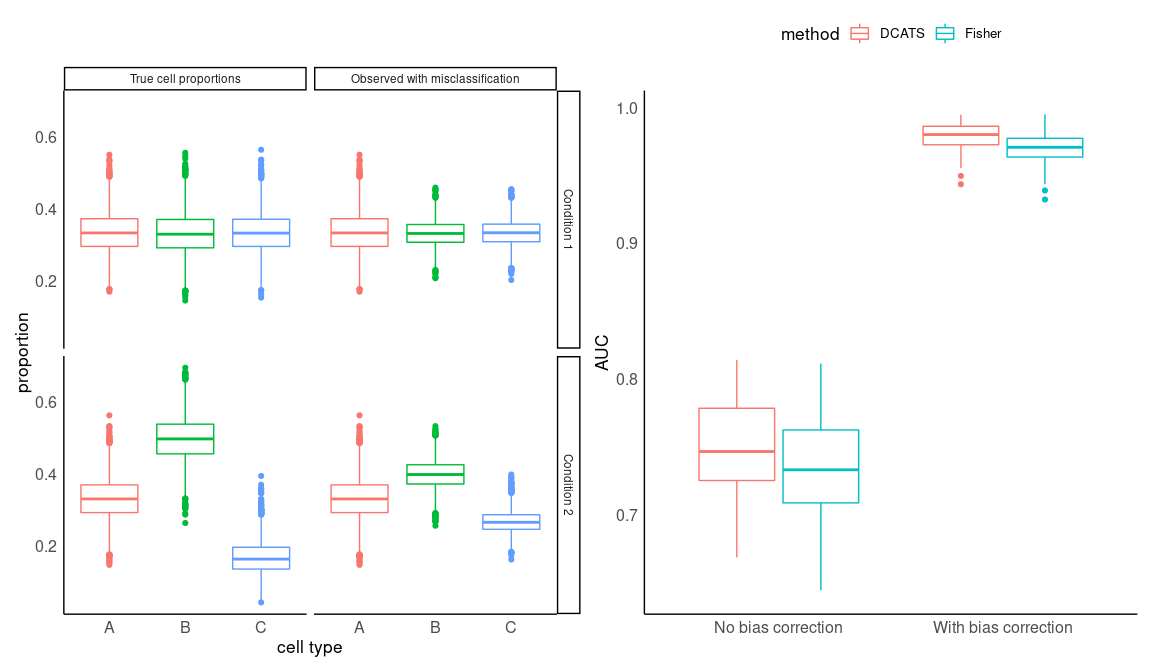


## Saving 12 x 7 in image



## Saving 12 x 7 in image





## Figure 2

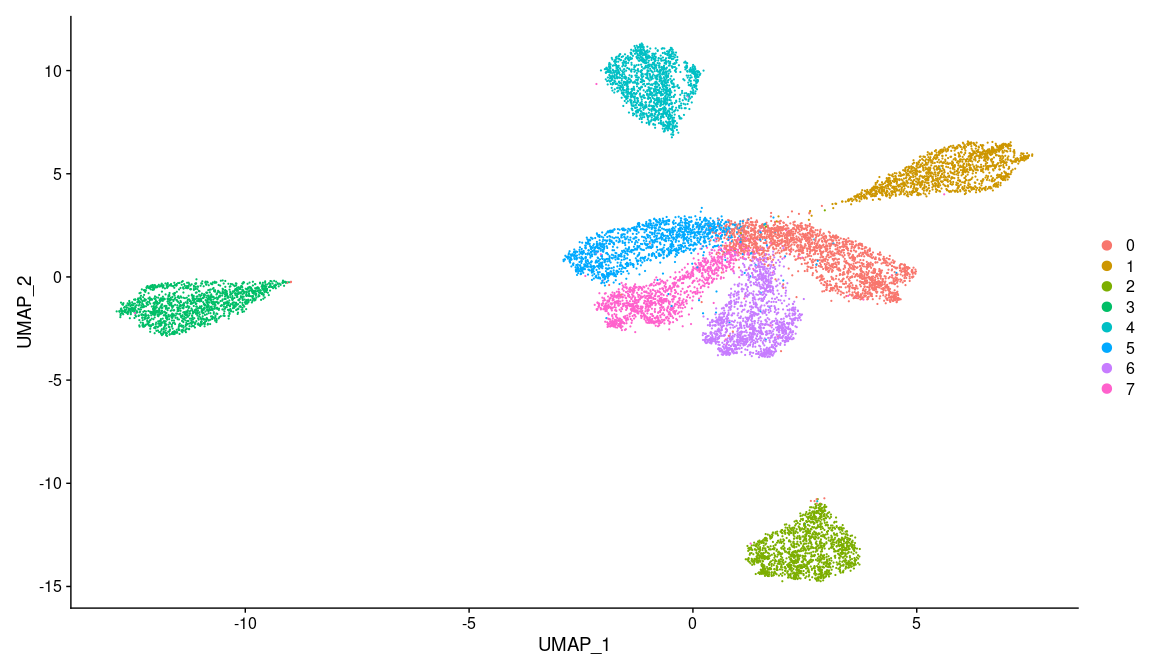
### Figure 2-A

The Distribution of cell pool

## Centering and scaling data matrix

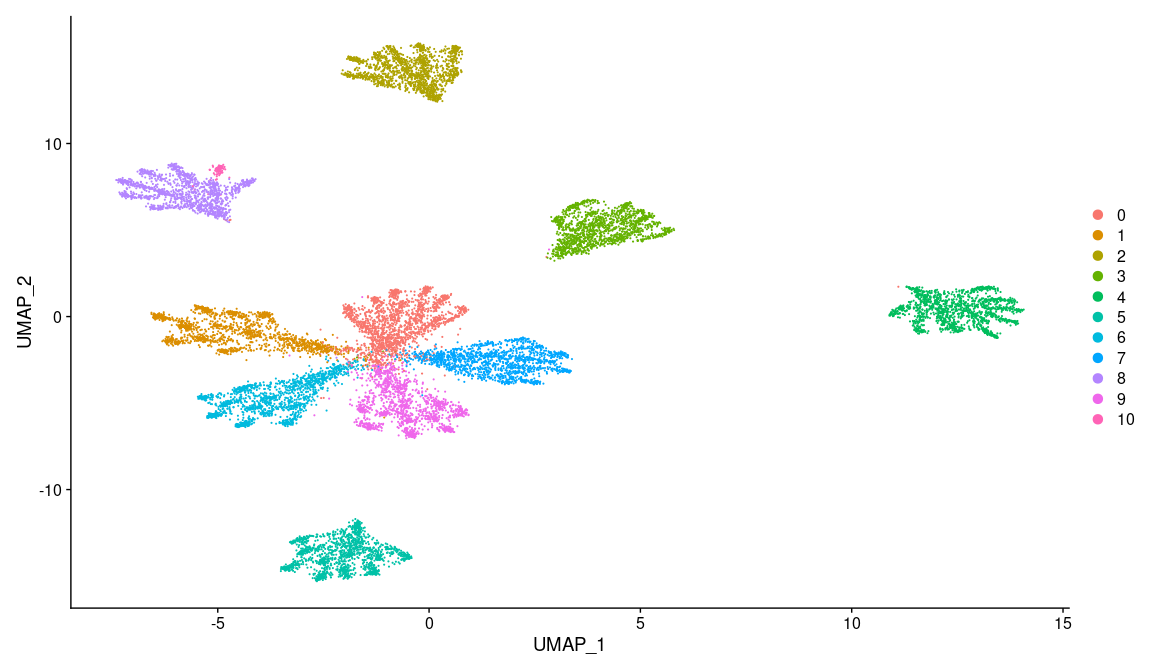
## PC\_ 1   
## Positive: Gene862, Gene593, Gene473, Gene94, Gene511, Gene508, Gene724, Gene830, Gene623, Gene584   
## Gene662, Gene396, Gene439, Gene214, Gene524, Gene714, Gene285, Gene485, Gene395, Gene19   
## Gene840, Gene191, Gene676, Gene88, Gene418, Gene111, Gene569, Gene713, Gene179, Gene434   
## 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



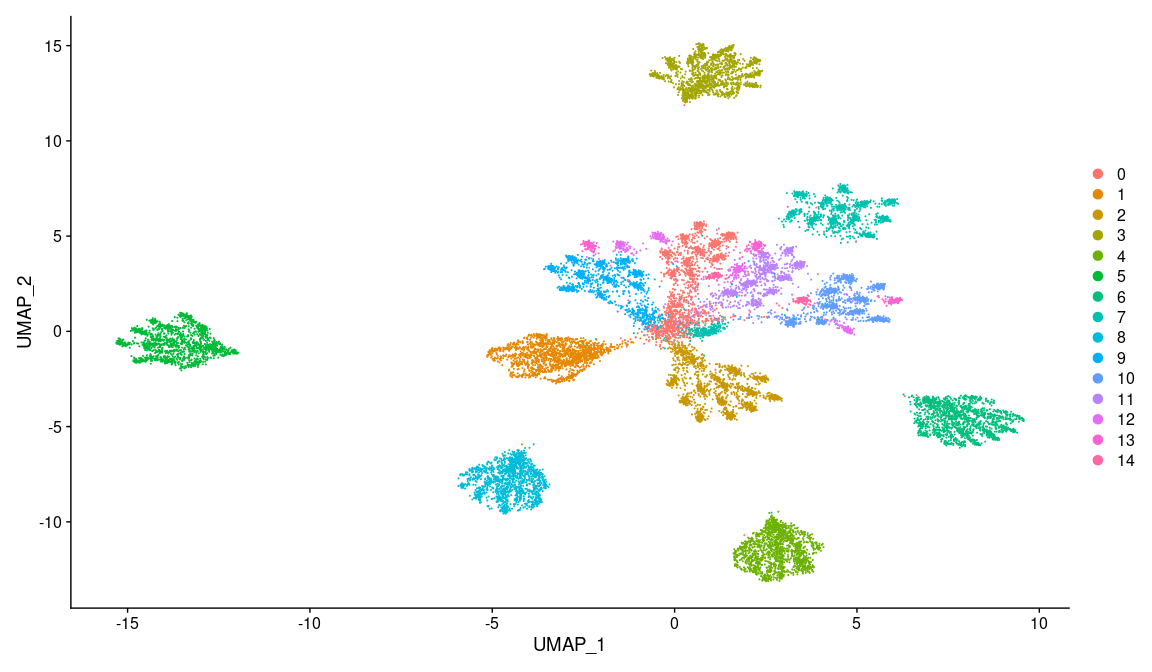
## Centering and scaling data matrix

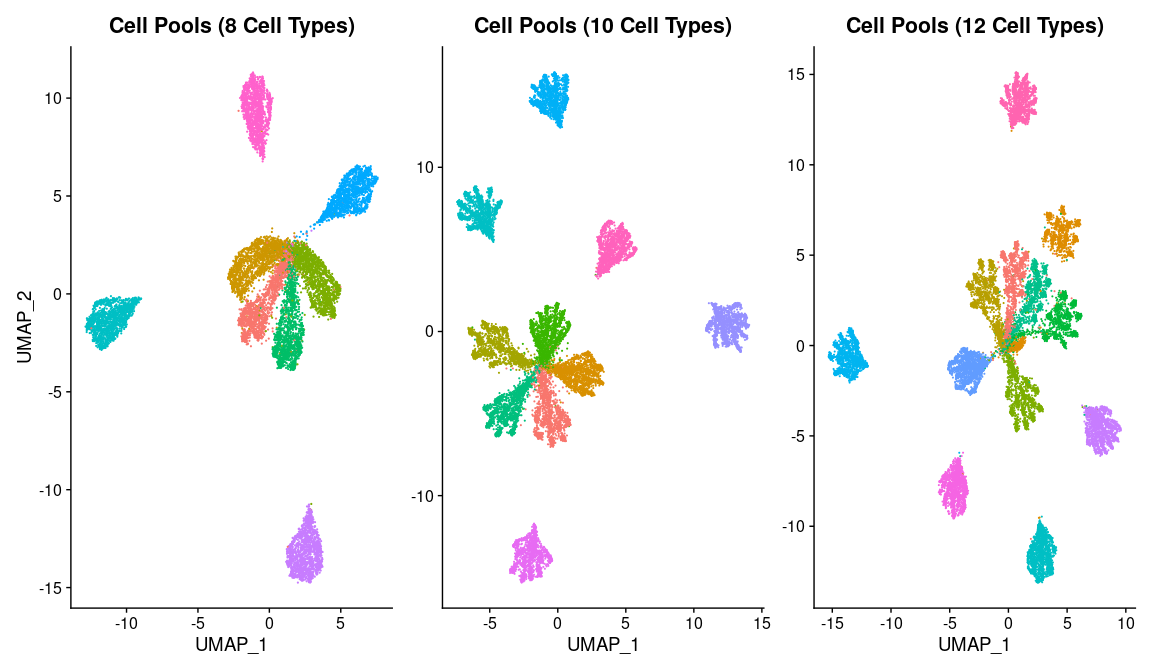
## PC\_ 1   
## Positive: Gene623, Gene412, Gene469, Gene313, Gene433, Gene400, Gene198, Gene589, Gene464, Gene973   
## Gene151, Gene251, Gene654, Gene340, Gene317, Gene56, Gene102, Gene524, Gene392, Gene872   
## Gene344, Gene766, Gene748, Gene980, Gene303, Gene873, Gene811, Gene652, Gene155, Gene485   
## 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



## 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

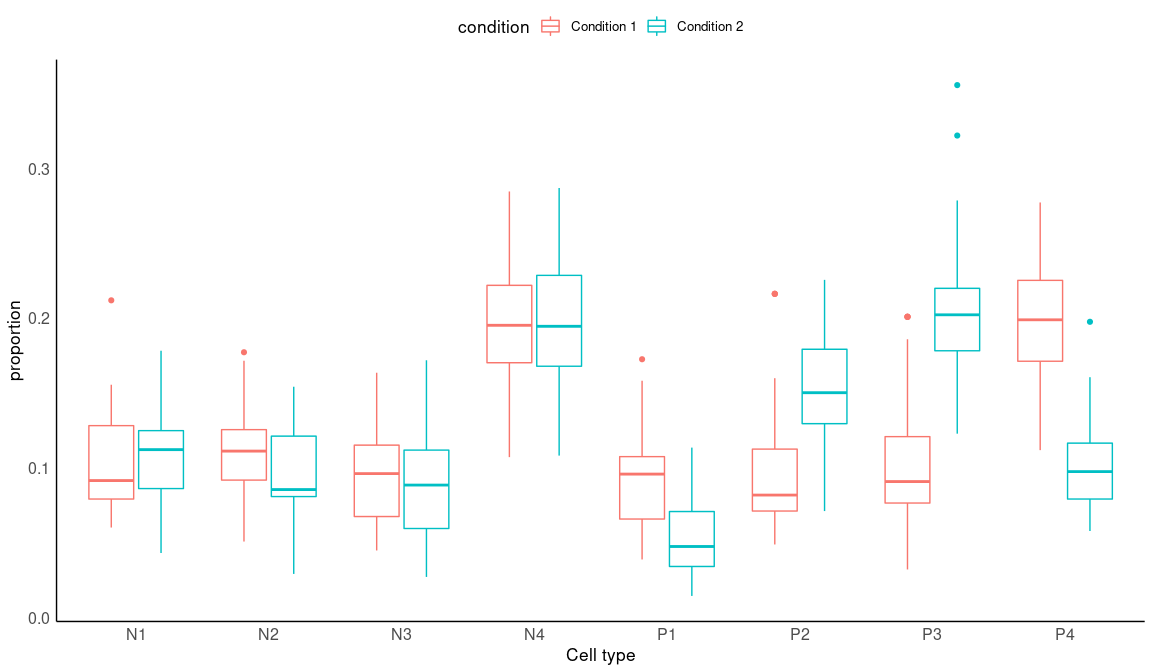


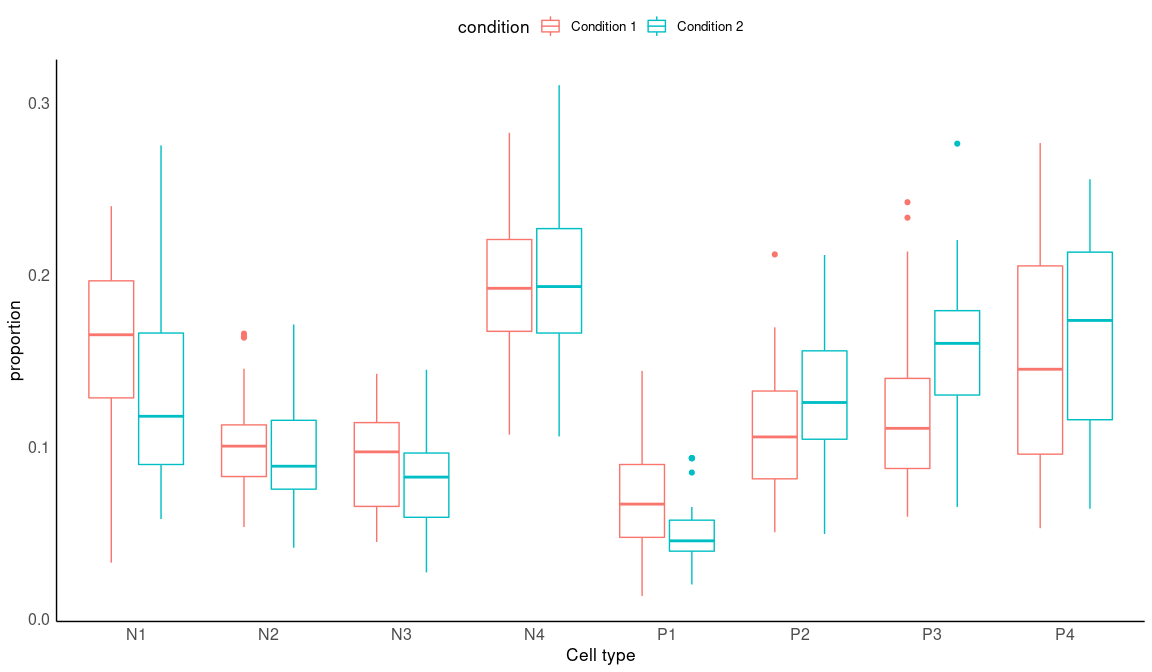


Draw the proportion of different cell types and ROC curves

## Warning: `data\_frame()` was deprecated in tibble 1.1.0.  
## Please use `tibble()` instead.  
## This warning is displayed once every 8 hours.  
## Call `lifecycle::last\_lifecycle\_warnings()` to see where this warning was generated.

## Warning in if (!is.na(oper[[idx]])) {: the condition has length > 1 and only the  
## first element will be used  
  
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## Setting levels: control = N, case = P

## Setting direction: controls > cases

## Setting levels: control = N, case = P

## Setting direction: controls > cases

## Setting levels: control = N, case = P

## Setting direction: controls > cases

## Setting levels: control = N, case = P

## Setting direction: controls > cases

## Setting levels: control = N, case = P

## Setting direction: controls > cases

## Setting levels: control = N, case = P

## Setting direction: controls < cases

Print one true\_matrix and knn\_matrix as example

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | A | B | C | D | E | F | G | H |
| 7 | 0.9925884 | 0.0000000 | 0.0074116 | 0.0000000 | 0.0000000 | 0.0000000 | 0.0000000 | 0.0000000 |
| 8 | 0.0000000 | 0.9996793 | 0.0003207 | 0.0000000 | 0.0000000 | 0.0000000 | 0.0000000 | 0.0000000 |
| 3 | 0.0000000 | 0.0000000 | 0.9616307 | 0.0004796 | 0.0163070 | 0.0100719 | 0.0000000 | 0.0115108 |
| 6 | 0.0016434 | 0.0000000 | 0.0061627 | 0.9921939 | 0.0000000 | 0.0000000 | 0.0000000 | 0.0000000 |
| 2 | 0.0000000 | 0.0000000 | 0.0557157 | 0.0019212 | 0.9178674 | 0.0033622 | 0.0000000 | 0.0211335 |
| 4 | 0.0000000 | 0.0000000 | 0.0507012 | 0.0016181 | 0.0253506 | 0.9099245 | 0.0000000 | 0.0124056 |
| 5 | 0.0000000 | 0.0000000 | 0.0012804 | 0.0000000 | 0.0000000 | 0.0000000 | 0.9987196 | 0.0000000 |
| 1 | 0.0000000 | 0.0000000 | 0.1407517 | 0.0007369 | 0.0324245 | 0.0140015 | 0.0000000 | 0.8120855 |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | A | B | C | D | E | F | G | H |
| A | 0.9985960 | 0.0000263 | 0.0010624 | 0.0000622 | 0.0001555 | 0.0000641 | 0.0000173 | 0.0000162 |
| B | 0.0000287 | 0.9991608 | 0.0006151 | 0.0000152 | 0.0001598 | 0.0000000 | 0.0000203 | 0.0000000 |
| C | 0.0018297 | 0.0009675 | 0.9375284 | 0.0021082 | 0.0187538 | 0.0094317 | 0.0006555 | 0.0287252 |
| D | 0.0000951 | 0.0000213 | 0.0018715 | 0.9972366 | 0.0001855 | 0.0003109 | 0.0000653 | 0.0002138 |
| E | 0.0003277 | 0.0003075 | 0.0229506 | 0.0002558 | 0.9404613 | 0.0119533 | 0.0000271 | 0.0237168 |
| F | 0.0001565 | 0.0000000 | 0.0133674 | 0.0004963 | 0.0138433 | 0.9546358 | 0.0000113 | 0.0174892 |
| G | 0.0000433 | 0.0000464 | 0.0009505 | 0.0001067 | 0.0000321 | 0.0000116 | 0.9987777 | 0.0000316 |
| H | 0.0000565 | 0.0000000 | 0.0582963 | 0.0004888 | 0.0393305 | 0.0250432 | 0.0000443 | 0.8767404 |

## [1] 0.9987421

## [1] 2.977109e-18

### Figure 2-B

#### Different numbers of replicates

## [1] "/storage/holab/linxy/DCATS/simulation/current/replicates2&2\_K8\_con100\_splatter3000&3000para.RData"  
## [2] "/storage/holab/linxy/DCATS/simulation/current/replicates3&3\_K8\_con100\_splatter3000&3000para.RData"  
## [3] "/storage/holab/linxy/DCATS/simulation/current/replicates4&4\_K8\_con100\_splatter3000&3000para.RData"

## Warning in if (!is.na(oper[[idx]])) {: the condition has length > 1 and only the  
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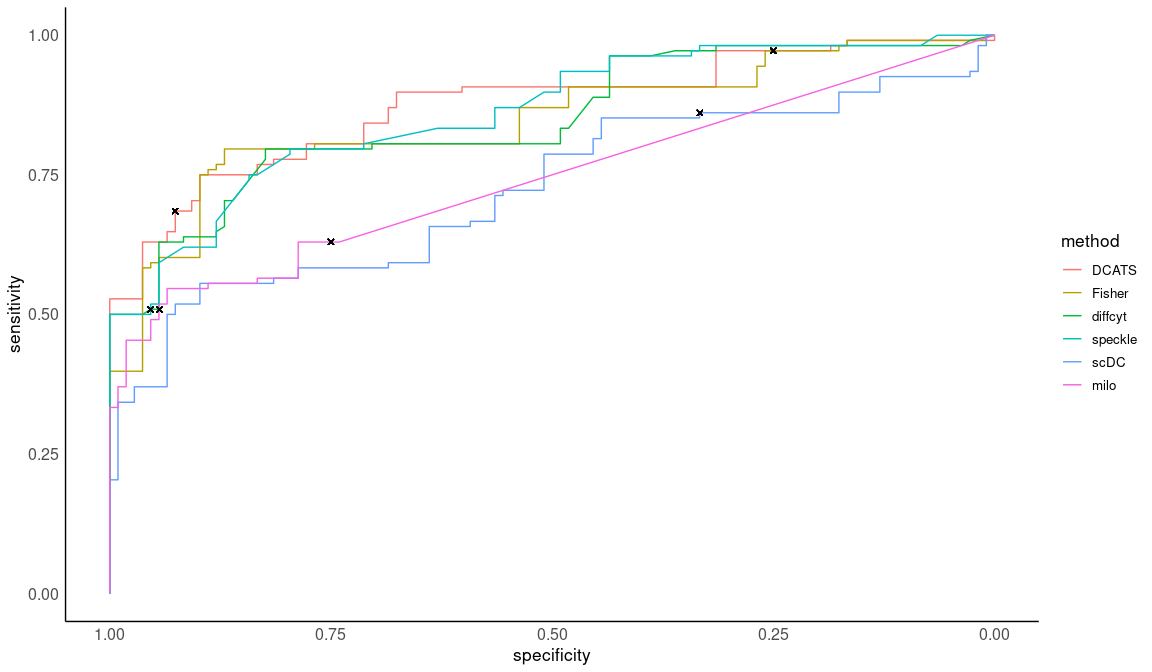
## Warning in if (!is.na(oper[[idx]])) {: the condition has length > 1 and only the  
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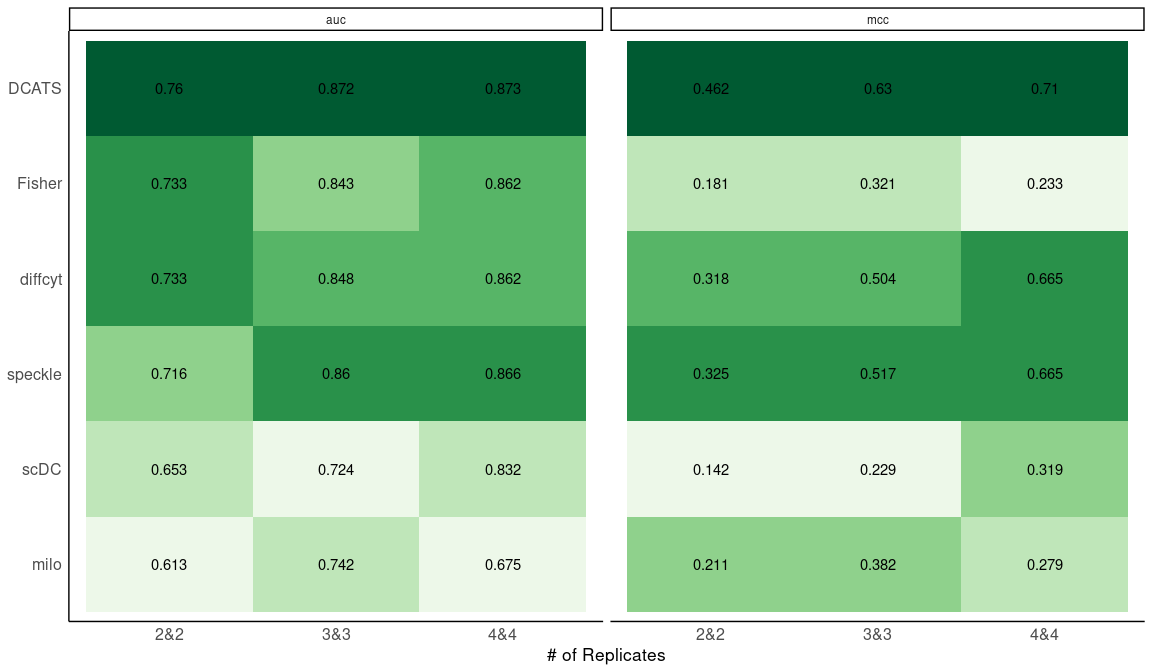
## Warning in if (!is.na(oper[[idx]])) {: the condition has length > 1 and only the  
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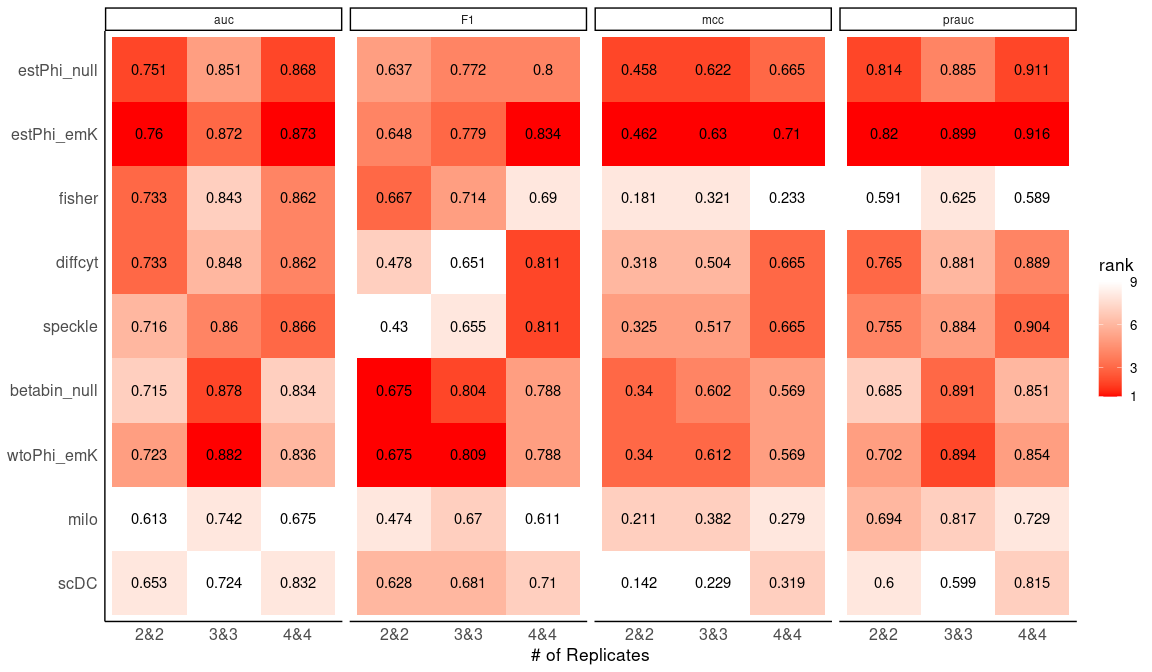
## method mcc auc sensitivity specificity F1 replicates  
## 1 estPhi\_emK 0.462 0.760 0.527 0.902 0.648 2&2  
## 2 estPhi\_null 0.458 0.751 0.509 0.911 0.637 2&2  
## 3 estPhi\_emU 0.451 0.743 0.598 0.839 0.680 2&2  
## 4 fisher 0.181 0.733 0.848 0.304 0.667 2&2  
## 5 diffcyt 0.318 0.733 0.339 0.920 0.478 2&2  
## 6 wtoPhi\_emK 0.340 0.723 0.688 0.652 0.675 2&2  
## 7 speckle 0.325 0.716 0.286 0.955 0.430 2&2  
## 8 betabin\_null 0.340 0.715 0.688 0.652 0.675 2&2  
## 9 scDC 0.142 0.653 0.732 0.402 0.628 2&2  
## 10 milo 0.211 0.613 0.366 0.821 0.474 2&2  
## 11 wtoPhi\_emK 0.612 0.882 0.824 0.787 0.809 3&3  
## 12 betabin\_null 0.602 0.878 0.815 0.787 0.804 3&3  
## 13 estPhi\_emK 0.630 0.872 0.685 0.926 0.779 3&3  
## 14 speckle 0.517 0.860 0.509 0.954 0.655 3&3  
## 15 estPhi\_emU 0.622 0.856 0.713 0.898 0.786 3&3  
## 16 estPhi\_null 0.622 0.851 0.676 0.926 0.772 3&3  
## 17 diffcyt 0.504 0.848 0.509 0.944 0.651 3&3  
## 18 fisher 0.321 0.843 0.972 0.250 0.714 3&3  
## 19 milo 0.382 0.742 0.630 0.750 0.670 3&3  
## 20 scDC 0.229 0.724 0.861 0.333 0.681 3&3  
## 21 estPhi\_emK 0.710 0.873 0.759 0.940 0.834 4&4  
## 22 estPhi\_emU 0.684 0.873 0.793 0.888 0.833 4&4  
## 23 estPhi\_null 0.665 0.868 0.707 0.940 0.800 4&4  
## 24 speckle 0.665 0.866 0.741 0.914 0.811 4&4  
## 25 diffcyt 0.665 0.862 0.741 0.914 0.811 4&4  
## 26 fisher 0.233 0.862 0.922 0.250 0.690 4&4  
## 27 wtoPhi\_emK 0.569 0.836 0.802 0.767 0.788 4&4  
## 28 betabin\_null 0.569 0.834 0.802 0.767 0.788 4&4  
## 29 scDC 0.319 0.832 0.888 0.388 0.710 4&4  
## 30 milo 0.279 0.675 0.569 0.707 0.611 4&4



## Warning in pal\_name(palette, type): Unknown palette RdYIBu



Simulation 2: Supplementary Plots

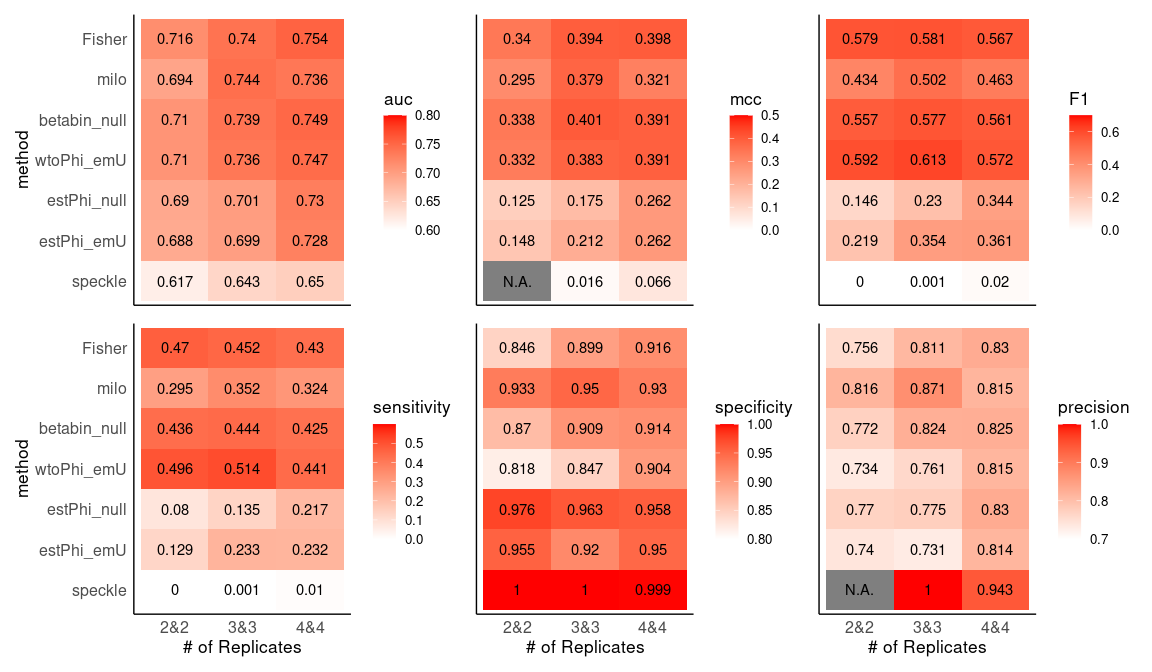


Details of statistics value

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| method | mcc | auc | prauc | sensitivity | specificity | precision | F1 | replicates |
| estPhi\_emK | 0.462 | 0.760 | 0.820 | 0.527 | 0.902 | 0.843 | 0.648 | 2&2 |
| estPhi\_null | 0.458 | 0.751 | 0.814 | 0.509 | 0.911 | 0.851 | 0.637 | 2&2 |
| diffcyt | 0.318 | 0.733 | 0.765 | 0.339 | 0.920 | 0.809 | 0.478 | 2&2 |
| Fisher | 0.181 | 0.733 | 0.591 | 0.848 | 0.304 | 0.549 | 0.667 | 2&2 |
| wtoPhi\_emK | 0.340 | 0.723 | 0.702 | 0.688 | 0.652 | 0.664 | 0.675 | 2&2 |
| speckle | 0.325 | 0.716 | 0.755 | 0.286 | 0.955 | 0.865 | 0.430 | 2&2 |
| betabin\_null | 0.340 | 0.715 | 0.685 | 0.688 | 0.652 | 0.664 | 0.675 | 2&2 |
| scDC | 0.142 | 0.653 | 0.600 | 0.732 | 0.402 | 0.550 | 0.628 | 2&2 |
| milo | 0.211 | 0.613 | 0.694 | 0.366 | 0.821 | 0.672 | 0.474 | 2&2 |
| wtoPhi\_emK | 0.612 | 0.882 | 0.894 | 0.824 | 0.787 | 0.795 | 0.809 | 3&3 |
| betabin\_null | 0.602 | 0.878 | 0.891 | 0.815 | 0.787 | 0.793 | 0.804 | 3&3 |
| estPhi\_emK | 0.630 | 0.872 | 0.899 | 0.685 | 0.926 | 0.902 | 0.779 | 3&3 |
| speckle | 0.517 | 0.860 | 0.884 | 0.509 | 0.954 | 0.917 | 0.655 | 3&3 |
| estPhi\_null | 0.622 | 0.851 | 0.885 | 0.676 | 0.926 | 0.901 | 0.772 | 3&3 |
| diffcyt | 0.504 | 0.848 | 0.881 | 0.509 | 0.944 | 0.902 | 0.651 | 3&3 |
| Fisher | 0.321 | 0.843 | 0.625 | 0.972 | 0.250 | 0.565 | 0.714 | 3&3 |
| milo | 0.382 | 0.742 | 0.817 | 0.630 | 0.750 | 0.716 | 0.670 | 3&3 |
| scDC | 0.229 | 0.724 | 0.599 | 0.861 | 0.333 | 0.564 | 0.681 | 3&3 |
| estPhi\_emK | 0.710 | 0.873 | 0.916 | 0.759 | 0.940 | 0.926 | 0.834 | 4&4 |
| estPhi\_null | 0.665 | 0.868 | 0.911 | 0.707 | 0.940 | 0.921 | 0.800 | 4&4 |
| speckle | 0.665 | 0.866 | 0.904 | 0.741 | 0.914 | 0.896 | 0.811 | 4&4 |
| diffcyt | 0.665 | 0.862 | 0.889 | 0.741 | 0.914 | 0.896 | 0.811 | 4&4 |
| Fisher | 0.233 | 0.862 | 0.589 | 0.922 | 0.250 | 0.552 | 0.690 | 4&4 |
| wtoPhi\_emK | 0.569 | 0.836 | 0.854 | 0.802 | 0.767 | 0.775 | 0.788 | 4&4 |
| betabin\_null | 0.569 | 0.834 | 0.851 | 0.802 | 0.767 | 0.775 | 0.788 | 4&4 |
| scDC | 0.319 | 0.832 | 0.815 | 0.888 | 0.388 | 0.592 | 0.710 | 4&4 |
| milo | 0.279 | 0.675 | 0.729 | 0.569 | 0.707 | 0.660 | 0.611 | 4&4 |

nhoods level

## method mcc auc sensitivity specificity F1 replicates prauc  
## 1 fisher 0.340 0.7157843 0.470 0.846 0.579 2&2 0.716  
## 2 wtoPhi\_emU 0.332 0.7096903 0.496 0.818 0.592 2&2 0.710  
## 3 betabin\_null 0.338 0.7095942 0.436 0.870 0.557 2&2 0.710  
## 4 milo 0.295 0.6937905 0.295 0.933 0.434 2&2 0.694  
## 5 estPhi\_null 0.125 0.6895417 0.080 0.976 0.146 2&2 0.690  
## 6 estPhi\_emU 0.148 0.6875149 0.129 0.955 0.219 2&2 0.688  
## 7 speckle NaN 0.6173524 0.000 1.000 0.000 2&2 0.617  
## 8 milo 0.379 0.7439506 0.352 0.950 0.502 3&3 0.744  
## 9 fisher 0.394 0.7403612 0.452 0.899 0.581 3&3 0.740  
## 10 betabin\_null 0.401 0.7393887 0.444 0.909 0.577 3&3 0.739  
## 11 wtoPhi\_emU 0.383 0.7361322 0.514 0.847 0.613 3&3 0.736  
## 12 estPhi\_null 0.175 0.7009994 0.135 0.963 0.230 3&3 0.701  
## 13 estPhi\_emU 0.212 0.6994401 0.233 0.920 0.354 3&3 0.699  
## 14 speckle 0.016 0.6428572 0.001 1.000 0.001 3&3 0.643  
## 15 fisher 0.398 0.7535549 0.430 0.916 0.567 4&4 0.754  
## 16 betabin\_null 0.391 0.7493532 0.425 0.914 0.561 4&4 0.749  
## 17 wtoPhi\_emU 0.391 0.7465912 0.441 0.904 0.572 4&4 0.747  
## 18 milo 0.321 0.7364727 0.324 0.930 0.463 4&4 0.736  
## 19 estPhi\_null 0.262 0.7304013 0.217 0.958 0.344 4&4 0.730  
## 20 estPhi\_emU 0.262 0.7279494 0.232 0.950 0.361 4&4 0.728  
## 21 speckle 0.066 0.6503482 0.010 0.999 0.020 4&4 0.650

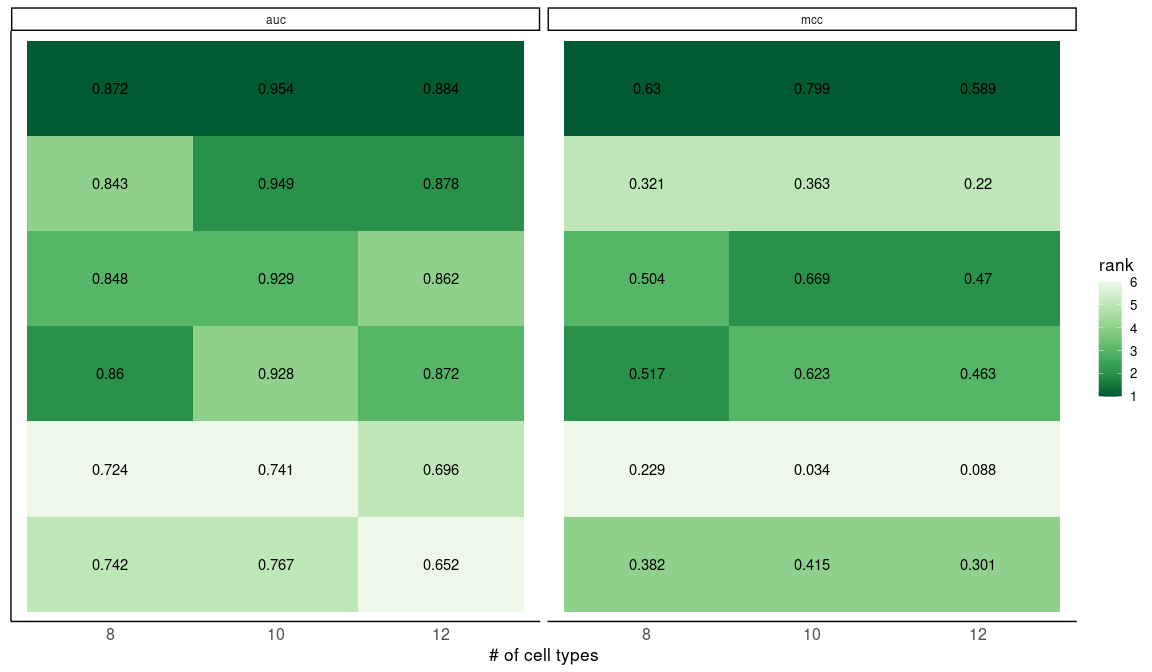


#### Different numbers of clusters

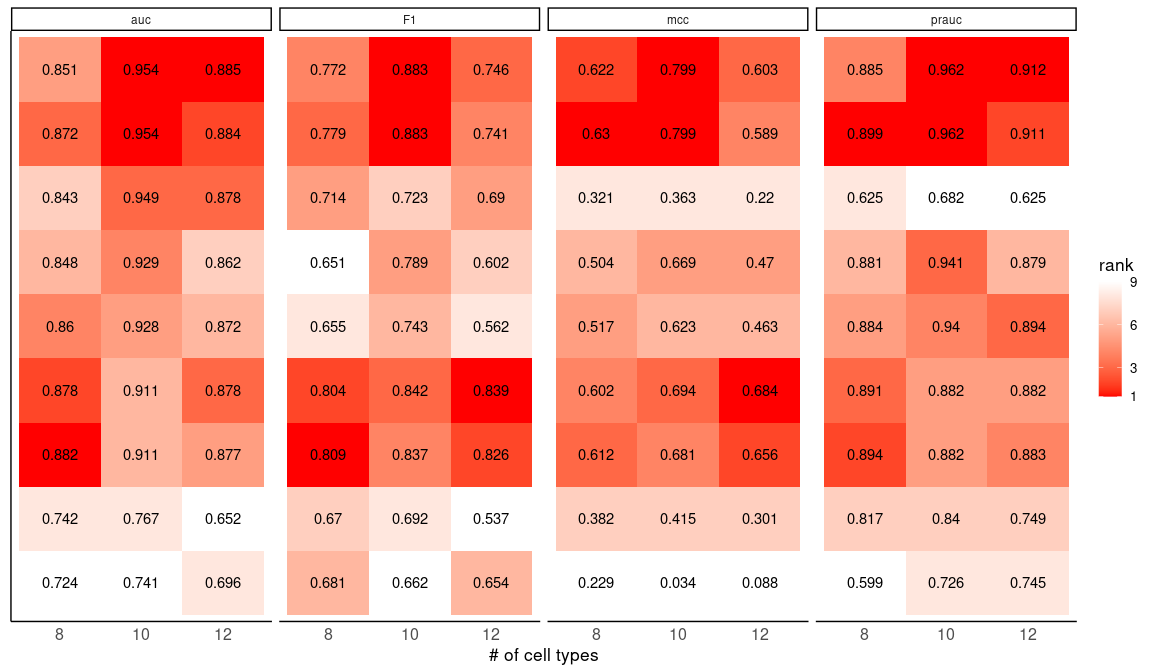
## [1] "/storage/holab/linxy/DCATS/simulation/current/replicates3&3\_K10\_con100\_splatter3000&3000para.RData"  
## [2] "/storage/holab/linxy/DCATS/simulation/current/replicates3&3\_K12\_con100\_splatter3000&3000para.RData"  
## [3] "/storage/holab/linxy/DCATS/simulation/current/replicates3&3\_K8\_con100\_splatter3000&3000para.RData"

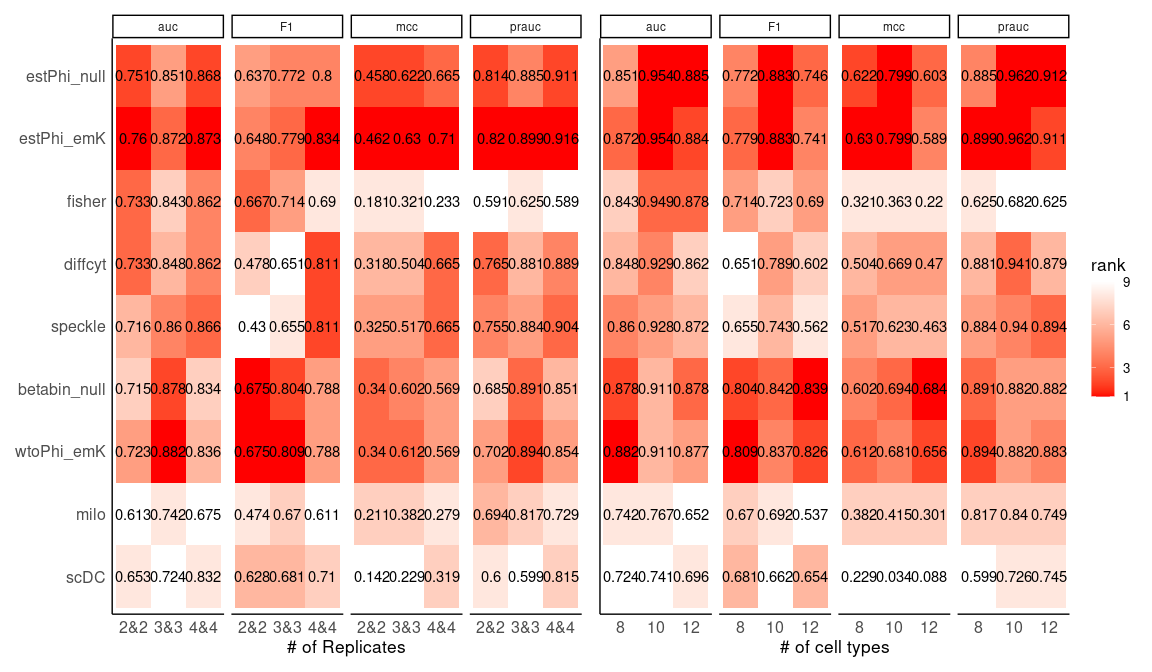
## method mcc auc sensitivity specificity F1 clustersN  
## 1 wtoPhi\_emK 0.612 0.882 0.824 0.787 0.809 8  
## 2 betabin\_null 0.602 0.878 0.815 0.787 0.804 8  
## 3 estPhi\_emK 0.630 0.872 0.685 0.926 0.779 8  
## 4 speckle 0.517 0.860 0.509 0.954 0.655 8  
## 5 estPhi\_null 0.622 0.851 0.676 0.926 0.772 8  
## 6 diffcyt 0.504 0.848 0.509 0.944 0.651 8  
## 7 fisher 0.321 0.843 0.972 0.250 0.714 8  
## 8 milo 0.382 0.742 0.630 0.750 0.670 8  
## 9 scDC 0.229 0.724 0.861 0.333 0.681 8  
## 10 estPhi\_null 0.799 0.954 0.807 0.980 0.883 10  
## 11 estPhi\_emK 0.799 0.954 0.807 0.980 0.883 10  
## 12 fisher 0.363 0.949 1.000 0.233 0.723 10  
## 13 diffcyt 0.669 0.929 0.673 0.967 0.789 10  
## 14 speckle 0.623 0.928 0.607 0.973 0.743 10  
## 15 betabin\_null 0.694 0.911 0.820 0.873 0.842 10  
## 16 wtoPhi\_emK 0.681 0.911 0.820 0.860 0.837 10  
## 17 milo 0.415 0.767 0.660 0.753 0.692 10  
## 18 scDC 0.034 0.741 0.967 0.047 0.662 10  
## 19 estPhi\_null 0.603 0.885 0.628 0.944 0.746 12  
## 20 estPhi\_emK 0.589 0.884 0.628 0.933 0.741 12  
## 21 betabin\_null 0.684 0.878 0.822 0.861 0.839 12  
## 22 fisher 0.220 0.878 0.950 0.194 0.690 12  
## 23 wtoPhi\_emK 0.656 0.877 0.817 0.839 0.826 12  
## 24 speckle 0.463 0.872 0.400 0.978 0.562 12  
## 25 diffcyt 0.470 0.862 0.450 0.956 0.602 12  
## 26 scDC 0.088 0.696 0.889 0.172 0.654 12  
## 27 milo 0.301 0.652 0.422 0.850 0.537 12

## Warning in pal\_name(palette, type): Unknown palette RdYIBu



Simulation 2: Supplementary Plot



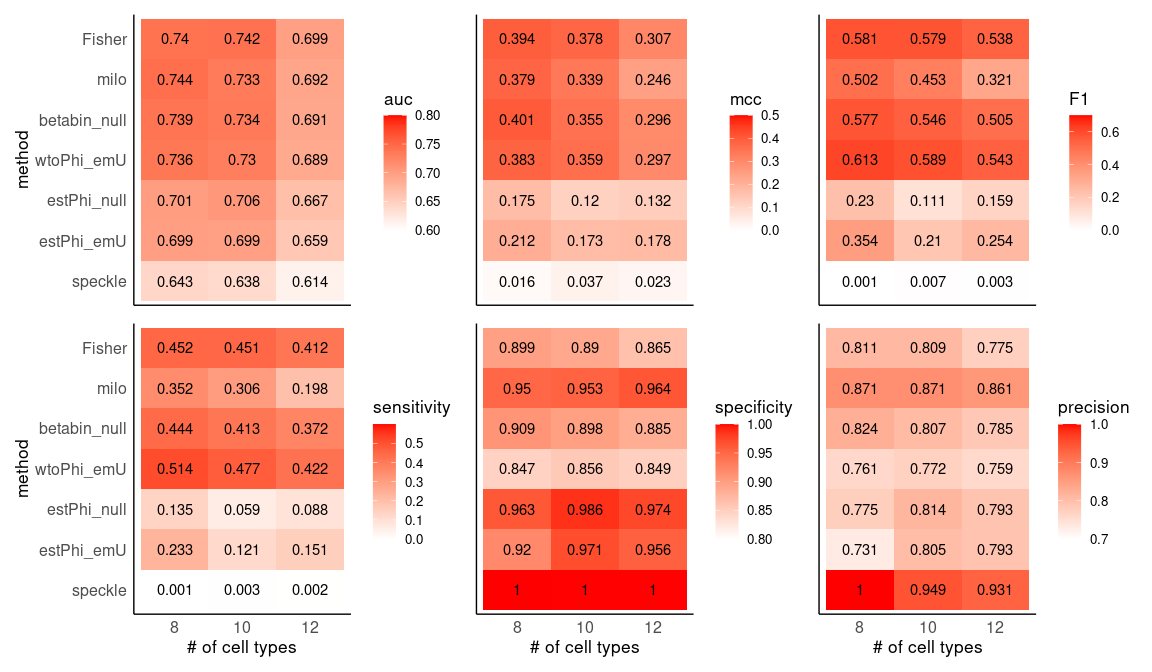


Details of statistics value

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| method | mcc | auc | prauc | sensitivity | specificity | precision | F1 | clustersN |
| wtoPhi\_emK | 0.612 | 0.882 | 0.894 | 0.824 | 0.787 | 0.795 | 0.809 | 8 |
| betabin\_null | 0.602 | 0.878 | 0.891 | 0.815 | 0.787 | 0.793 | 0.804 | 8 |
| estPhi\_emK | 0.630 | 0.872 | 0.899 | 0.685 | 0.926 | 0.902 | 0.779 | 8 |
| speckle | 0.517 | 0.860 | 0.884 | 0.509 | 0.954 | 0.917 | 0.655 | 8 |
| estPhi\_null | 0.622 | 0.851 | 0.885 | 0.676 | 0.926 | 0.901 | 0.772 | 8 |
| diffcyt | 0.504 | 0.848 | 0.881 | 0.509 | 0.944 | 0.902 | 0.651 | 8 |
| Fisher | 0.321 | 0.843 | 0.625 | 0.972 | 0.250 | 0.565 | 0.714 | 8 |
| milo | 0.382 | 0.742 | 0.817 | 0.630 | 0.750 | 0.716 | 0.670 | 8 |
| scDC | 0.229 | 0.724 | 0.599 | 0.861 | 0.333 | 0.564 | 0.681 | 8 |
| estPhi\_null | 0.799 | 0.954 | 0.962 | 0.807 | 0.980 | 0.976 | 0.883 | 10 |
| estPhi\_emK | 0.799 | 0.954 | 0.962 | 0.807 | 0.980 | 0.976 | 0.883 | 10 |
| Fisher | 0.363 | 0.949 | 0.682 | 1.000 | 0.233 | 0.566 | 0.723 | 10 |
| diffcyt | 0.669 | 0.929 | 0.941 | 0.673 | 0.967 | 0.953 | 0.789 | 10 |
| speckle | 0.623 | 0.928 | 0.940 | 0.607 | 0.973 | 0.958 | 0.743 | 10 |
| betabin\_null | 0.694 | 0.911 | 0.882 | 0.820 | 0.873 | 0.866 | 0.842 | 10 |
| wtoPhi\_emK | 0.681 | 0.911 | 0.882 | 0.820 | 0.860 | 0.854 | 0.837 | 10 |
| milo | 0.415 | 0.767 | 0.840 | 0.660 | 0.753 | 0.728 | 0.692 | 10 |
| scDC | 0.034 | 0.741 | 0.726 | 0.967 | 0.047 | 0.503 | 0.662 | 10 |
| estPhi\_null | 0.603 | 0.885 | 0.912 | 0.628 | 0.944 | 0.919 | 0.746 | 12 |
| estPhi\_emK | 0.589 | 0.884 | 0.911 | 0.628 | 0.933 | 0.904 | 0.741 | 12 |
| betabin\_null | 0.684 | 0.878 | 0.882 | 0.822 | 0.861 | 0.855 | 0.839 | 12 |
| Fisher | 0.220 | 0.878 | 0.625 | 0.950 | 0.194 | 0.541 | 0.690 | 12 |
| wtoPhi\_emK | 0.656 | 0.877 | 0.883 | 0.817 | 0.839 | 0.835 | 0.826 | 12 |
| speckle | 0.463 | 0.872 | 0.894 | 0.400 | 0.978 | 0.947 | 0.562 | 12 |
| diffcyt | 0.470 | 0.862 | 0.879 | 0.450 | 0.956 | 0.910 | 0.602 | 12 |
| scDC | 0.088 | 0.696 | 0.745 | 0.889 | 0.172 | 0.518 | 0.654 | 12 |
| milo | 0.301 | 0.652 | 0.749 | 0.422 | 0.850 | 0.738 | 0.537 | 12 |

nhoods level

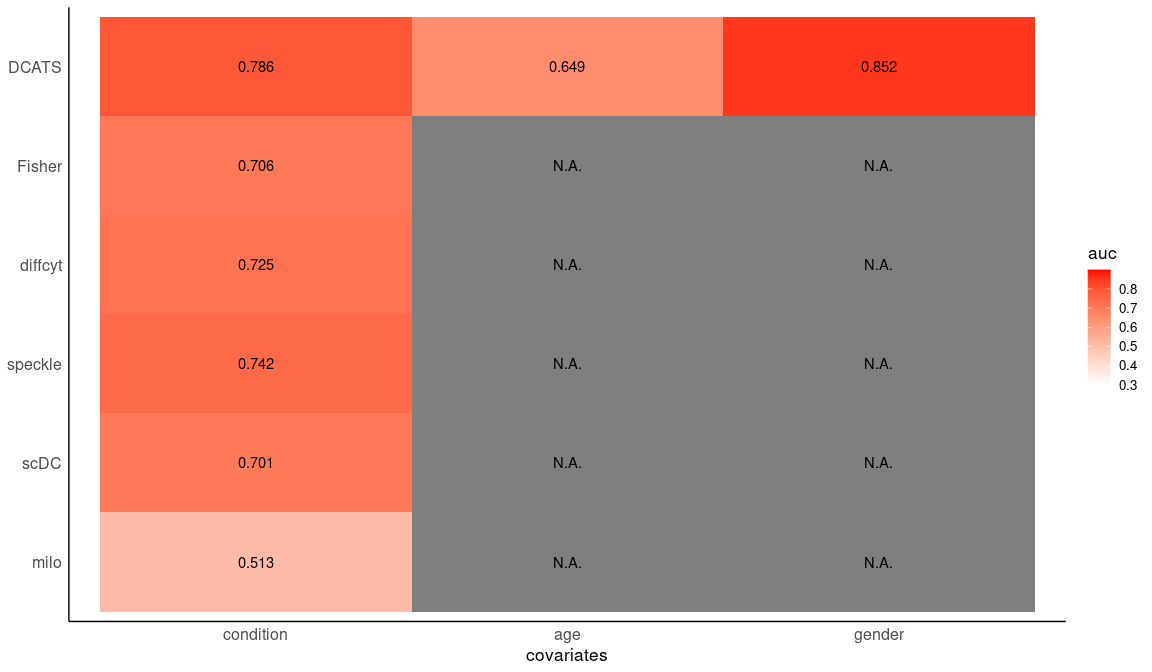
## method mcc auc sensitivity specificity F1 clustersN prauc  
## 1 milo 0.379 0.7439506 0.352 0.950 0.502 8 0.744  
## 2 fisher 0.394 0.7403612 0.452 0.899 0.581 8 0.740  
## 3 betabin\_null 0.401 0.7393887 0.444 0.909 0.577 8 0.739  
## 4 wtoPhi\_emU 0.383 0.7361322 0.514 0.847 0.613 8 0.736  
## 5 estPhi\_null 0.175 0.7009994 0.135 0.963 0.230 8 0.701  
## 6 estPhi\_emU 0.212 0.6994401 0.233 0.920 0.354 8 0.699  
## 7 speckle 0.016 0.6428572 0.001 1.000 0.001 8 0.643  
## 8 fisher 0.378 0.7419091 0.451 0.890 0.579 10 0.742  
## 9 betabin\_null 0.355 0.7336701 0.413 0.898 0.546 10 0.734  
## 10 milo 0.339 0.7330529 0.306 0.953 0.453 10 0.733  
## 11 wtoPhi\_emU 0.359 0.7301010 0.477 0.856 0.589 10 0.730  
## 12 estPhi\_null 0.120 0.7064403 0.059 0.986 0.111 10 0.706  
## 13 estPhi\_emU 0.173 0.6985041 0.121 0.971 0.210 10 0.699  
## 14 speckle 0.037 0.6383595 0.003 1.000 0.007 10 0.638  
## 15 fisher 0.307 0.6987307 0.412 0.865 0.538 12 0.699  
## 16 milo 0.246 0.6924343 0.198 0.964 0.321 12 0.692  
## 17 betabin\_null 0.296 0.6910424 0.372 0.885 0.505 12 0.691  
## 18 wtoPhi\_emU 0.297 0.6891288 0.422 0.849 0.543 12 0.689  
## 19 estPhi\_null 0.132 0.6670580 0.088 0.974 0.159 12 0.667  
## 20 estPhi\_emU 0.178 0.6589271 0.151 0.956 0.254 12 0.659  
## 21 speckle 0.023 0.6143789 0.002 1.000 0.003 12 0.614



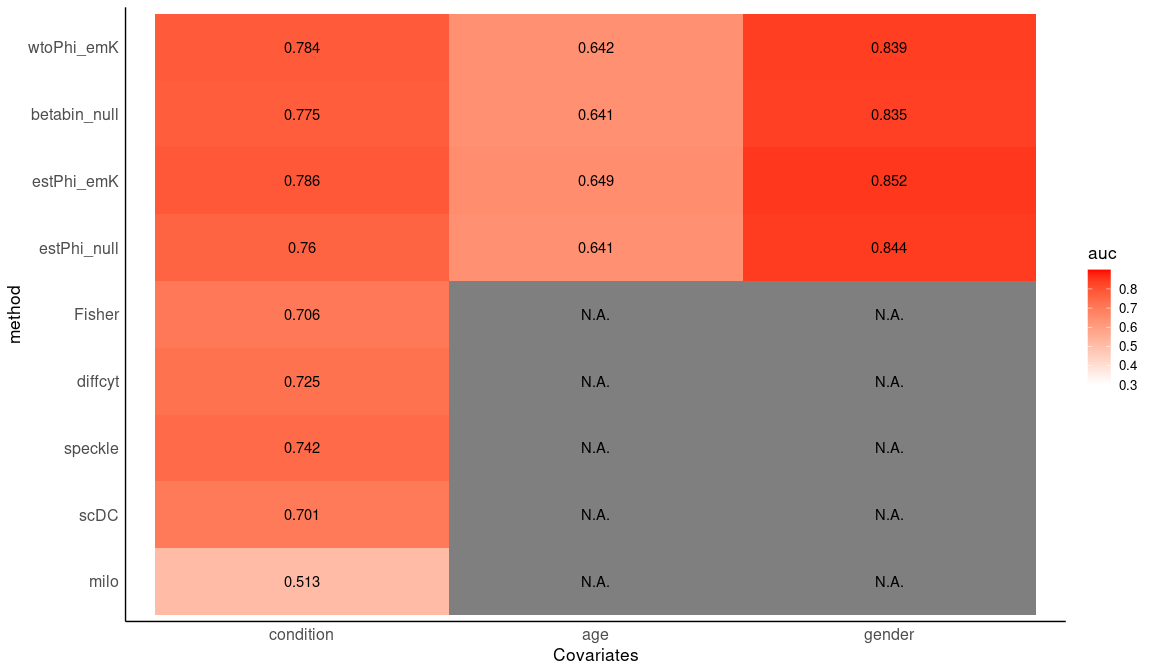
### Figure 2 - C

## 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

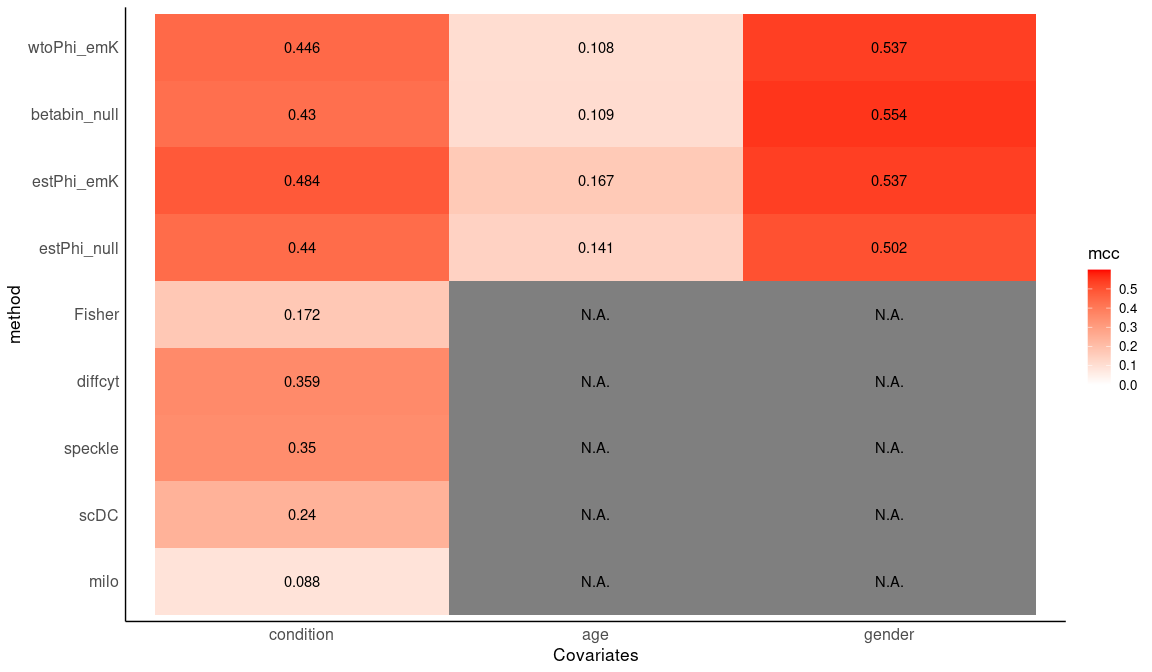
## method mcc auc prauc sensitivity specificity  
## 1 estPhi\_emK 0.48368770 0.7863194 0.8323688 0.54166667 0.9083333  
## 2 wtoPhi\_emK 0.44563426 0.7835764 0.8246389 0.60000000 0.8333333  
## 3 estPhi\_emSVM 0.46917346 0.7790972 0.8275914 0.52500000 0.9083333  
## 4 wtoPhi\_emSVM 0.42849448 0.7785417 0.8219258 0.59166667 0.8250000  
## 5 wtoPhi\_emU 0.45515785 0.7757292 0.8190422 0.60000000 0.8416667  
## 6 betabin\_null 0.43033148 0.7746528 0.8195118 0.58333333 0.8333333  
## 7 wtoPhi\_emT 0.40973294 0.7744792 0.8199141 0.59166667 0.8083333  
## 8 estPhi\_emU 0.40737326 0.7621528 0.8107808 0.55833333 0.8333333  
## 9 estPhi\_null 0.44001528 0.7595139 0.8034698 0.49166667 0.9083333  
## 10 estPhi\_emT 0.41502868 0.7580208 0.7943756 0.56666667 0.8333333  
## 11 speckle 0.35013164 0.7424306 0.7819901 0.29166667 0.9666667  
## 12 diffcyt 0.35854742 0.7245486 0.7729244 0.31666667 0.9583333  
## 13 fisher 0.17229220 0.7064583 0.5828199 0.88333333 0.2500000  
## 14 scDC 0.24041118 0.7011111 0.7569040 0.82500000 0.3916667  
## 15 milo 0.08751899 0.5125347 0.6322917 0.03333333 0.9916667  
## 16 estPhi\_emK 0.16728422 0.6488194 0.6467654 0.20000000 0.9166667  
## 17 estPhi\_emSVM 0.16336601 0.6473958 0.6504345 0.20833333 0.9083333  
## 18 estPhi\_emU 0.13159034 0.6460417 0.6471863 0.22500000 0.8750000  
## 19 wtoPhi\_emK 0.10770347 0.6420486 0.6224978 0.28333333 0.8083333  
## 20 estPhi\_null 0.14062174 0.6408333 0.6325675 0.16666667 0.9250000  
## 21 betabin\_null 0.10904995 0.6406250 0.6191436 0.27500000 0.8166667  
## 22 wtoPhi\_emT 0.08812102 0.6401736 0.6128798 0.27500000 0.8000000  
## 23 wtoPhi\_emSVM 0.08812102 0.6373958 0.6197886 0.27500000 0.8000000  
## 24 wtoPhi\_emU 0.09851380 0.6354514 0.6189081 0.27500000 0.8083333  
## 25 estPhi\_emT 0.13416408 0.6309375 0.6273675 0.21666667 0.8833333  
## 26 estPhi\_emK 0.53743077 0.8515278 0.8718671 0.56666667 0.9333333  
## 27 estPhi\_emSVM 0.52663879 0.8478125 0.8691380 0.56666667 0.9250000  
## 28 estPhi\_emU 0.54344685 0.8478125 0.8697115 0.63333333 0.8916667  
## 29 estPhi\_null 0.50209993 0.8436458 0.8606659 0.52500000 0.9333333  
## 30 wtoPhi\_emK 0.53677805 0.8386111 0.8473468 0.65833333 0.8666667  
## 31 wtoPhi\_emSVM 0.55189883 0.8355556 0.8452450 0.67500000 0.8666667  
## 32 betabin\_null 0.55381862 0.8353125 0.8467215 0.66666667 0.8750000  
## 33 wtoPhi\_emU 0.53491732 0.8345486 0.8444899 0.66666667 0.8583333  
## 34 wtoPhi\_emT 0.52923838 0.8321528 0.8392081 0.65000000 0.8666667  
## 35 estPhi\_emT 0.48420012 0.8283333 0.8391192 0.60000000 0.8666667  
## precision F1 factor  
## 1 0.8552632 0.6632653 condition  
## 2 0.7826087 0.6792453 condition  
## 3 0.8513514 0.6494845 condition  
## 4 0.7717391 0.6698113 condition  
## 5 0.7912088 0.6824645 condition  
## 6 0.7777778 0.6666667 condition  
## 7 0.7553191 0.6635514 condition  
## 8 0.7701149 0.6473430 condition  
## 9 0.8428571 0.6210526 condition  
## 10 0.7727273 0.6538462 condition  
## 11 0.8974359 0.4402516 condition  
## 12 0.8837209 0.4662577 condition  
## 13 0.5408163 0.6708861 condition  
## 14 0.5755814 0.6780822 condition  
## 15 0.8000000 0.0640000 condition  
## 16 0.7058824 0.3116883 age  
## 17 0.6944444 0.3205128 age  
## 18 0.6428571 0.3333333 age  
## 19 0.5964912 0.3841808 age  
## 20 0.6896552 0.2684564 age  
## 21 0.6000000 0.3771429 age  
## 22 0.5789474 0.3728814 age  
## 23 0.5789474 0.3728814 age  
## 24 0.5892857 0.3750000 age  
## 25 0.6500000 0.3250000 age  
## 26 0.8947368 0.6938776 gender  
## 27 0.8831169 0.6903553 gender  
## 28 0.8539326 0.7272727 gender  
## 29 0.8873239 0.6596859 gender  
## 30 0.8315789 0.7348837 gender  
## 31 0.8350515 0.7465438 gender  
## 32 0.8421053 0.7441860 gender  
## 33 0.8247423 0.7373272 gender  
## 34 0.8297872 0.7289720 gender  
## 35 0.8181818 0.6923077 gender



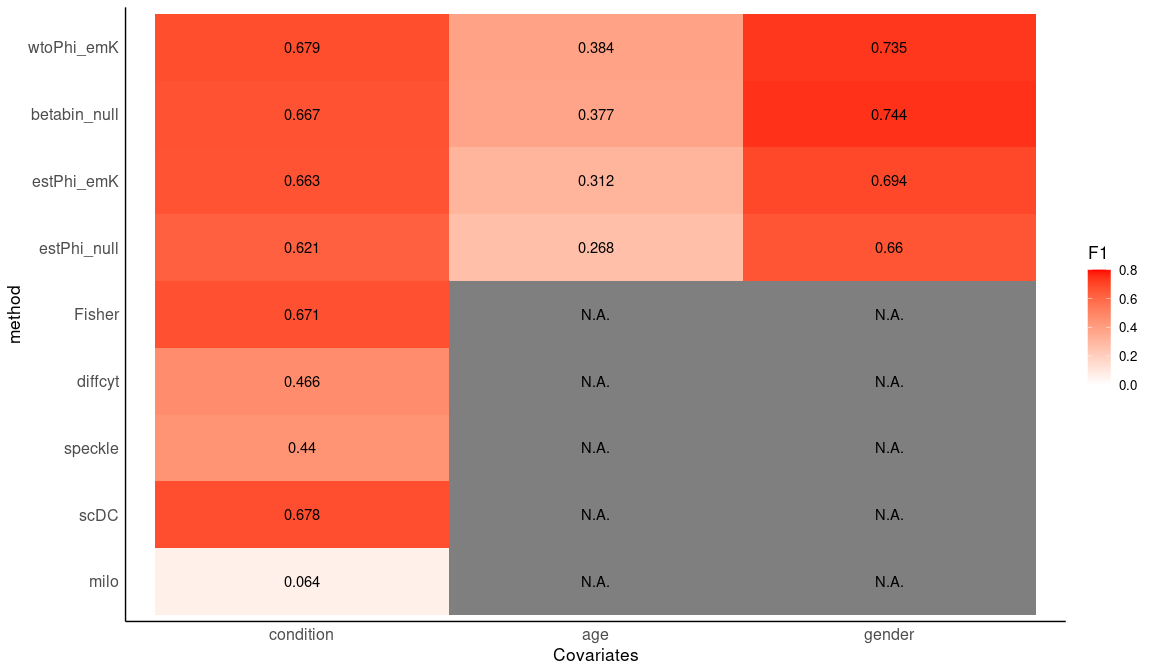
## Saving 12 x 7 in image



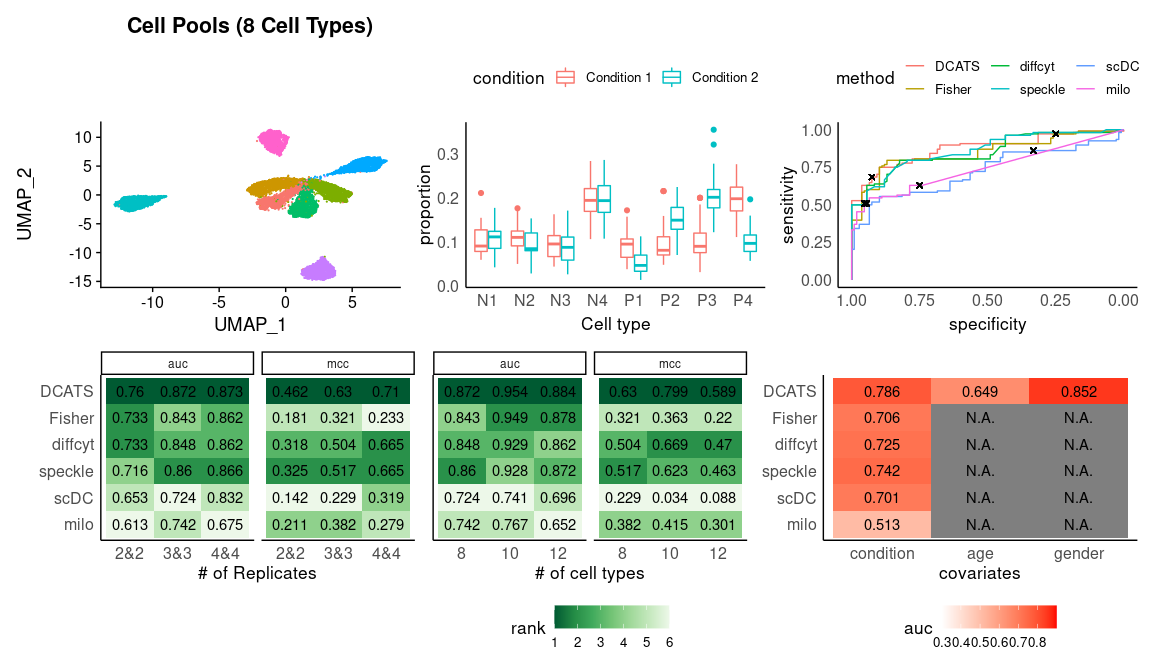
## Saving 12 x 7 in image



## 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 |

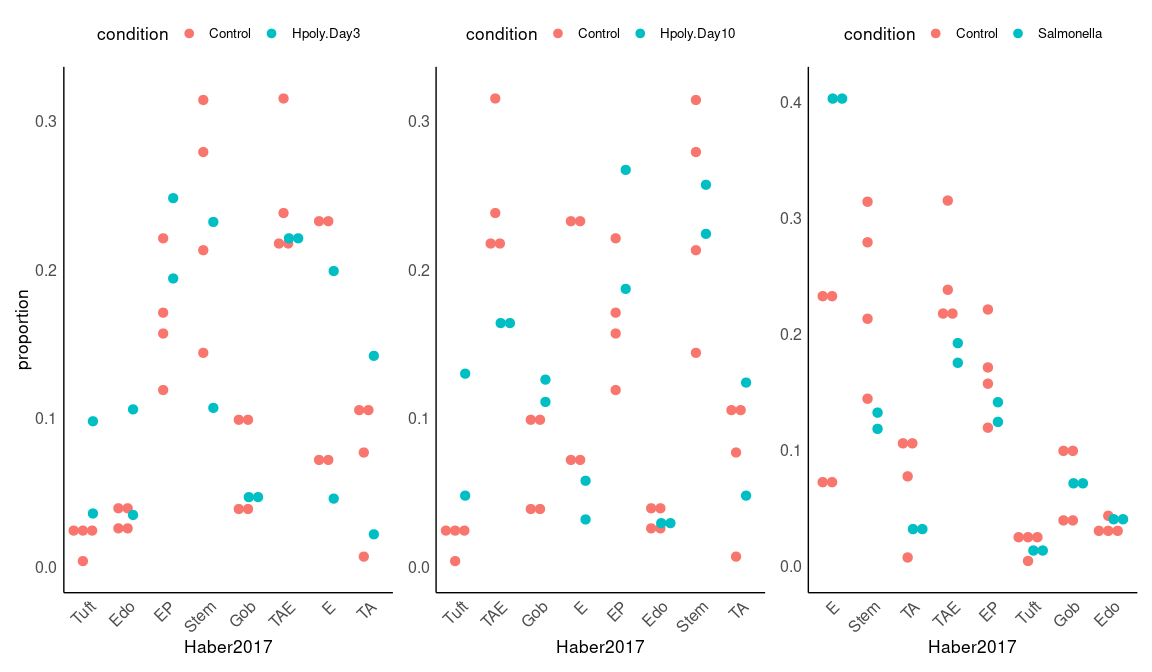
|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Tuft | TA.Early | Goblet | Enterocyte | Enterocyte.Progenitor | Endocrine | Stem | TA |
| origin | P | P | P | P | N | N | N | N |
| DCATS | \*\* | \* | n.s. | \*\*\* | n.s. | n.s. | n.s. | n.s. |
| fisher | \*\*\*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

Supplementary Figures: Distribution of each cell type after bias correction

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

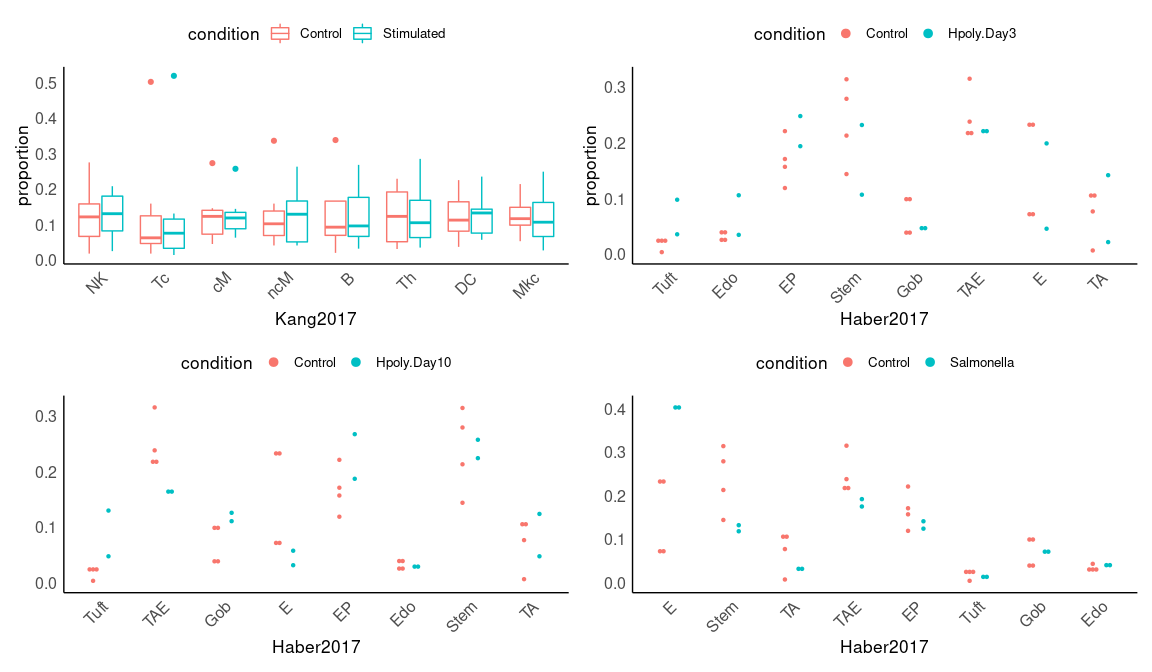
## cell batch  
## 1 AAACATACATTTCC-1 SNG-1016  
## 2 AAACATACCAGAAA-1 SNG-1256  
## 3 AAACATACCATGCA-1 SNG-1488  
## 4 AAACATACCTCGCT-1 SNG-1256  
## 5 AAACATACCTGGTA-1 SNG-1039  
## 6 AAACATACGATGAA-1 SNG-1488

## `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 |

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## Figure 4

### real-world data 3

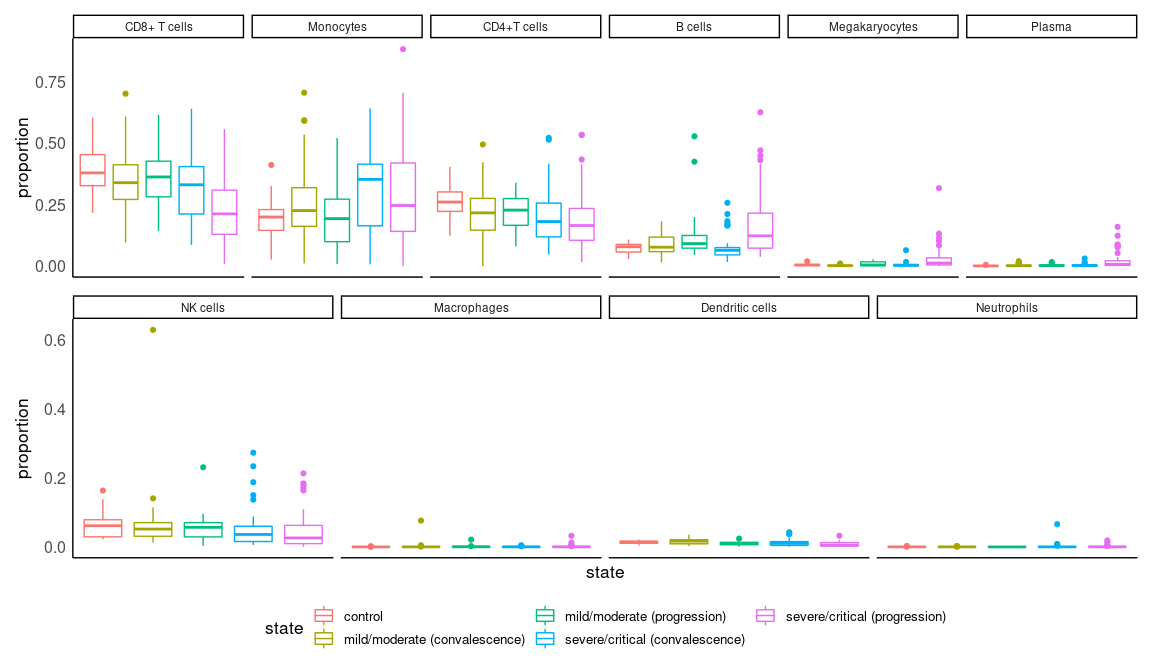
Test between different groups

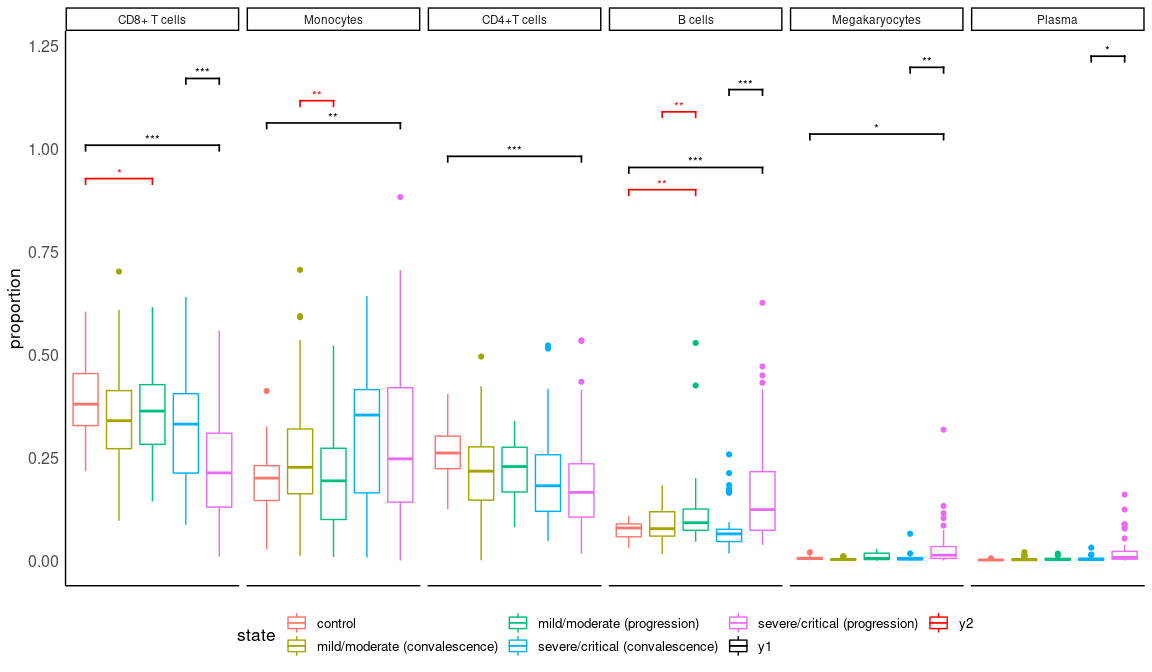
control vs mild/moderate\_progression

control vs severe/critical\_progression

mild/moderate\_convalescence vs mild/moderate\_progression

severe/critical\_convalescence vs severe/critical\_progression





### UMAP plot