

# Signature Scoring

Abinet Joan

2024-04-22 14:27:53 +0200

## Contents

<b>Loading packages</b>	<b>1</b>
<b>Loading data</b>	<b>1</b>
<b>Testing for M2 signature</b>	<b>1</b>
Loading signature . . . . .	2
Testing signature . . . . .	2
<b>Testing for M1 signature</b>	<b>2</b>
Loading signature . . . . .	3
Testing signature . . . . .	3
<b>Signature satM</b>	<b>3</b>

## Loading packages

```
suppressMessages(library(dplyr))
suppressMessages(library(Seurat))
suppressMessages(library(patchwork))
suppressMessages(library(ggplot2))
suppressMessages(library(RColorBrewer))
suppressMessages(library(stringr))
```

## Loading data

```
myeloid_cells_clustered <-
readRDS("../3-Visualisation_Clustering/Myeloid_cells_Final.rds")

colors <- c("#B2DF8A", "#ABD61C", "#1F78B4", "#A6CEE3", "#E31A1C", "#E377C2", "#600078",
"#33A02C", "#FDBF6F", "#526317", "#D4AAC6", "#784620")
```

## Testing for M2 signature

M2 signatures (gene downregulated in M1 vs M2) [https://www.gsea-msigdb.org/gsea/msigdb/mouse/geneset/COATES\\_MACROPHAGE\\_M1\\_VS\\_M2\\_DN.html?keywords=macrophage](https://www.gsea-msigdb.org/gsea/msigdb/mouse/geneset/COATES_MACROPHAGE_M1_VS_M2_DN.html?keywords=macrophage)

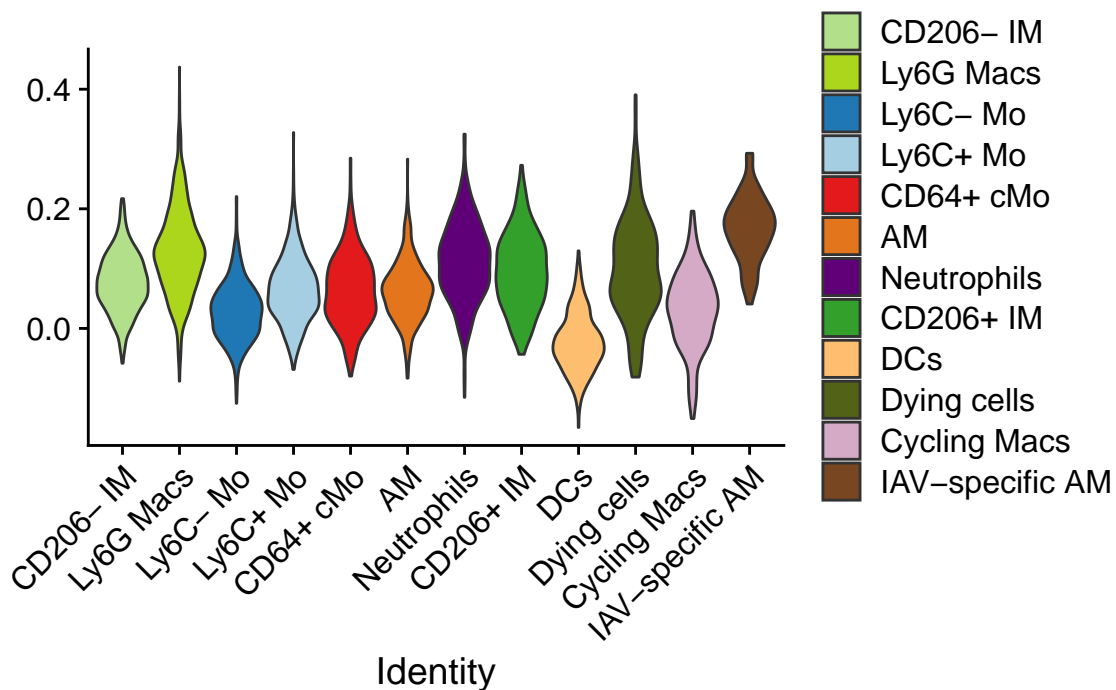
## Loading signature

```
M2_sigDatabase <-  
read.table("M1-M2_signature/COATES_MACROPHAGE_M1_VS_M2_DN.v2023.2.Mm.tsv", sep = "\t")  
  
M2_signatures <- M2_sigDatabase[18,2]  
  
M2_signatures <- strsplit(M2_signatures, ",")[[1]]  
  
M2_signatures <- M2_signatures[M2_signatures != ""]  
  
M2_signatures <- unique(M2_signatures)
```

## Testing signature

```
DefaultAssay(myeloid_cells_clustered) <- "RNA"  
myeloid_cells_clustered <- AddModuleScore(myeloid_cells_clustered,  
  features = list(M2_signatures),  
  name="M2")
```

```
VlnPlot(myeloid_cells_clustered, features = "M21", cols = colors, pt.size= 0, group.by =  
"CellType")+ ggtitle("")
```



```
#ggsave("Signature_M2_vln.pdf", height = 12, width = 19, units = "cm")
```

## Testing for M1 signature

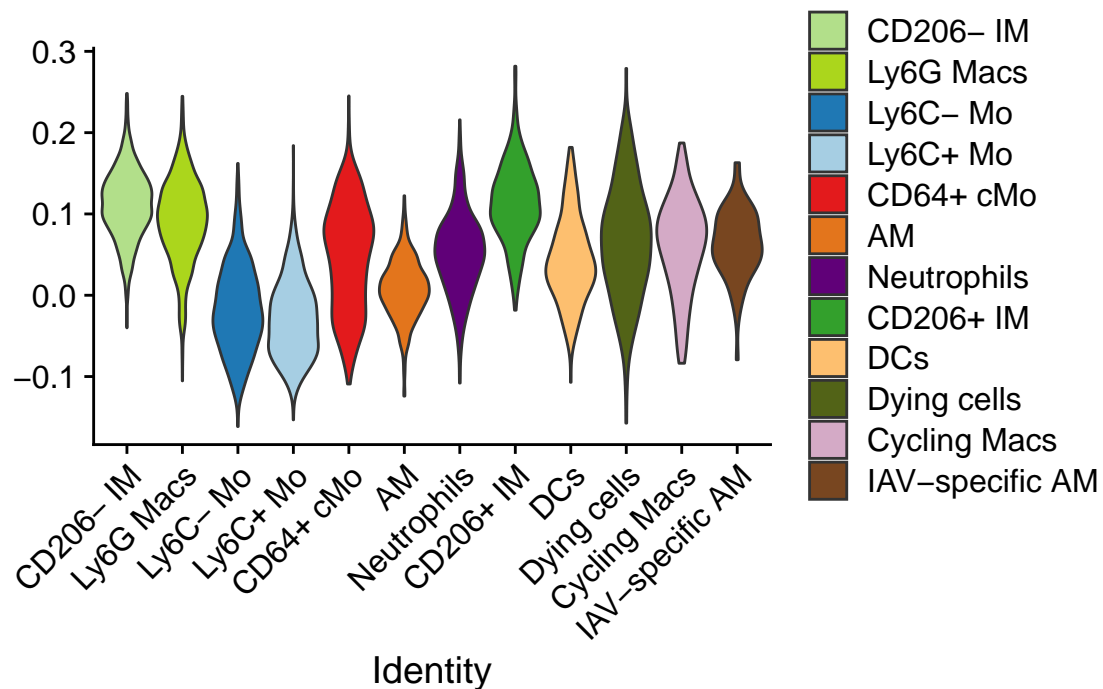
M1 signatures (gene downregulated in M1 vs M2) [https://www.gsea-msigdb.org/gsea/msigdb/mouse/geneset/COATES\\_MACROPHAGE\\_M1\\_VS\\_M2\\_DN.html?keywords=macrophage](https://www.gsea-msigdb.org/gsea/msigdb/mouse/geneset/COATES_MACROPHAGE_M1_VS_M2_DN.html?keywords=macrophage)

## Loading signature

```
M1_sigDatabase <-  
read.table("M1-M2_signature/COATES_MACROPHAGE_M1_VS_M2_UP.v2023.2.Mm.tsv", sep = "\t")  
  
M1_signatures <- M1_sigDatabase[18,2]  
  
M1_signatures <- strsplit(M1_signatures, ",")[[1]]  
  
M1_signatures <- M1_signatures[M1_signatures != ""]  
  
M1_signatures <- unique(M1_signatures)
```

## Testing signature

```
myeloid_cells_clustered <- AddModuleScore(myeloid_cells_clustered,  
  features = list(M1_signatures),  
  name="M1")  
  
VlnPlot(myeloid_cells_clustered, features = "M1", cols = colors, pt.size= 0, group.by =  
"CellType")+ ggtitle("")
```



```
#ggsave("Signature_M1_vln.pdf", height = 12, width = 19, units = "cm")
```

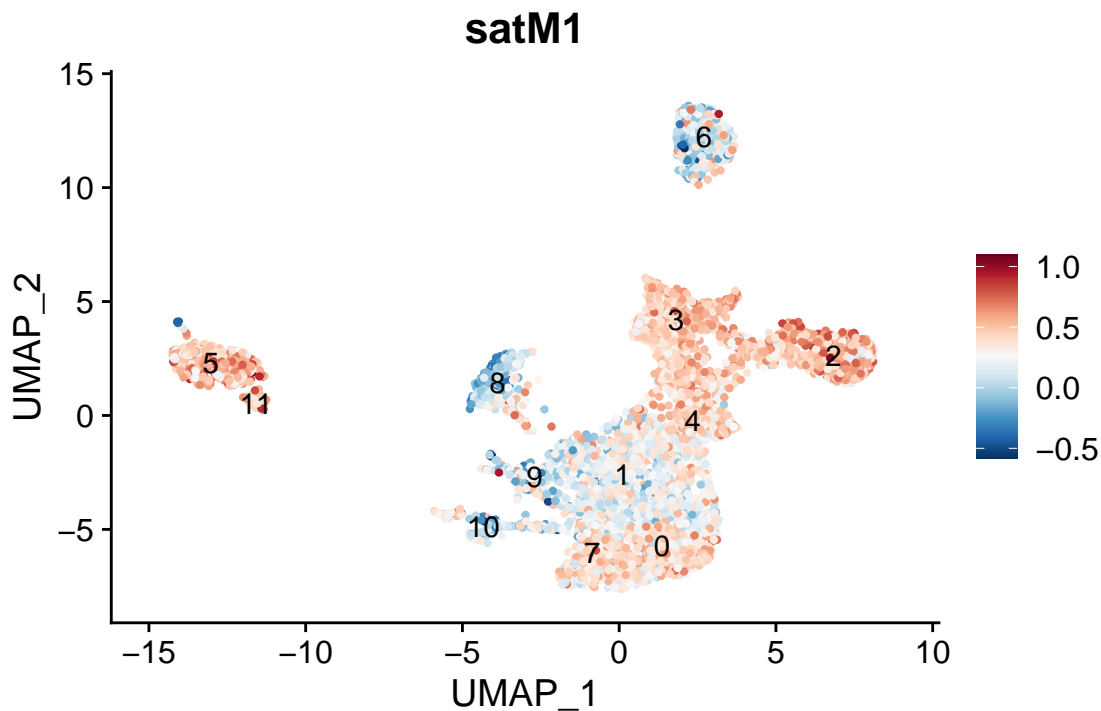
## Signature satM

```
signature_satM <- c("Csflr", "Lyz1", "Lyz2", "Cd68", "Cd14", "Cybb", "Itgb2", "Mpo",
"Elane", "Prtn3", "Csf2ra", "Lyz11", "Cybb1", "Fes", "Ltf", "Prg2", "Epx", "Ear1", "Ear2",
"Ear3")

myeloid_cells_clustered <- AddModuleScore(myeloid_cells_clustered,
features = list(signature_satM),
name="satM")
```

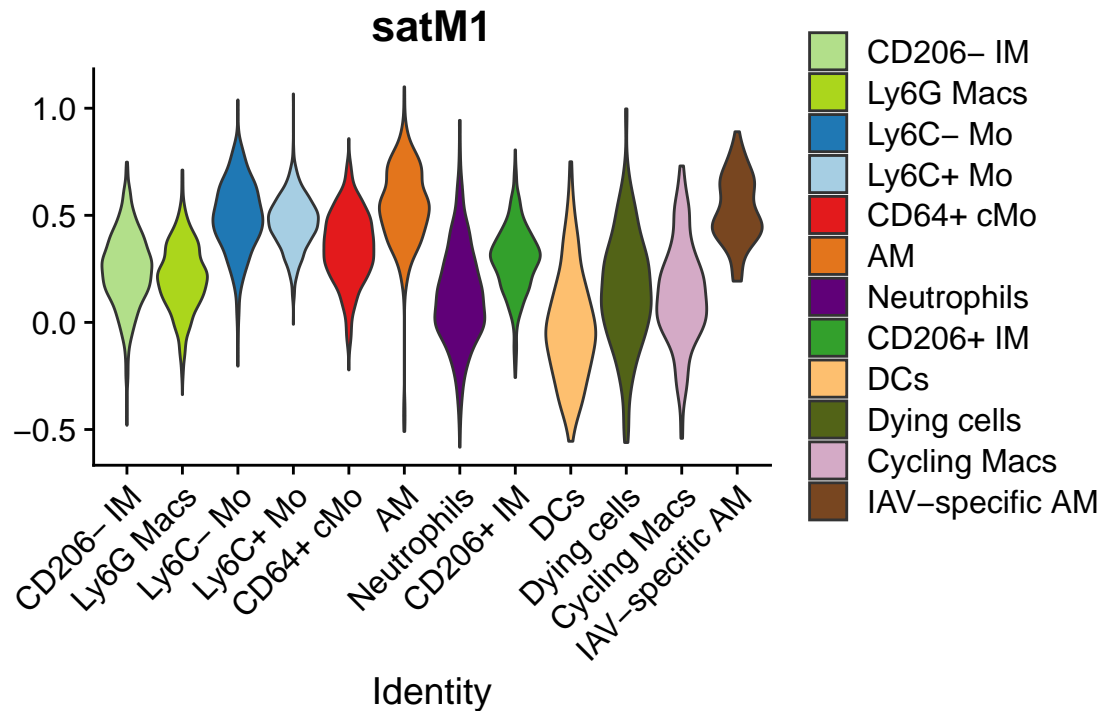
```
FeaturePlot(myeloid_cells_clustered, features = "satM1", label = T, pt.size = 0.8) +
scale_colour_gradientn(colours = rev(brewer.pal(n = 11, name = "RdBu")))
```

```
## Scale for colour is already present.
## Adding another scale for colour, which will replace the existing scale.
```



```
#ggsave("Signature_satM.pdf", width = 9, height = 6)
```

```
VlnPlot(myeloid_cells_clustered, features = "satM1", cols = colors , pt.size= 0, group.by
= "CellType")
```



```
#ggsave("Signature_Satm_vln.pdf", height = 12 , width = 19, units = "cm")
```

```
sessionInfo()
```

```
## R version 4.3.3 (2024-02-29)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 22.04.4 LTS
##
## Matrix products: default
## BLAS: /usr/lib/x86_64-linux-gnu/openblas-pthread/libblas.so.3
## LAPACK: /usr/lib/x86_64-linux-gnu/openblas-pthread/libopenblas-p0.3.20.so; LAPACK version 3.10.0
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
##  [3] LC_TIME=fr_BE.UTF-8      LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=fr_BE.UTF-8  LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=fr_BE.UTF-8     LC_NAME=C
##  [9] LC_ADDRESS=C             LC_TELEPHONE=C
## [11] LC_MEASUREMENT=fr_BE.UTF-8 LC_IDENTIFICATION=C
##
## time zone: Europe/Brussels
## tzcode source: system (glibc)
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods    base
##
## other attached packages:
## [1] stringr_1.5.0      RColorBrewer_1.1-3 ggplot2_3.4.2      patchwork_1.1.2
## [5] SeuratObject_4.1.3 Seurat_4.3.0       dplyr_1.1.2
##
## loaded via a namespace (and not attached):
```

## [1] deldir_1.0-9	pbapply_1.7-2	gridExtra_2.3
## [4] rlang_1.1.1	magrittr_2.0.3	RcppAnnoy_0.0.21
## [7] spatstat.geom_3.2-4	matrixStats_1.0.0	ggribes_0.5.4
## [10] compiler_4.3.3	png_0.1-8	vcvrs_0.6.3
## [13] reshape2_1.4.4	pkgconfig_2.0.3	fastmap_1.1.1
## [16] ellipsis_0.3.2	labeling_0.4.2	utf8_1.2.3
## [19] promises_1.2.0.1	rmarkdown_2.23	purrr_1.0.1
## [22] xfun_0.39	jsonlite_1.8.7	goftest_1.2-3
## [25] highr_0.10	later_1.3.1	spatstat.utils_3.0-3
## [28] irlba_2.3.5.1	parallel_4.3.3	cluster_2.1.6
## [31] R6_2.5.1	ica_1.0-3	stringi_1.7.12
## [34] spatstat.data_3.0-1	reticulate_1.30	parallelly_1.36.0
## [37] lmtest_0.9-40	scattermore_1.2	Rcpp_1.0.11
## [40] knitr_1.43	tensor_1.5	future.apply_1.11.0
## [43] zoo_1.8-12	sctransform_0.3.5	httpuv_1.6.11
## [46] Matrix_1.6-1	splines_4.3.3	igraph_1.5.0.1
## [49] tidyselect_1.2.0	rstudioapi_0.14	abind_1.4-5
## [52] yaml_2.3.7	spatstat.random_3.1-5	codetools_0.2-19
## [55] miniUI_0.1.1.1	spatstat.explore_3.2-1	listenv_0.9.0
## [58] lattice_0.22-5	tibble_3.2.1	plyr_1.8.8
## [61] withr_2.5.0	shiny_1.7.4.1	ROCR_1.0-11
## [64] evaluate_0.21	Rtsne_0.16	future_1.33.0
## [67] survival_3.5-8	polycip_1.10-4	fitdistrplus_1.1-11
## [70] pillar_1.9.0	KernSmooth_2.23-22	plotly_4.10.2
## [73] generics_0.1.3	sp_2.0-0	munsell_0.5.0
## [76] scales_1.2.1	globals_0.16.2	xtable_1.8-4
## [79] glue_1.6.2	lazyeval_0.2.2	tools_4.3.3
## [82] data.table_1.14.8	RANN_2.6.1	dotCall64_1.0-2
## [85] leiden_0.4.3	cowplot_1.1.1	grid_4.3.3
## [88] tidyr_1.3.0	colorspace_2.1-0	nlme_3.1-163
## [91] cli_3.6.1	spatstat.sparse_3.0-2	spam_2.9-1
## [94] fansi_1.0.4	viridisLite_0.4.2	uwot_0.1.16
## [97] gtable_0.3.3	digest_0.6.33	progressr_0.13.0
## [100] ggrepel_0.9.3	farver_2.1.1	htmlwidgets_1.6.2
## [103] htmltools_0.5.5	lifecycle_1.0.3	httr_1.4.6
## [106] mime_0.12	MASS_7.3-60	