

Building novartisA.Rda

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July 23, 2009

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1 Executive Summary

1.1 Introduction

In this report, we extract the “A” set replicates from the complete set of Novartis U95A NCI-60 quantifications.

1.2 Methods

We loaded the previously assembled novartisAll Rda file. We loaded cell line information from the drug sensitivity data. We loaded the most recent lists of cell lines in each drug predictor from the Potti et al. [1] web site.

We extracted the A set quantifications from the full data matrix, and used the orderings of cell lines in the reported signature lists to reorder the data columns in the quantification matrix.

1.3 Results

We created a “novartisA” matrix of array quantifications and an identically ordered “novartisAInfo” data frame of sample information. We stored these in RDataObjects as “novartisA.Rda.”

2 Options and Libraries

```
> options(width = 80)
```

3 Loading and Parsing Data

3.1 NovartisAll.Rda

We begin by loading the novartisAll Rda file assembled earlier.

```
> rdaList <- c("novartisAll")
> for (rdaFile in rdaList) {
+   rdaFullFile <- file.path("RDataObjects", paste(rdaFile, "Rda",
+     sep = "."))
+   if (file.exists(rdaFullFile)) {
+     cat("loading ", rdaFullFile, " from cache\n")
+     load(rdaFullFile)
```

```
+   }
+   else {
+       cat("building ", rdaFullFile, " from raw data\n")
+       Stangle(file.path("RNowebSource", paste("buildRda", rdaFile,
+         "Rnw", sep = ".")))
+       source(paste("buildRda", rdaFile, "R", sep = "."))
+   }
+ }
```

```
loading RDataObjects/novartisAll.Rda from cache
```

3.2 NCI60 Cell Line Info

Next, we load in information about the NCI-60 cell lines extracted from the drug sensitivity information.

```
> nci60Info <- read.table(file.path("RawData", "NCI60", "nci60Info.csv"),
+   sep = ",", header = TRUE, colClasses = c("character", "character",
+   "numeric", "numeric"), row.names = 1)
> nci60Info[1:3, ]
```

		PANEL	PANELNBR	CELLNBR
NCI-H23	Non-Small Cell Lung		1	1
NCI-H522	Non-Small Cell Lung		1	3
A549/ATCC	Non-Small Cell Lung		1	4

3.3 Lists of Cell Lines in Predictors

Next, we load in the most recent (August 2008) lists of cell lines in each drug prediction signature available from the Potti et al. [1] web site, <http://data.genome.duke.edu/NatureMedicine.php>. We reorganized the contents of the relevant file, "Celllines_in_each_predictor1.xls," as a csv file for easier loading and parsing.

```
> signatureCellLines <- read.table(file.path("RawData", "PottiNatMed",
+   "cellLinesInEachPredictor1_reorg.csv"), header = TRUE, sep = ",")
> signatureCellLines[1:3, ]

  CellLine    Status    Drug
1    EKVX Resistant Docetaxel
2   IGROV1 Resistant Docetaxel
3  OVCAR-4 Resistant Docetaxel

> which(is.na(match(signatureCellLines[, "CellLine"], rownames(nci60Info))))

[1] 124

> dim(signatureCellLines)

[1] 124  3

> signatureCellLines[123:124, ]
```

```

      CellLine      Status      Drug
123      SN12C Resistant Fluorouracil
124      OVkar-8 Resistant Fluorouracil

> signatureCellLines[124, "CellLine"] <- "OVCAR-8"
> signatureCellLines[, "CellLine"] <- as.factor(as.character(signatureCellLines[,
+      "CellLine"]))

```

There is a variant spelling for the name of the last cell line involved, but this is easily fixed.

4 Ordering Cell Line Panels

Now we want to check the ordering of the cell line panels in the signatures used by Potti et al. [1]. We use the panel numbers for this purpose as opposed to the panel names, because the panel names for some cell lines (e.g., MDA-MB-435) have changed over time.

```

> panelNumbers <- tapply(nci60Info[as.character(signatureCellLines[,
+      "CellLine"]), "PANELNBR"], signatureCellLines[, c("Status",
+      "Drug")], FUN = function(x) {
+      x
+ })
> panelNumbers["Resistant", ]

```

```

$Cyclophosphamide
[1] 12 5 5 5 1 10 10 10

```

```

$Docetaxel
[1] 1 6 6 9 9 9 9

```

```

$Doxorubicin
[1] 5 4 4 1 1 6 6 6 6 6 6 9

```

```

$Etoposide
[1] 5 5 4 4 1 10 6 6

```

```

$Fluorouracil
[1] 5 5 4 1 10 9 6

```

```

$Paclitaxel
[1] 7 4 1 1 10 10 6 9

```

```

$Topotecan
[1] 7 7 5 5 4 4 4 1 10 4

```

```

> panelNumbers["Sensitive", ]

```

```

$Cyclophosphamide
[1] 7 7 7 5 4 4 1 9

```

```

$Docetaxel
[1] 7 12 4 1 10 10 1

$Doxorubicin
[1] 12 12 5 1 10 10 10 10 10 10

$Etoposide
[1] 12 5 5 4 1 1 10 11 9

$Fluorouracil
[1] 5 4 4 1 10 10 9 9

$Paclitaxel
[1] 12 12 5 5 4 4 4 6 1

$Topotecan
[1] 12 12 12 5 1 1 1 10 6 9 9 9 9

```

But for a few exceptions, the panel order used appears to be

$$7 > 12 > 5 > 4 > 1 > 10 > (6, 11) > 9,$$

corresponding to Leukemia (Blood), Central Nervous System (Brain), Breast, Colon, Non-Small Cell Lung (Lung), Melanoma, Ovarian, Prostate, Renal.

5 Ordering Lines Within Panels

5.1 Leukemia

```

> nci60Info[nci60Info[, "PANELNBR"] == 7, ]
      PANEL PANELNBR CELLNBR
CCRF-CEM  Leukemia      7      3
K-562     Leukemia      7      5
MOLT-4     Leukemia      7      6
HL-60(TB) Leukemia      7      8
RPMI-8226 Leukemia      7     10
SR         Leukemia      7     19

> signatureCellLines[nci60Info[as.character(signatureCellLines[,
+   "CellLine"]), "PANELNBR"] == 7, ]
      CellLine  Status      Drug
8  HL-60(TB) Sensitive  Docetaxel
45      K-562 Resistant  Topotecan
46 RPMI-8226 Resistant  Topotecan
64  CCRF-CEM Resistant  Paclitaxel
94      K-562 Sensitive Cyclophosphamide
95      MOLT-4 Sensitive Cyclophosphamide
96 HL-60(TB) Sensitive Cyclophosphamide

```

The ordering is consistent with CELLNBR.

5.2 Central Nervous System

```
> nci60Info[nci60Info[, "PANELNBR"] == 12, ]
```

	PANEL	PANELNBR	CELLNBR
SNB-19 Central Nervous System		12	2
SNB-75 Central Nervous System		12	5
U251 Central Nervous System		12	9
SF-268 Central Nervous System		12	14
SF-295 Central Nervous System		12	15
SF-539 Central Nervous System		12	16

```
> signatureCellLines[nci60Info[as.character(signatureCellLines[,  
+ "CellLine"]), "PANELNBR"] == 12, ]
```

	CellLine	Status	Drug
9	SF-539	Sensitive	Docetaxel
15	SF-539	Sensitive	Etoposide
32	SF-539	Sensitive	Topotecan
33	SNB-75	Sensitive	Topotecan
34	U251	Sensitive	Topotecan
55	SF-295	Sensitive	Paclitaxel
56	SF-539	Sensitive	Paclitaxel
72	SF-539	Sensitive	Doxorubicin
73	SNB-75	Sensitive	Doxorubicin
102	SNB-19	Resistant	Cyclophosphamide

Here, CELLNBR doesn't seem to track very well. Alphabetic ordering does, so we'll use that.

5.3 Breast

```
> nci60Info[nci60Info[, "PANELNBR"] == 5, ]
```

	PANEL	PANELNBR	CELLNBR
MCF7	Breast	5	1
NCI/ADR-RES	Ovarian	5	2
MDA-MB-231/ATCC	Breast	5	5
HS 578T	Breast	5	6
MDA-MB-435	Melanoma	5	11
BT-549	Breast	5	13
T-47D	Breast	5	14

```
> signatureCellLines[nci60Info[as.character(signatureCellLines[,  
+ "CellLine"]), "PANELNBR"] == 5, ]
```

	CellLine	Status	Drug
16	BT-549	Sensitive	Etoposide
17	MDA-MB-231/ATCC	Sensitive	Etoposide
24	MCF7	Resistant	Etoposide
25	NCI/ADR-RES	Resistant	Etoposide

35	HS 578T	Sensitive	Topotecan
47	MDA-MB-435	Resistant	Topotecan
48	MDA-MB-231/ATCC	Resistant	Topotecan
57	HS 578T	Sensitive	Paclitaxel
58	MDA-MB-435	Sensitive	Paclitaxel
74	MDA-MB-435	Sensitive	Doxorubicin
82	NCI/ADR-RES	Resistant	Doxorubicin
97	MCF7	Sensitive	Cyclophosphamide
103	HS 578T	Resistant	Cyclophosphamide
104	MDA-MB-231/ATCC	Resistant	Cyclophosphamide
105	MDA-MB-435	Resistant	Cyclophosphamide
110	MCF7	Sensitive	Fluorouracil
118	NCI/ADR-RES	Resistant	Fluorouracil
119	MDA-MB-435	Resistant	Fluorouracil

Again, alphabetic order looks better than CELLNBR. We have conflicting information about the relative placement of MDA-MB-231/ATCC and MDA-MB-435 from the Topotecan Resistant group ordering and the Cyclophosphamide Resistant group ordering, so we leave that one alone. We place NCI/ADR-RES before MDA-MB-435 based on the Fluorouracil Resistant ordering.

5.4 Colon

```
> nci60Info[nci60Info[, "PANELNBR"] == 4, ]
```

	PANEL	PANELNBR	CELLNBR
HT29	Colon	4	1
HCC-2998	Colon	4	2
HCT-116	Colon	4	3
SW-620	Colon	4	9
COLO 205	Colon	4	10
HCT-15	Colon	4	15
KM12	Colon	4	17

```
> signatureCellLines[nci60Info[as.character(signatureCellLines[,
+ "CellLine"]), "PANELNBR"] == 4, ]
```

	CellLine	Status	Drug
10	HT29	Sensitive	Docetaxel
18	HCC-2998	Sensitive	Etoposide
26	HCT-15	Resistant	Etoposide
27	SW-620	Resistant	Etoposide
49	HCC-2998	Resistant	Topotecan
50	HCT-116	Resistant	Topotecan
51	HCT-15	Resistant	Topotecan
54	COLO 205	Resistant	Topotecan
59	COLO 205	Sensitive	Paclitaxel
60	HCC-2998	Sensitive	Paclitaxel
61	HT29	Sensitive	Paclitaxel
65	SW-620	Resistant	Paclitaxel

```

83   HCT-15 Resistant      Doxorubicin
84   HT29 Resistant       Doxorubicin
98   HCC-2998 Sensitive   Cyclophosphamide
99   HCT-116 Sensitive   Cyclophosphamide
111  COLO 205 Sensitive   Fluorouracil
112  HCT-116 Sensitive   Fluorouracil
120  SW-620 Resistant     Fluorouracil

```

There are ambiguities here, so we choose an alphabetic ordering.

5.5 Non-Small Cell Lung Cancer

```

> nci60Info[nci60Info[, "PANELNBR"] == 1, ]

              PANEL PANELNBR CELLNBR
NCI-H23   Non-Small Cell Lung      1      1
NCI-H522   Non-Small Cell Lung      1      3
A549/ATCC Non-Small Cell Lung      1      4
EKVX      Non-Small Cell Lung      1      8
NCI-H226   Non-Small Cell Lung      1     13
NCI-H322M Non-Small Cell Lung      1     17
NCI-H460   Non-Small Cell Lung      1     21
HOP-62     Non-Small Cell Lung      1     26
HOP-92     Non-Small Cell Lung      1     29

> signatureCellLines[nci60Info[as.character(signatureCellLines[,
+   "CellLine"]), "PANELNBR"] == 1, ]

      CellLine      Status      Drug
1      EKVX Resistant      Docetaxel
11     HOP-62 Sensitive      Docetaxel
14    NCI-H522 Sensitive      Docetaxel
19     HOP-62 Sensitive      Etoposide
20    NCI-H226 Sensitive      Etoposide
28    NCI-H322M Resistant      Etoposide
36     HOP-62 Sensitive      Topotecan
37    NCI-H226 Sensitive      Topotecan
38    NCI-H23 Sensitive      Topotecan
52    NCI-H322M Resistant      Topotecan
63    NCI-H522 Sensitive      Paclitaxel
66   A549/ATCC Resistant      Paclitaxel
67      EKVX Resistant      Paclitaxel
75    NCI-H23 Sensitive      Doxorubicin
85      EKVX Resistant      Doxorubicin
86    NCI-H322M Resistant      Doxorubicin
100   NCI-H460 Sensitive Cyclophosphamide
106   NCI-H226 Resistant Cyclophosphamide
113   NCI-H460 Sensitive   Fluorouracil
121      EKVX Resistant   Fluorouracil

```

The data is consistent with alphabetic ordering, so we use that.

5.6 Melanoma

```
> nci60Info[nci60Info[, "PANELNBR"] == 10, ]
```

	PANEL	PANELNBR	CELLNBR
LOX IMVI	Melanoma	10	1
MALME-3M	Melanoma	10	2
SK-MEL-2	Melanoma	10	5
SK-MEL-5	Melanoma	10	7
SK-MEL-28	Melanoma	10	8
M14	Melanoma	10	14
UACC-62	Melanoma	10	20
UACC-257	Melanoma	10	21

```
> signatureCellLines[nci60Info[as.character(signatureCellLines[,
+ "CellLine"]), "PANELNBR"] == 10, ]
```

	CellLine	Status	Drug
12	SK-MEL-2	Sensitive	Docetaxel
13	SK-MEL-5	Sensitive	Docetaxel
21	M14	Sensitive	Etoposide
29	UACC-257	Resistant	Etoposide
39	LOX IMVI	Sensitive	Topotecan
53	SK-MEL-28	Resistant	Topotecan
68	MALME-3M	Resistant	Paclitaxel
69	SK-MEL-28	Resistant	Paclitaxel
76	M14	Sensitive	Doxorubicin
77	MALME-3M	Sensitive	Doxorubicin
78	SK-MEL-2	Sensitive	Doxorubicin
79	SK-MEL-28	Sensitive	Doxorubicin
80	SK-MEL-5	Sensitive	Doxorubicin
81	UACC-62	Sensitive	Doxorubicin
107	M14	Resistant	Cyclophosphamide
108	MALME-3M	Resistant	Cyclophosphamide
109	SK-MEL-2	Resistant	Cyclophosphamide
114	LOX IMVI	Sensitive	Fluorouracil
115	SK-MEL-5	Sensitive	Fluorouracil
122	M14	Resistant	Fluorouracil

Alphabetic looks fine here.

5.7 Ovarian

```
> nci60Info[nci60Info[, "PANELNBR"] == 6, ]
```

	PANEL	PANELNBR	CELLNBR
OVCAR-3	Ovarian	6	1
OVCAR-4	Ovarian	6	2
OVCAR-5	Ovarian	6	3
OVCAR-8	Ovarian	6	5

```
IGROV1 Ovarian      6      10
SK-OV-3 Ovarian     6      11
```

```
> signatureCellLines[nci60Info[as.character(signatureCellLines[,
+   "CellLine"]), "PANELNBR"] == 6, ]
```

	CellLine	Status	Drug
2	IGROV1	Resistant	Docetaxel
3	OVCAR-4	Resistant	Docetaxel
30	OVCAR-4	Resistant	Etoposide
31	OVCAR-5	Resistant	Etoposide
40	OVCAR-8	Sensitive	Topotecan
62	OVCAR-3	Sensitive	Paclitaxel
70	OVCAR-8	Resistant	Paclitaxel
87	IGROV1	Resistant	Doxorubicin
88	OVCAR-3	Resistant	Doxorubicin
89	OVCAR-4	Resistant	Doxorubicin
90	OVCAR-5	Resistant	Doxorubicin
91	OVCAR-8	Resistant	Doxorubicin
92	SK-OV-3	Resistant	Doxorubicin
124	OVCAR-8	Resistant	Fluorouracil

Alphabetic looks fine here.

5.8 Prostate

```
> nci60Info[nci60Info[, "PANELNBR"] == 11, ]
```

	PANEL	PANELNBR	CELLNBR
PC-3	Prostate	11	1
DU-145	Prostate	11	3

```
> signatureCellLines[nci60Info[as.character(signatureCellLines[,
+   "CellLine"]), "PANELNBR"] == 11, ]
```

	CellLine	Status	Drug
22	PC-3	Sensitive	Etoposide

No real evidence here, but we'll go with alphabetic in keeping with most of the rest.

5.9 Renal

```
> nci60Info[nci60Info[, "PANELNBR"] == 9, ]
```

	PANEL	PANELNBR	CELLNBR
UO-31	Renal	9	4
SN12C	Renal	9	8
A498	Renal	9	13
CAKI-1	Renal	9	15
RXF 393	Renal	9	16

786-0	Renal	9	18
ACHN	Renal	9	23
TK-10	Renal	9	24

```
> signatureCellLines[nci60Info[as.character(signatureCellLines[,
+   "CellLine"]), "PANELNBR"] == 9, ]
```

	CellLine	Status	Drug
4	786-0	Resistant	Docetaxel
5	CAKI-1	Resistant	Docetaxel
6	SN12C	Resistant	Docetaxel
7	TK-10	Resistant	Docetaxel
23	786-0	Sensitive	Etoposide
41	A498	Sensitive	Topotecan
42	ACHN	Sensitive	Topotecan
43	CAKI-1	Sensitive	Topotecan
44	UO-31	Sensitive	Topotecan
71	786-0	Resistant	Paclitaxel
93	CAKI-1	Resistant	Doxorubicin
101	TK-10	Sensitive	Cyclophosphamide
116	A498	Sensitive	Fluorouracil
117	UO-31	Sensitive	Fluorouracil
123	SN12C	Resistant	Fluorouracil

Alphabetic works here.

6 The Final Ordering

```
> tempOrder <- c("CCRF-CEM", "K-562", "MOLT-4", "HL-60(TB)", "RPMI-8226",
+   "SR", "SF-268", "SF-295", "SF-539", "SNB-19", "SNB-75", "U251",
+   "BT-549", "HS 578T", "MCF7", "MDA-MB-231/ATCC", "NCI/ADR-RES",
+   "MDA-MB-435", "T-47D", "COLO 205", "HCC-2998", "HCT-116",
+   "HCT-15", "HT29", "KM12", "SW-620", "A549/ATCC", "EKVX",
+   "HOP-62", "HOP-92", "NCI-H226", "NCI-H23", "NCI-H322M", "NCI-H460",
+   "NCI-H522", "LOX IMVI", "M14", "MALME-3M", "SK-MEL-2", "SK-MEL-28",
+   "SK-MEL-5", "UACC-257", "UACC-62", "DU-145", "PC-3", "IGROV1",
+   "OVCAR-3", "OVCAR-4", "OVCAR-5", "OVCAR-8", "SK-OV-3", "786-0",
+   "A498", "ACHN", "CAKI-1", "RXF 393", "SN12C", "TK-10", "UO-31")
```

7 Extracting and Ordering Quantifications and Info

7.1 The Quantifications

```
> novartisA <- novartisAll[, grep("A$", colnames(novartisAll))]
> colnames(novartisA) <- substr(colnames(novartisA), 1, nchar(colnames(novartisA)) -
+   2)
> novartisA <- novartisA[, tempOrder]
> dim(novartisA)
```

```
[1] 12625    59

> novartisA[1:3, 1:3]

      CCRF-CEM      K-562      MOLT-4
36460_at  41.16584  95.75866  68.12313
36461_at  80.50482  98.03310  97.47627
36462_at 113.68166 200.20106 248.60211
```

7.2 The Info

```
> novartisAInfo <- nci60Info[colnames(novartisA), ]
```

8 Save Rda File

Finally, we save the quantification matrix and the annotation information.

```
> save(novartisA, novartisAInfo, file = file.path("RDataObjects",
+      "novartisA.Rda"))
```

9 Appendix

9.1 File Location

```
> getwd()

[1] "/Users/kabagg/ReproRsch/WebSite"
```

9.2 Saves

9.3 SessionInfo

```
> sessionInfo()

R version 2.8.1 (2008-12-22)
i386-apple-darwin8.11.1

locale:
en_US.UTF-8/en_US.UTF-8/C/C/en_US.UTF-8/en_US.UTF-8

attached base packages:
[1] stats      graphics  grDevices  utils      datasets  methods   base
```

References

- [1] Potti A, Dressman HK, Bild A, et al: Genomic signatures to guide the use of chemotherapeutics. *Nat Med*, **12**:1294-1300, 2006.