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NaviCell Web Service for Data Visualization

Eric Bonnet

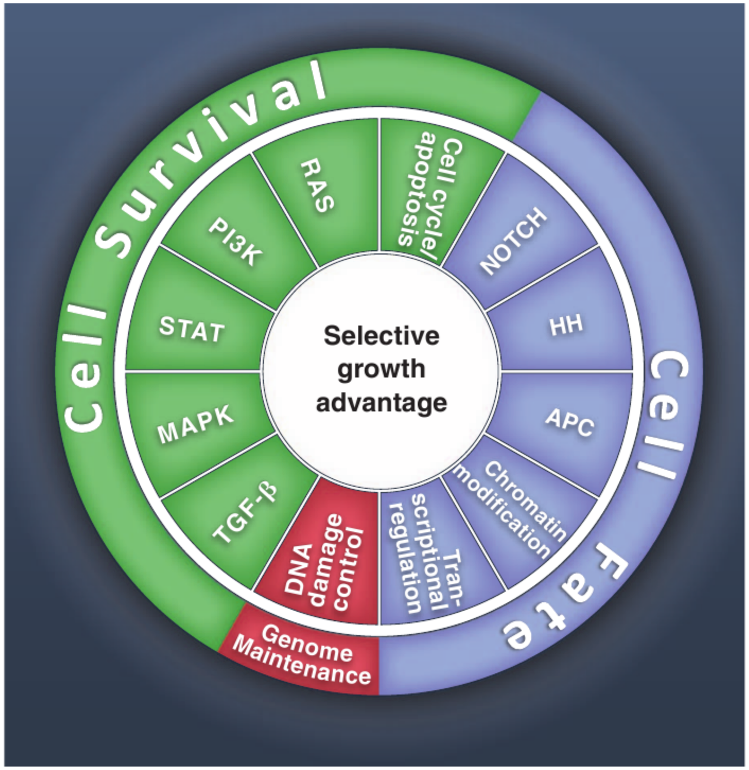
Computational Systems Biology of Cancer
Institut Curie - INSERM U900 - Mines ParisTech

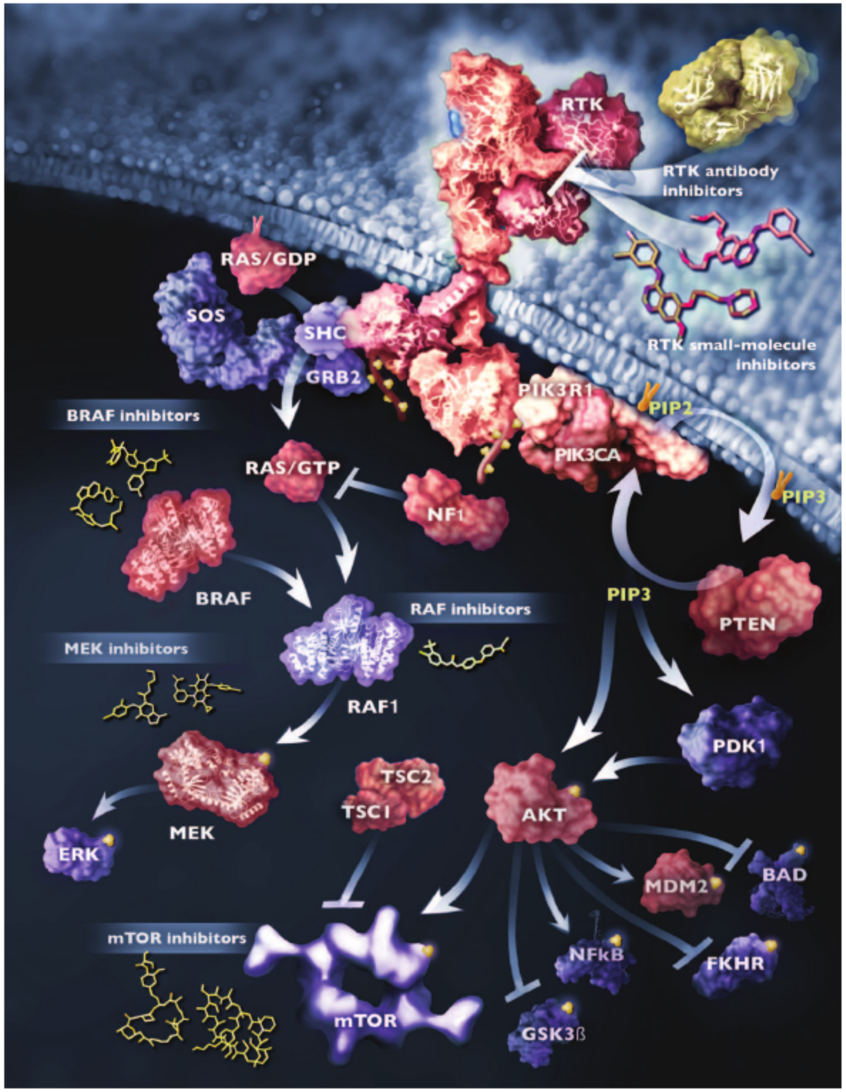
UseR! Conference Aalborg - 02/07/2015

Instituts thématiques Inserm
Institut national de la santé et de la recherche médicale

MINES ParisTech

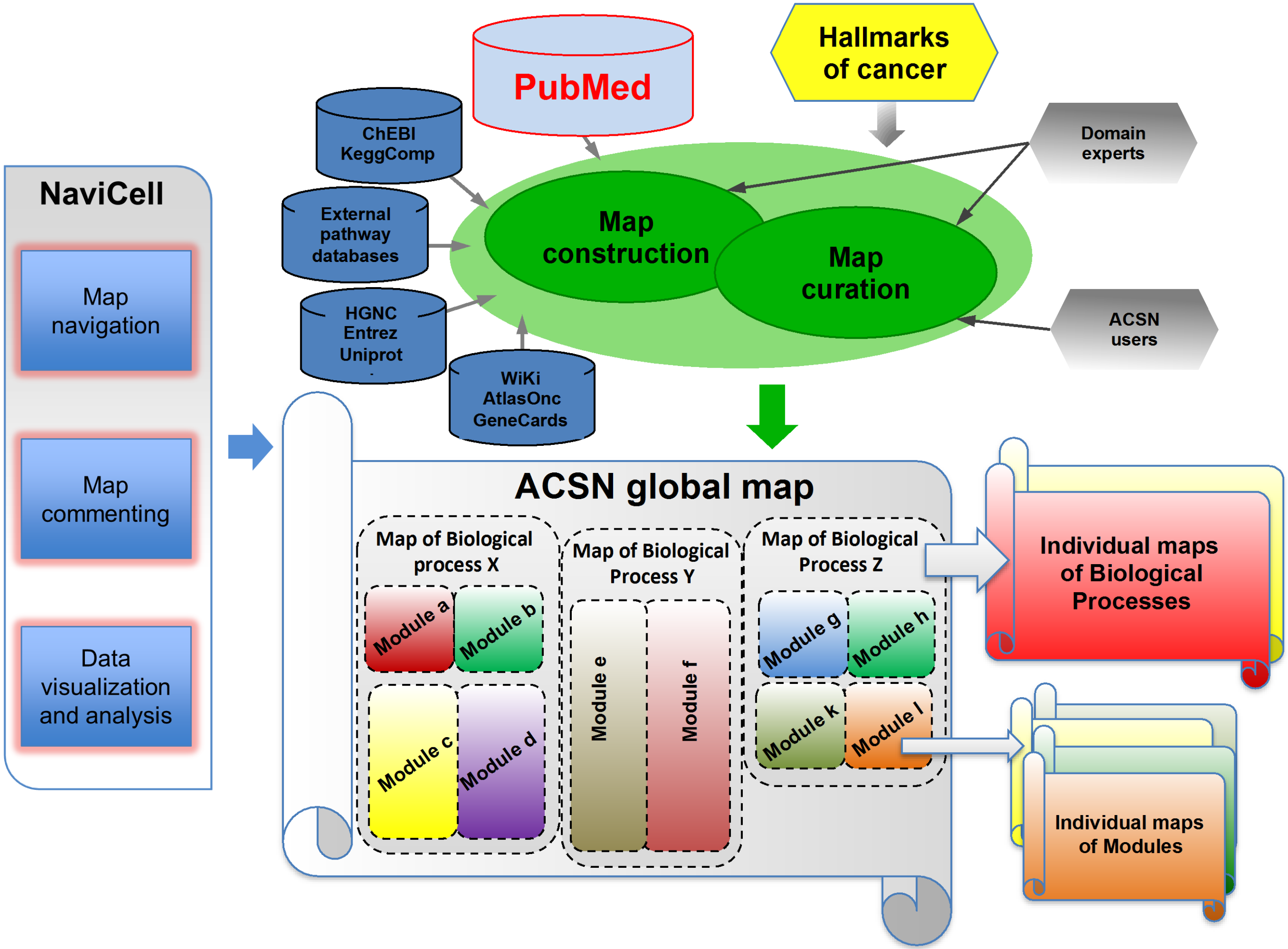
Cancer pathways



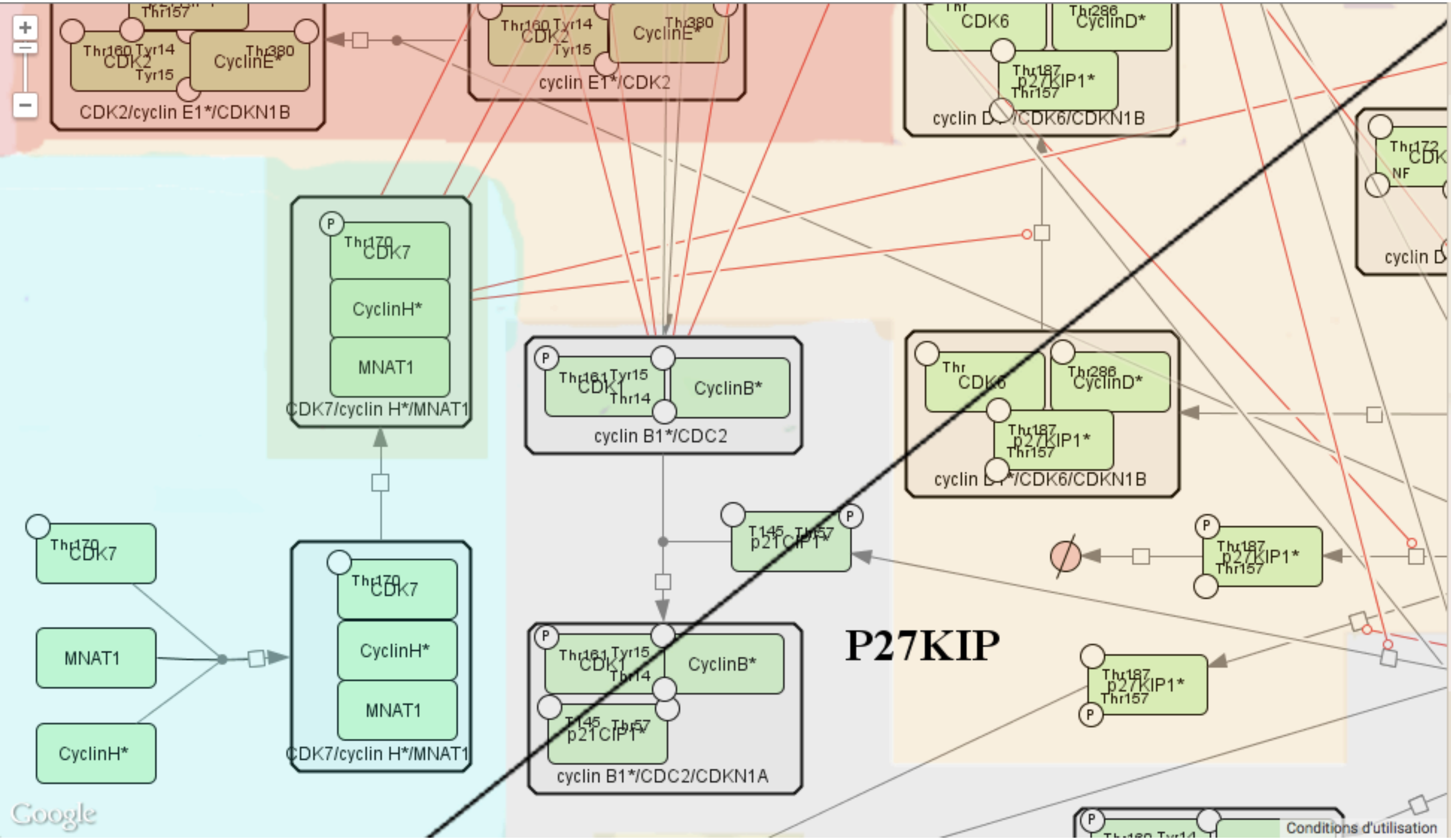


We believe that greater knowledge of these pathways and the ways in which they function is the most pressing need in basic cancer research. Successful research on this topic should allow the development of agents that target, albeit indirectly, defective tumor suppressor genes.

Large-scale maps of molecular interactions

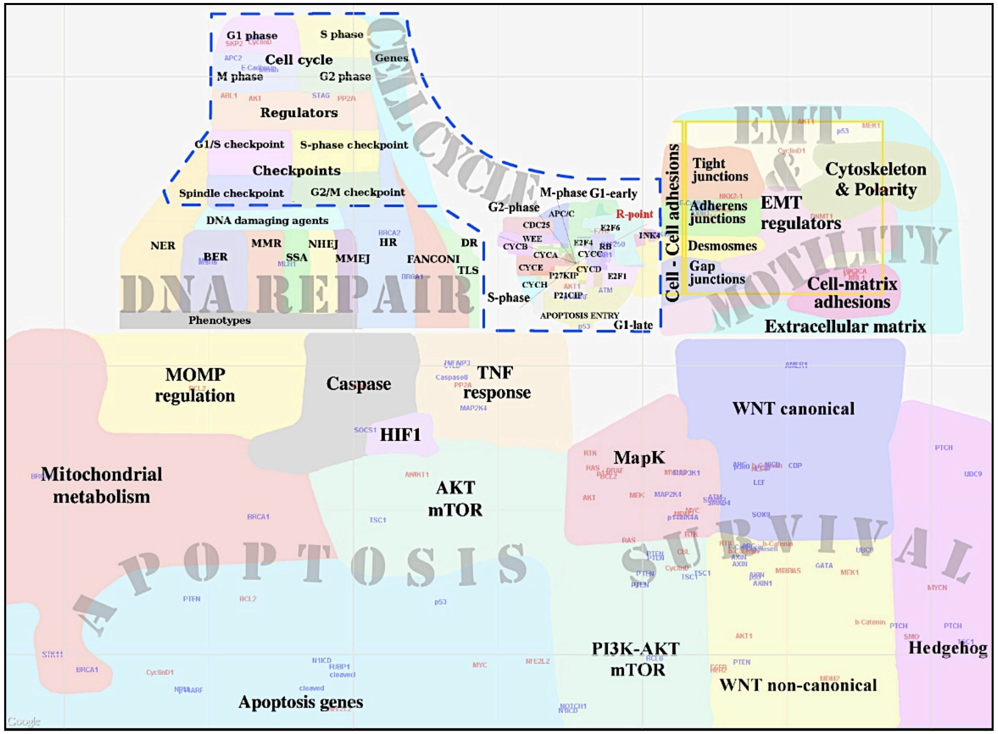


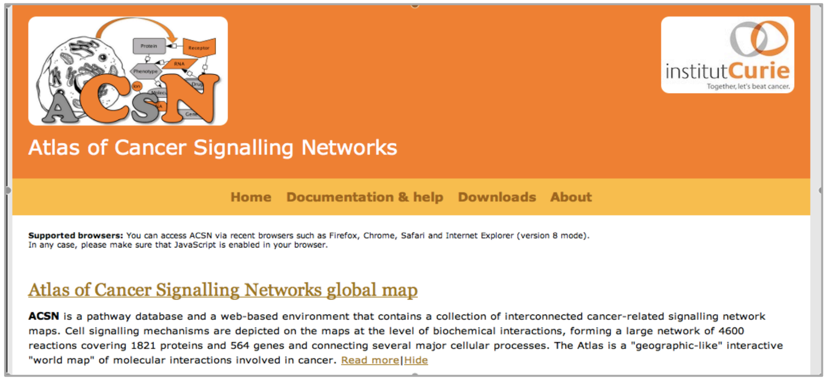
P27KIP


CDK2/cyclin E1*/CDKN1B
Thr160 Tyr14
CDK2
Tyr15
Thr157
CyclinE*
Thr380
cyclin E1*/CDK2
cyclin D1*/CDK6/CDKN1B
CDK6
Thr
CyclinD*
Thr286
p27KIP1*
Thr187
Thr157
Thr172
CDK
NF
cyclin D
CDK7/cyclin H*/MNAT1
P
Thr170
CDK7
CyclinH*
MNAT1
cyclin B1*/CDC2
Thr161 Tyr15
CDK1
Thr14
CyclinB*
p21CIP1*
T145 Thr57
cyclin B1*/CDC2/CDKN1A
Thr160 Tyr14
Google
Conditions d'utilisation

Atlas of Cancer Signalling Networks

Resource of knowledge on molecular mechanisms and analytical tool





Atlas of Cancer Signalling Networks

Home Documentation & help Downloads About

Supported browsers: You can access ACSN via recent browsers such as Firefox, Chrome, Safari and Internet Explorer (version 8 mode).
In any case, please make sure that JavaScript is enabled in your browser.

Atlas of Cancer Signalling Networks global map

ACSN is a pathway database and a web-based environment that contains a collection of interconnected cancer-related signalling network maps. Cell signalling mechanisms are depicted on the maps at the level of biochemical interactions, forming a large network of 4600 reactions covering 1821 proteins and 564 genes and connecting several major cellular processes. The Atlas is a "geographic-like" interactive "world map" of molecular interactions involved in cancer. Read more|Hide

http://acsn.curie.fr

- ✓ 5 maps of biological processes
- ✓ 52 functional modules
- ✓ 4826 reactions
- ✓ 2371 proteins
- ✓ 5979 chemical species
- ✓ 2822 references

- ✓ Cancer-related
- ✓ Manually curated
- ✓ Comprehensive and up-to-date
- ✓ Interconnected
- ✓ Browsable and zoomable

Applicable for:

- ✓ Data integration
- ✓ Network−based data analysis
- ✓ Modeling synthetic interactions
- ✓ Prediction drug resistance mechanisms

Kuperstein et al., (2015) **Atlas of Cancer Signaling Network: a systems biology resource for integrative analysis of cancer data with Google Maps.** Oncogenesis, in press.

NaviCell technology

- **Web-based environment** for ease of use.
- **Easy and intuitive map browsing** using Google Maps engine^{TM}.
- **Semantic zooming** to visualize different levels of map details.
- **Web blog** for collaborative map annotation and comments.
- **“-Omics” data visualization** web service.

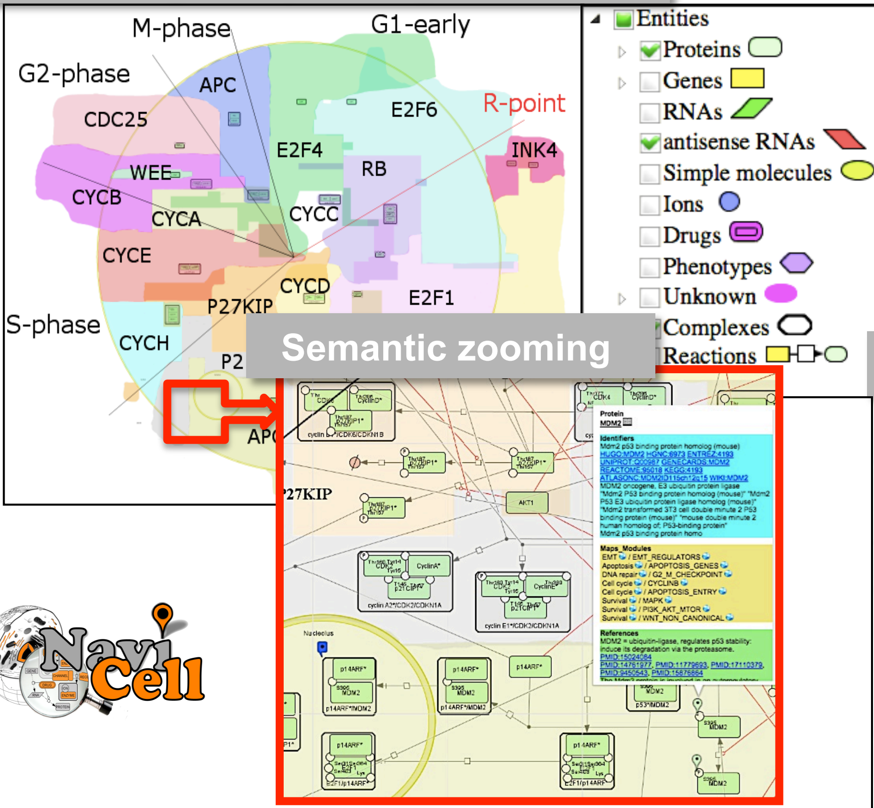
Bonnet E, et al.(2015) **NaviCell Web Service for network-based data visualization.** Nucleic Acids Research (2015) doi: 10.1093/nar/gkv450

Kuperstein I, et al. (2013) **NaviCell: a web-based environment for navigation, curation and maintenance of large molecular interaction maps**. doi:10.1186/1752-0509-7-100

NaviCell web interface

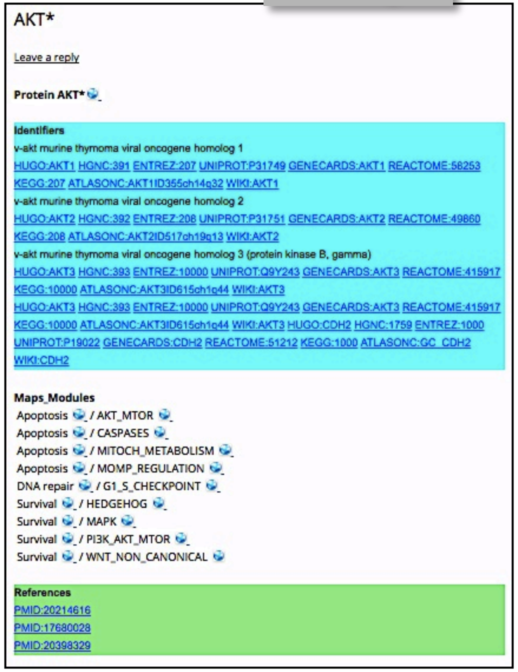
NaviCell = Map (Google Maps engine) + Blog (WordPress) + ToolBox

Google maps navigation



Semantic zooming

Blog



AKT*

Leave a reply

Protein AKT*

Identifiers

v-akt murine thymoma viral oncogene homolog 1
HUGO:AKT1 HGNC:391 ENTREZ:207 UNIPROT:P31749 GENECARDS:AKT1 REACTOME:58253 KEGG:207 ATLASONC:AKT1ID355ch14q32 WIKI:AKT1
v-akt murine thymoma viral oncogene homolog 2
HUGO:AKT2 HGNC:392 ENTREZ:208 UNIPROT:P31751 GENECARDS:AKT2 REACTOME:49860 KEGG:208 ATLASONC:AKT2ID517ch19q13 WIKI:AKT2
v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)
HUGO:AKT3 HGNC:393 ENTREZ:10000 UNIPROT:Q9Y243 GENECARDS:AKT3 REACTOME:415917 KEGG:10000 ATLASONC:AKT3ID615ch1q44 WIKI:AKT3
HUGO:AKT3 HGNC:393 ENTREZ:10000 UNIPROT:Q9Y243 GENECARDS:AKT3 REACTOME:415917 KEGG:10000 ATLASONC:AKT3ID615ch1q44 WIKI:AKT3 HUGO:CDH2 HGNC:1759 ENTREZ:1000 UNIPROT:P19022 GENECARDS:CDH2 REACTOME:51212 KEGG:1000 ATLASONC:GC_CDH2 WIKI:CDH2

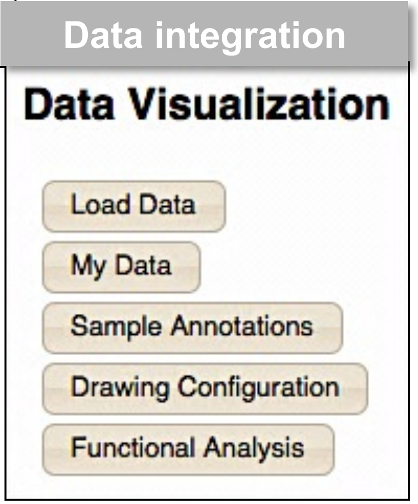
Maps_Modules

Apoptosis / AKT_MTOR
Apoptosis / CASPASES
Apoptosis / MITOCH_METABOLISM
Apoptosis / MOMP_REGULATION
DNA repair / G1_S_CHECKPOINT
Survival / HEDGEHOG
Survival / MAPK
Survival / PI3K_AKT_MTOR
Survival / WNT_NON_CANONICAL

References

PMID:20214616
PMID:17680028
PMID:20398329

Data integration



- ✓ Google engine (navigation, search, markers, callout window)
- ✓ Semantic zooming
- ✓ Entity annotation post

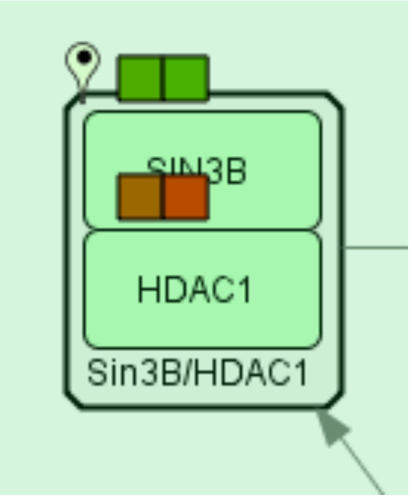
- ✓ Data integration and visualization (on line)
- ✓ Entity neighborhood study
- ✓ Functional analysis (enrichment of modules)

http://navicell.curie.fr

Data visualization:
biological data types

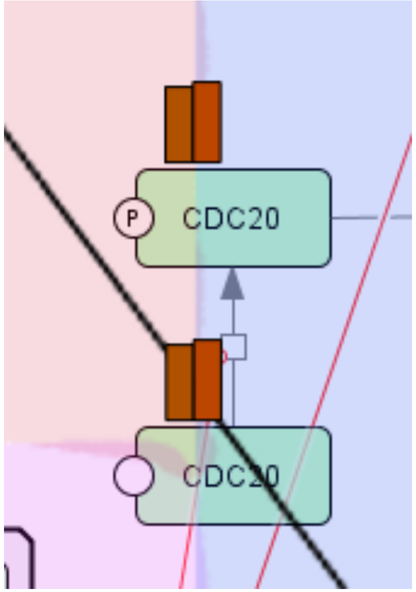
- Expression data (mRNA, protein, microRNA) **[continuous]**
- Copy-number data **[discrete ordered]**
- Mutation data **[discrete unordered]**
- Gene lists

Data visualization:
Graphical representations (1)



Heatmaps:

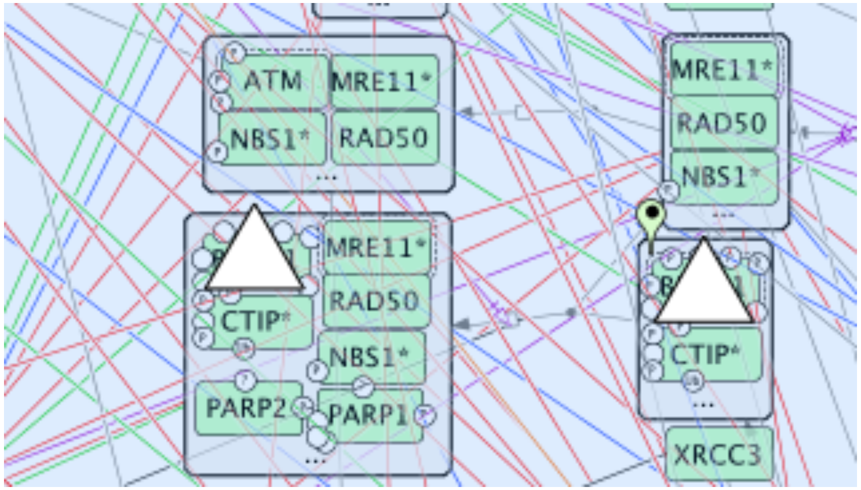
- Fixed shape and size
- Color gradient (continuous data) or solid values (discrete data)
- Multiple sample/groups on x-axis



Barplots:

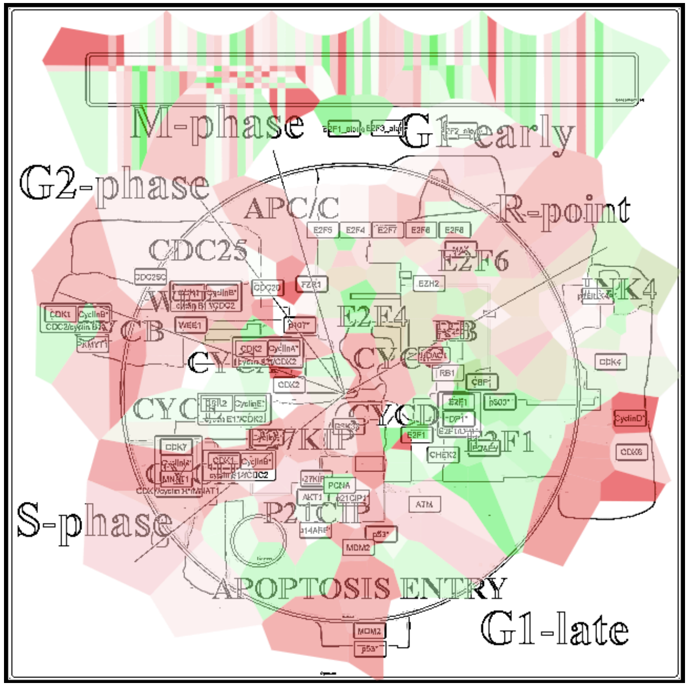
- Fixed shape
- Variable size
- Color gradient (continuous data) or solid values (discrete data)
- Multiple sample/groups on x-axis

Data visualization:
Graphical representations (2)



Glyphs:

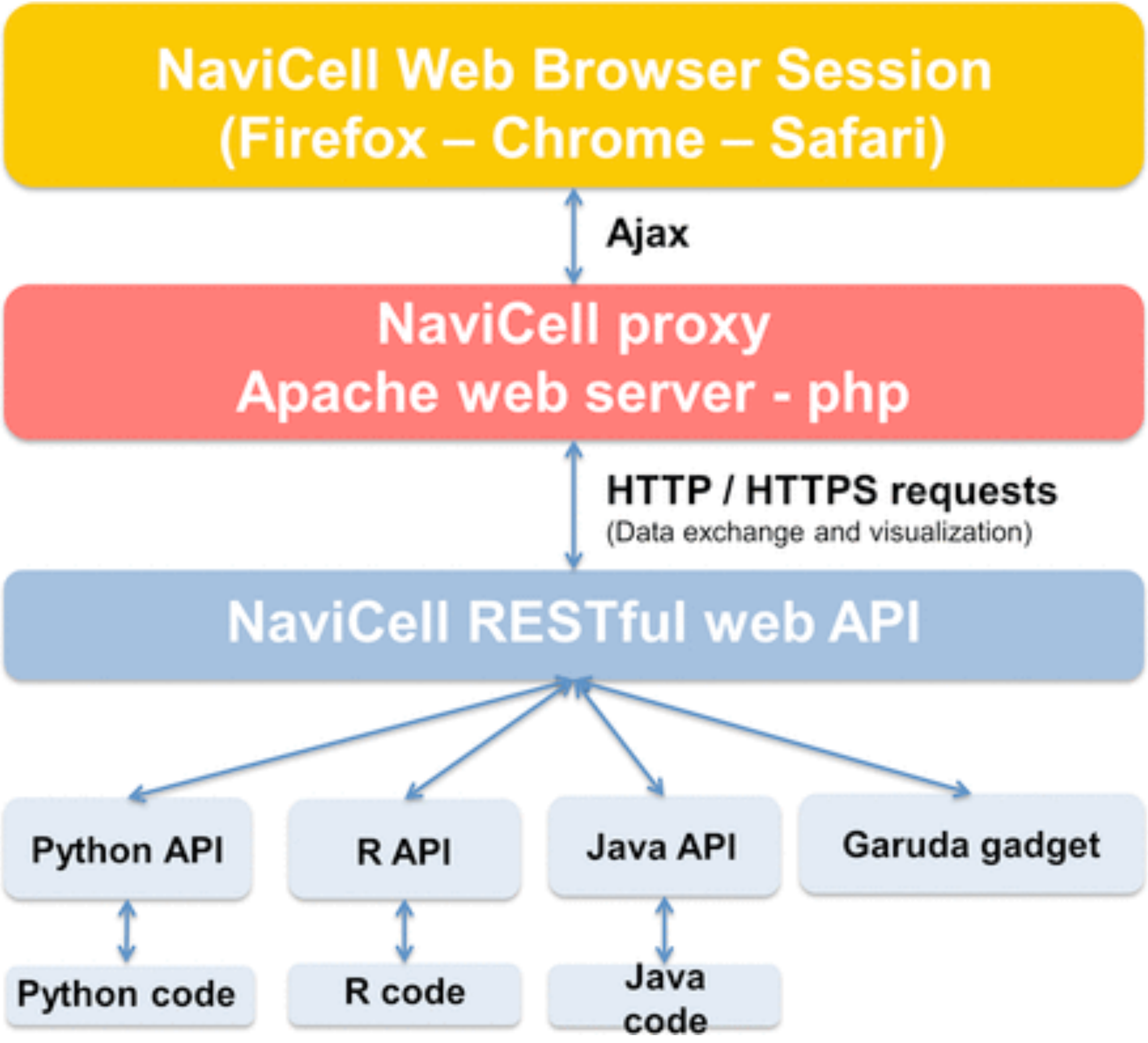
- Variable shape (5)
- Variable size
- Color gradient (continuous data) or solid values (discrete data)
- Multiple dataset on shape, size and color properties.

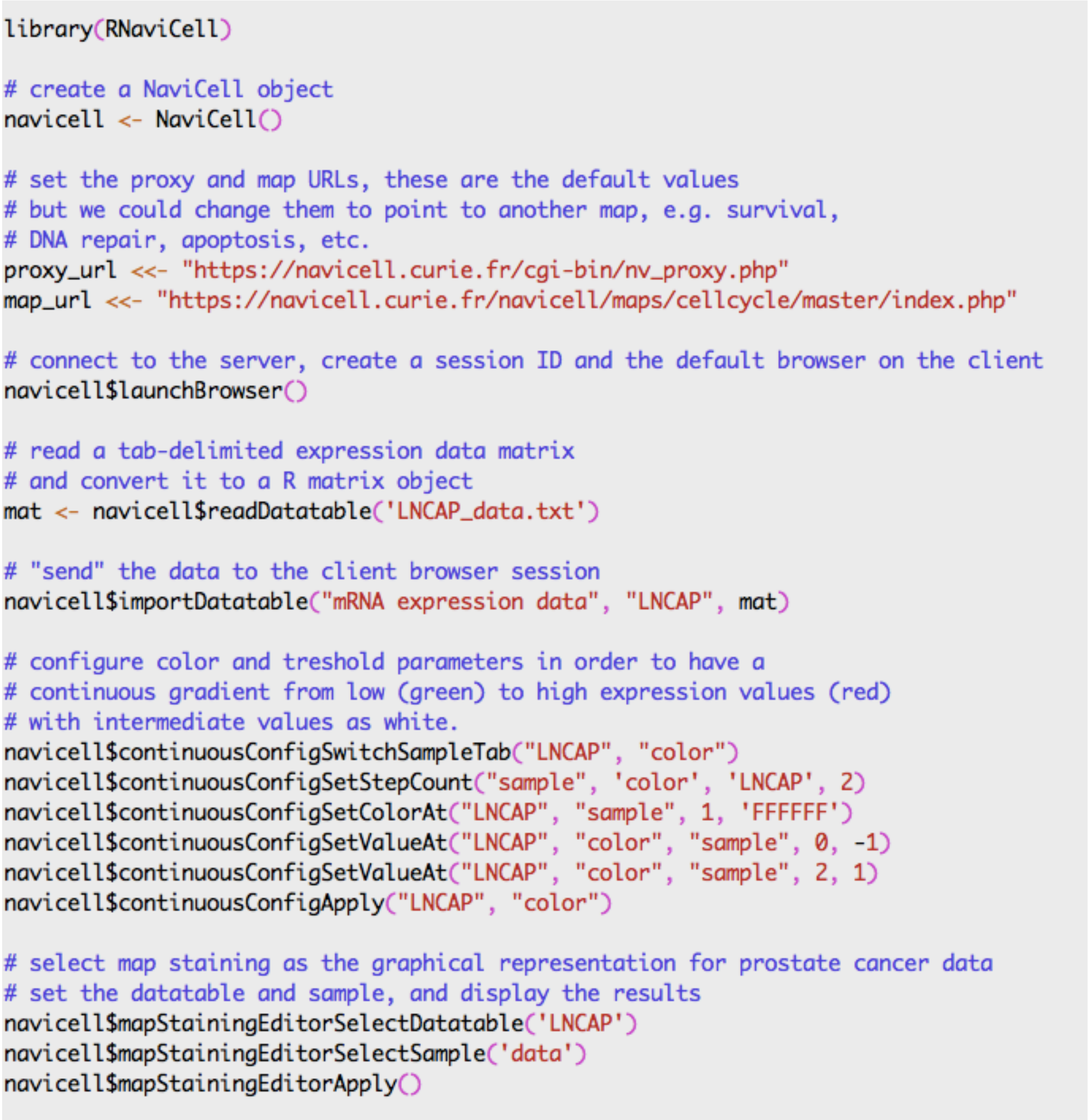


Map staining:

- Polygons shapes defined around each entity of the map
- Color gradient (continuous data) or solid values (discrete data)
- One sample/group

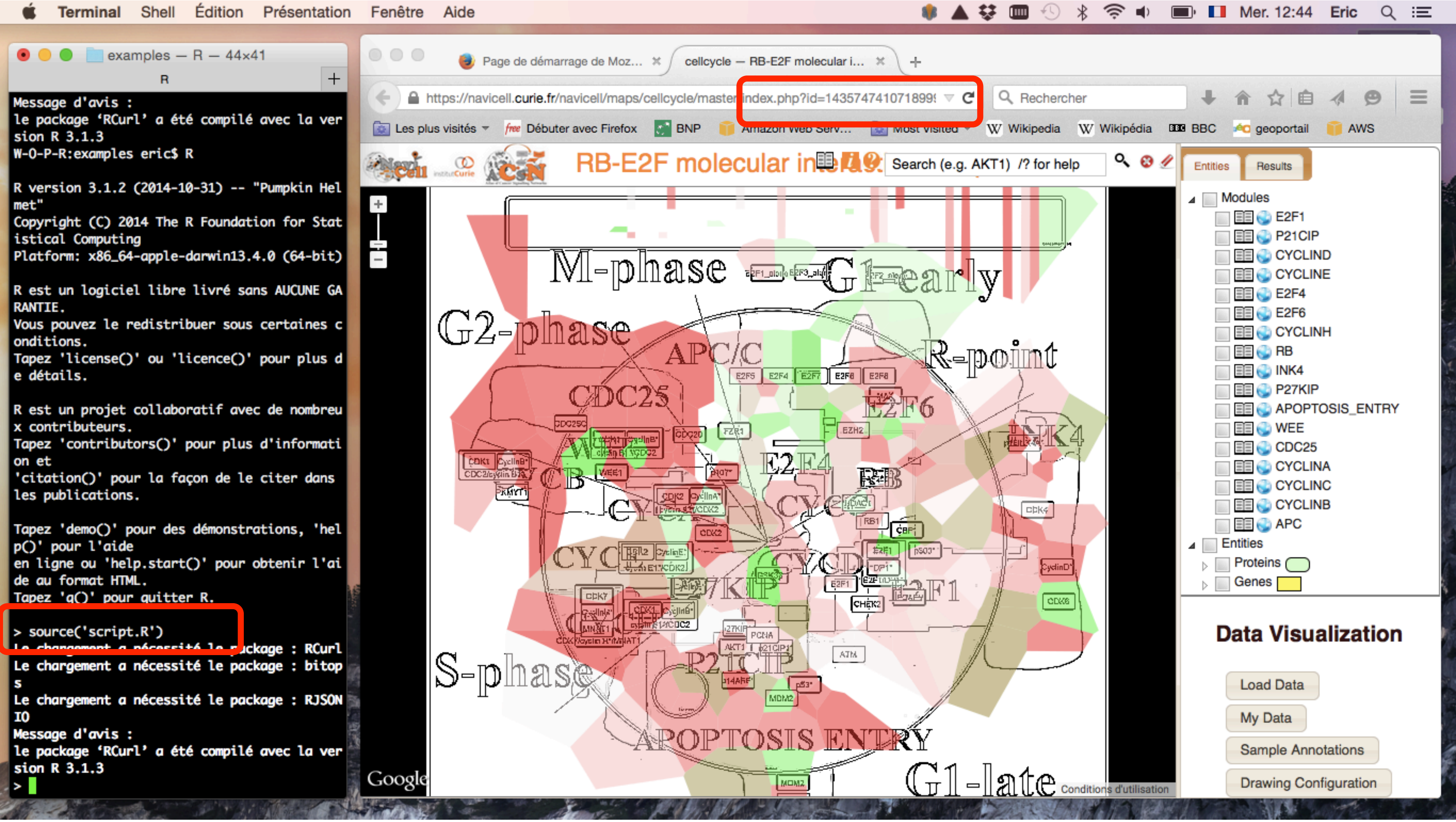
NaviCell server mode





```
library(RNaviCell)

# create a NaviCell object
navicell <- NaviCell()

# set the proxy and map URLs, these are the default values
# but we could change them to point to another map, e.g. survival,
# DNA repair, apoptosis, etc.
proxy_url <<- "https://navicell.curie.fr/cgi-bin/nv_proxy.php"
map_url <<- "https://navicell.curie.fr/navicell/maps/cellcycle/master/index.php"

# connect to the server, create a session ID and the default browser on the client
navicell$launchBrowser()

# read a tab-delimited expression data matrix
# and convert it to a R matrix object
mat <- navicell$readDatatable('LNCAP_data.txt')

# "send" the data to the client browser session
navicell$importDatatable("mRNA expression data", "LNCAP", mat)

# configure color and treshold parameters in order to have a
# continuous gradient from low (green) to high expression values (red)
# with intermediate values as white.
navicell$continuousConfigSwitchSampleTab("LNCAP", "color")
navicell$continuousConfigSetStepCount("sample", 'color', 'LNCAP', 2)
navicell$continuousConfigSetColorAt("LNCAP", "sample", 1, 'FFFFFF')
navicell$continuousConfigSetValueAt("LNCAP", "color", "sample", 0, -1)
navicell$continuousConfigSetValueAt("LNCAP", "color", "sample", 2, 1)
navicell$continuousConfigApply("LNCAP", "color")

# select map staining as the graphical representation for prostate cancer data
# set the datatable and sample, and display the results
navicell$mapStainingEditorSelectDatatable('LNCAP')
navicell$mapStainingEditorSelectSample('data')
navicell$mapStainingEditorApply()
```

https://github.com/eb00/RNaviCell https://github.com/eb00/RNaviCell/wiki/Tutorial



```
Message d'avis :
le package ‘RCurl’ a été compilé avec la ver
sion R 3.1.3
W-O-P-R:examples eric$ R

R version 3.1.2 (2014-10-31) -- "Pumpkin Hel
met"
Copyright (C) 2014 The R Foundation for Stat
istical Computing
Platform: x86_64-apple-darwin13.4.0 (64-bit)

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R est un projet collaboratif avec de nombreu
x contributeurs.
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on et
'citation()' pour la façon de le citer dans
les publications.

Tapez 'demo()' pour des démonstrations, 'hel
p()' pour l'aide
en ligne ou 'help.start()' pour obtenir l'ai
de au format HTML.
Tapez 'q()' pour quitter R.

> source('script.R')
Le chargement a nécessité le package : RCurl
Le chargement a nécessité le package : bitop
s
Le chargement a nécessité le package : RJSON
IO
Message d'avis :
le package ‘RCurl’ a été compilé avec la ver
sion R 3.1.3
> 
```
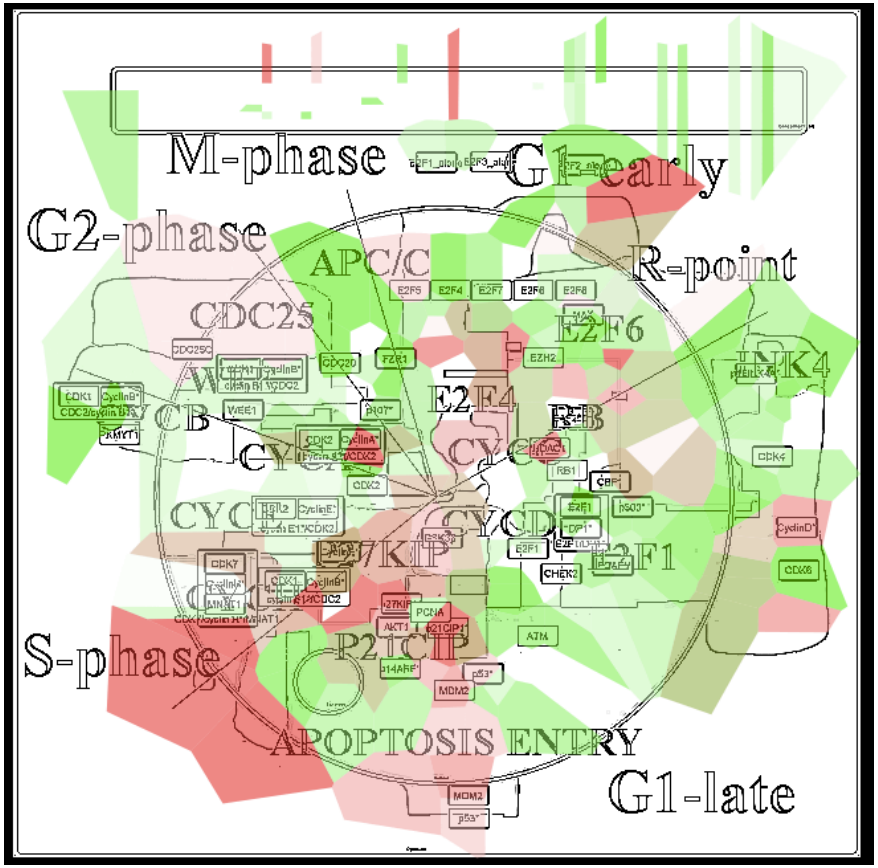
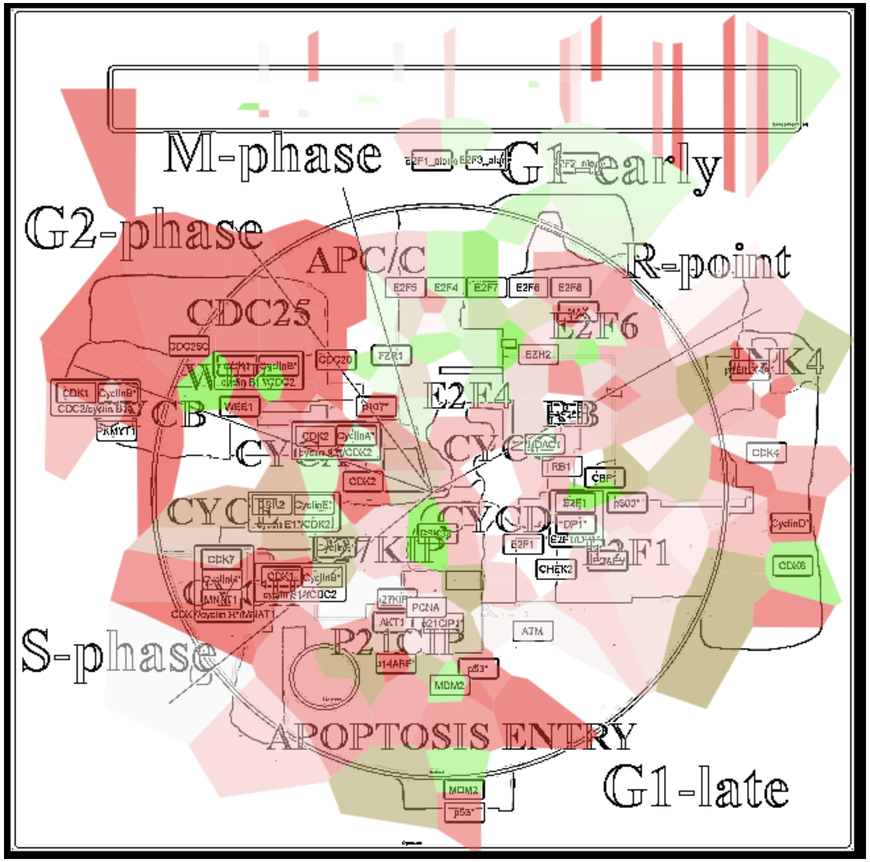

Comparing 2 prostate cancer cell lines expression on the cell cycle map



LNCAP
Hormone treatment sensitive



DU145
Hormone treatment resistant

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Thanks to

Eric Viara

Laurence Calzone

Inna Kuperstein

David Cohen

Andrei Zinovyev

Emmanuel Barillot

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Inserm

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