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
Atlas of Cancer Signalling Networks

Resource of knowledge on molecular mechanisms and analytical tool

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


http://acsn.curie.fr
NaviCell technology

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


Google maps navigation

- M-phase
- G2-phase
- APC
- CDC25
- WEE1
- CYCB
- E2F4
- E2F6
- RB
- INK4
- G1-early
- R-point
- CYCA
- CYCC
- CYCE
- P27KIP1
- E2F1
- CYCD
- P2
- APE1
- S-phase

Semantic zooming

- Proteins
- Genes
- RNA
- Antisense RNAs
- Simple molecules
- Ions
- Drugs
- Phenotypes
- Complexes
- Reactions

Data integration

- Entities
- Proteins
- Genes
- RNAs
- Antisense RNAs
- Simple molecules
- Ions
- Drugs
- Phenotypes
- Complexes
- Reactions

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

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

- Data integration and visualization (online)
- 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

NaviCell Web Browser Session
(Firefox – Chrome – Safari)

Ajax

NaviCell proxy
Apache web server - php

HTTP / HTTPS requests
(Data exchange and visualization)

NaviCell RESTful web API

Python API
Python code

R API
R code

Java API
Java code

Garuda gadget
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 threshold 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()
Comparing 2 prostate cancer cell lines expression on the cell cycle map

LNCAP
Hormone treatment sensitive

DU145
Hormone treatment resistant
Thanks to
Eric Viara
Laurence Calzone
Inna Kuperstein
David Cohen
Andrei Zinovyev
Emmanuel Barillot