



Garuda

The way biology connects

Samik Ghosh,
The Systems Biology Institute,
Tokyo

The Garuda Alliance

www.garuda-alliance.org

ECCB, September 2014

Computational Tools and Platforms



Landscape

Computational tools and platforms drive analysis of experimental data

- A wide variety of tools and techniques are available
 - Genomic analysis
 - Proteomic analysis
 - Pathways and network analysis
 - Simulation and modeling at multiple scales

Landscape

- Complexity and multiple dimensions of analysis characterize biomedical research
- It is extremely challenging to develop a single tools which covers these dimensions
- The focus is shifting to “platforms”



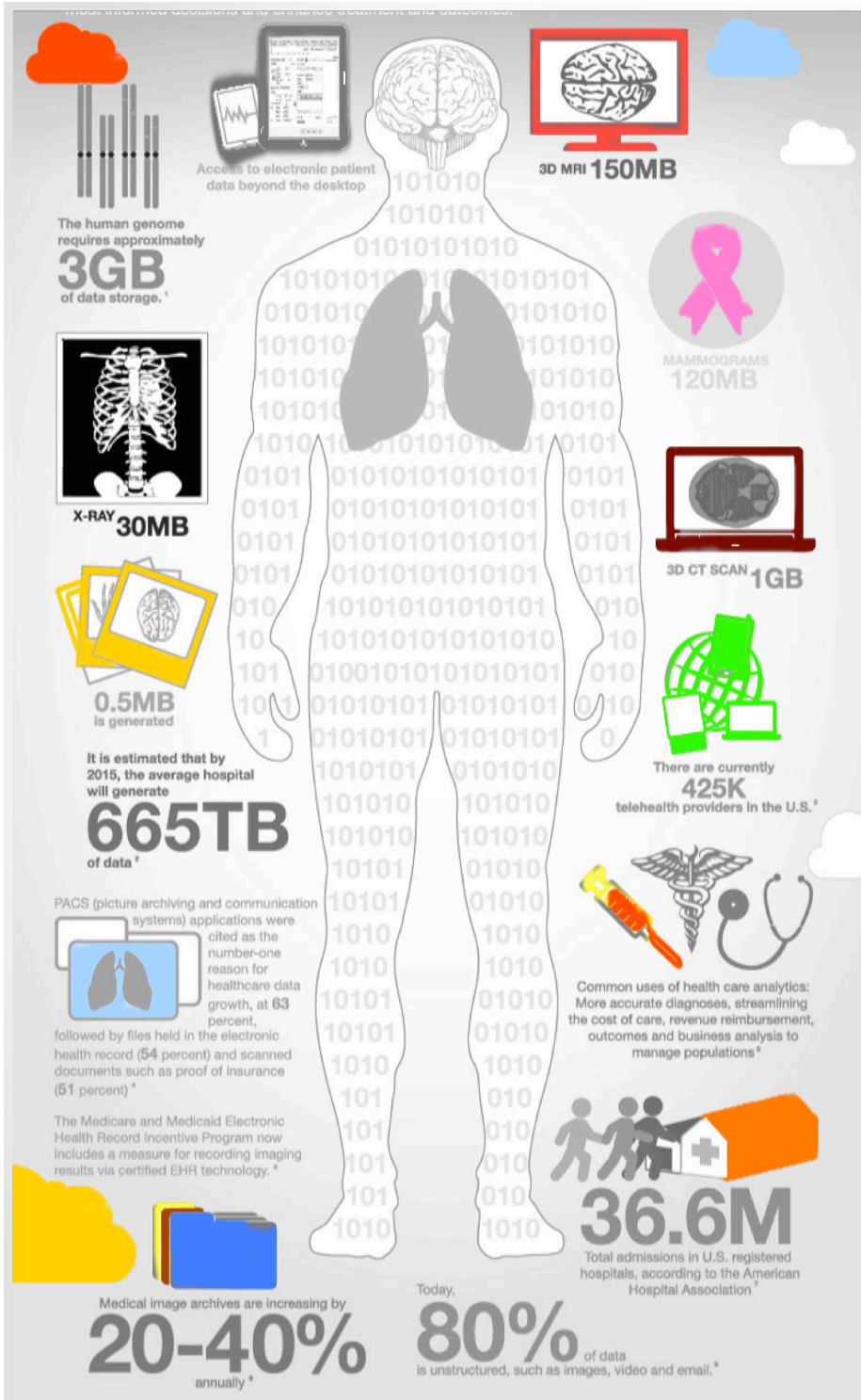
Why Garuda?



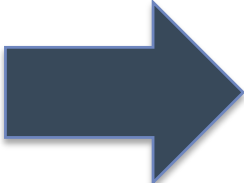
Data Diversity

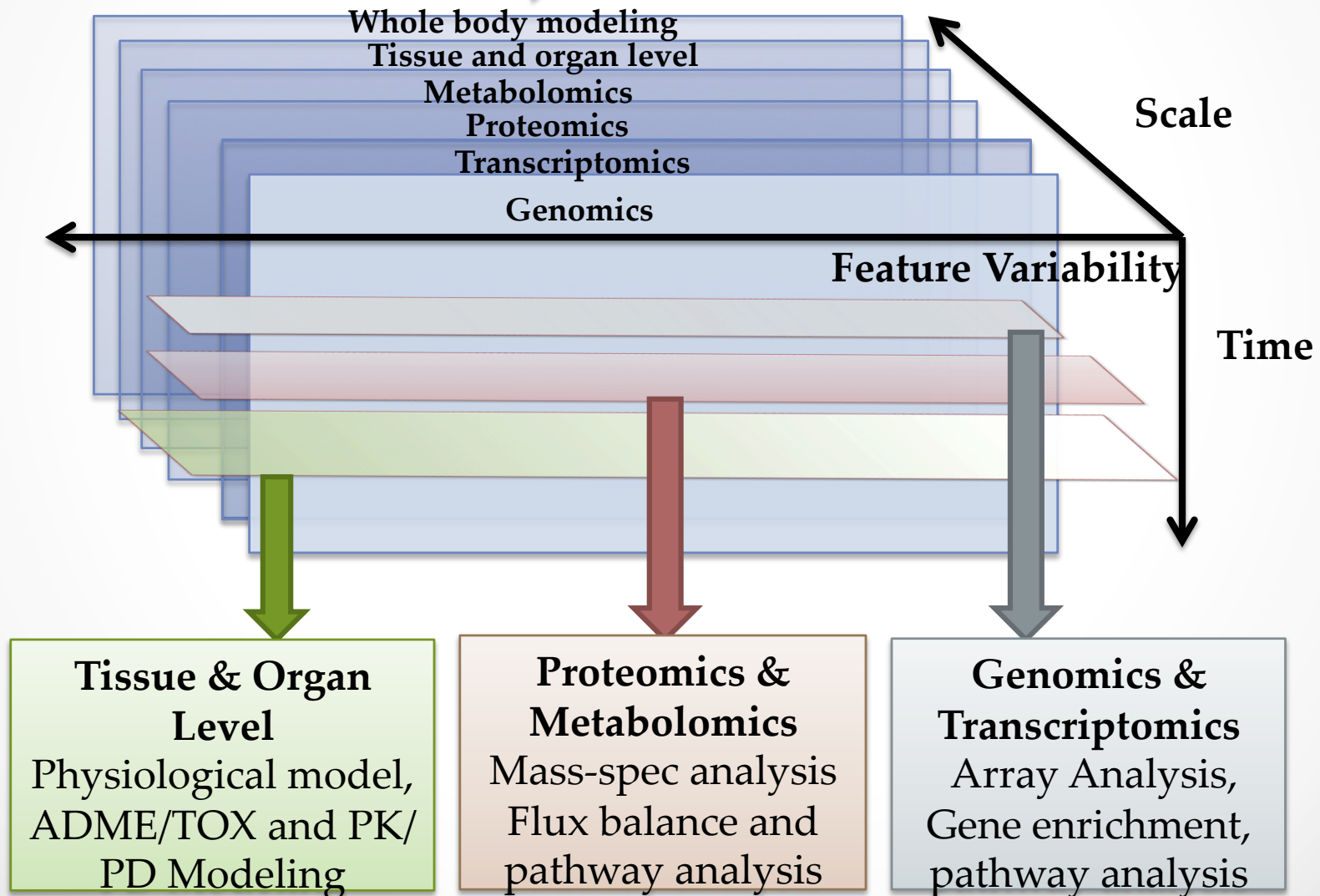
Biological data has:

- High Variety
- High Variability
- High Volume
- Need Veracity
- Need Visualization



Analytics Diversity

HD Data  HD Analytics



Analytics Diversity

Plethora of databases, tools and services

Database



Modeling



Informatics



Networks



Analytics Challenges

Discoverability: which, how, what



Analytics Challenges

Where should I go....



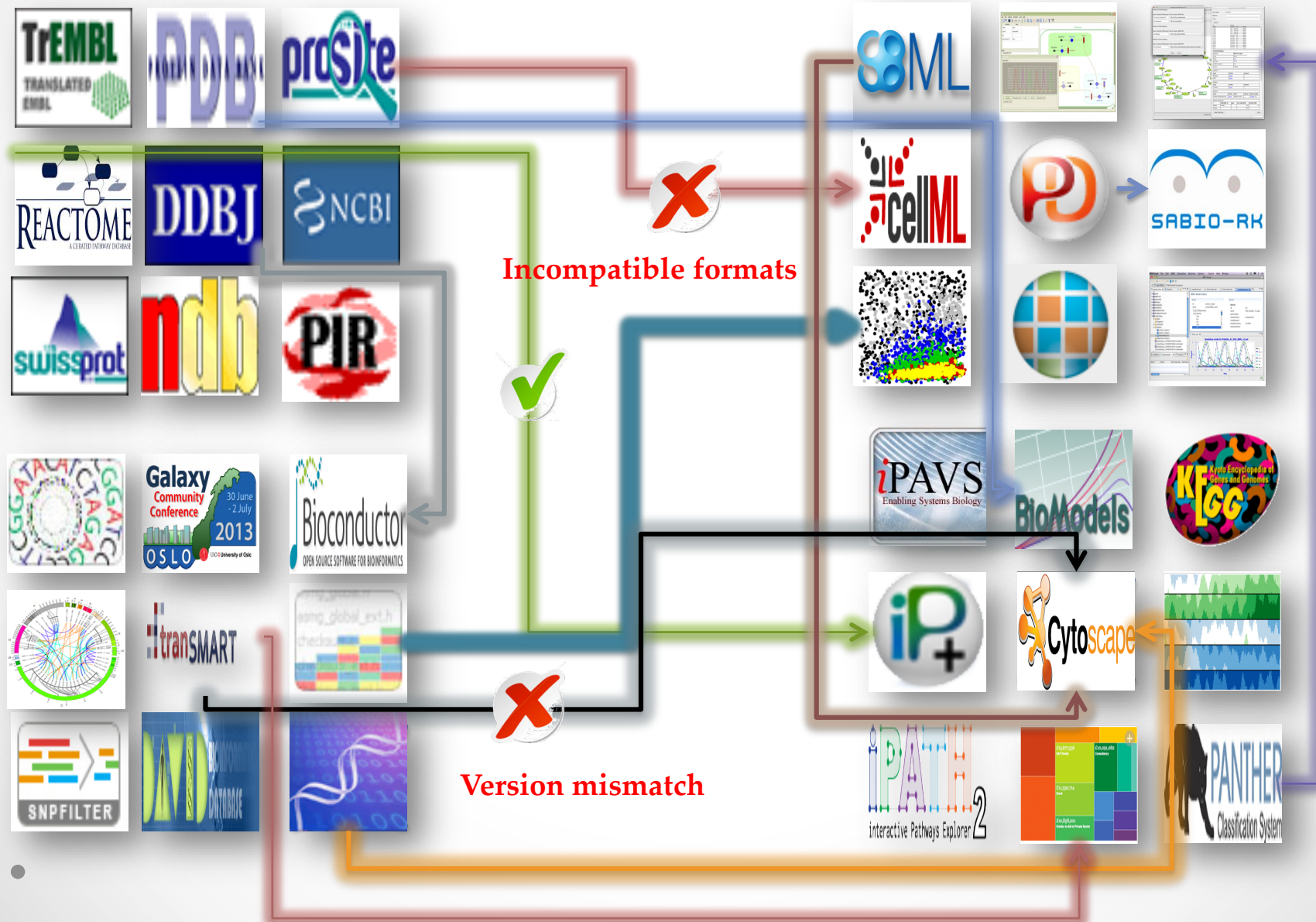
Analytics Challenges

Navigability: how to walk through multiple tools



Analytics Challenges

Navigability: road-blocks, dead-ends



Need for a Platform



Platform Needs

A platform for bio-medical research which is

- Open – Interface with multiple analytics tools
- Discoverable - One stop access
- Navigable – Reduce friction in using multiple tools

nature
REVIEWS **GENETICS**

Software for systems biology: from tools to integrated platforms

Samik Ghosh¹, Yukiko Matsuoka^{1,2}, Yoshiyuki Asai³, Kun-Yi Hsin³ & Hiroaki

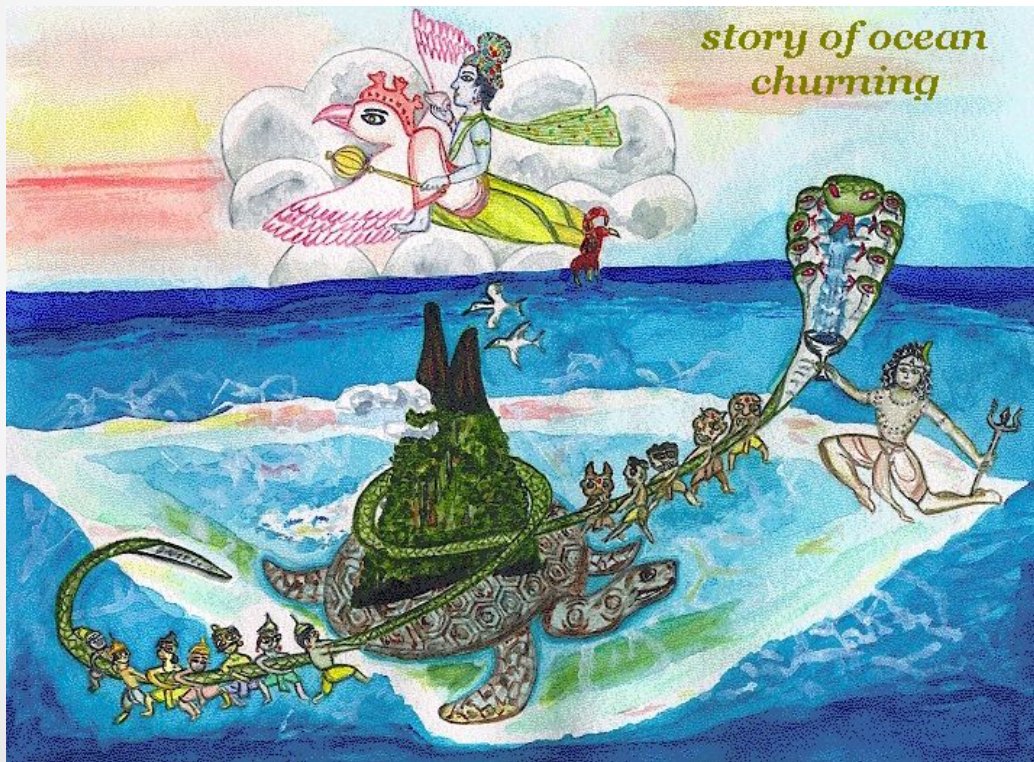
Kitano^{1,3,4} [About the authors](#)

What is Garuda?



What is Garuda?

The Myth....

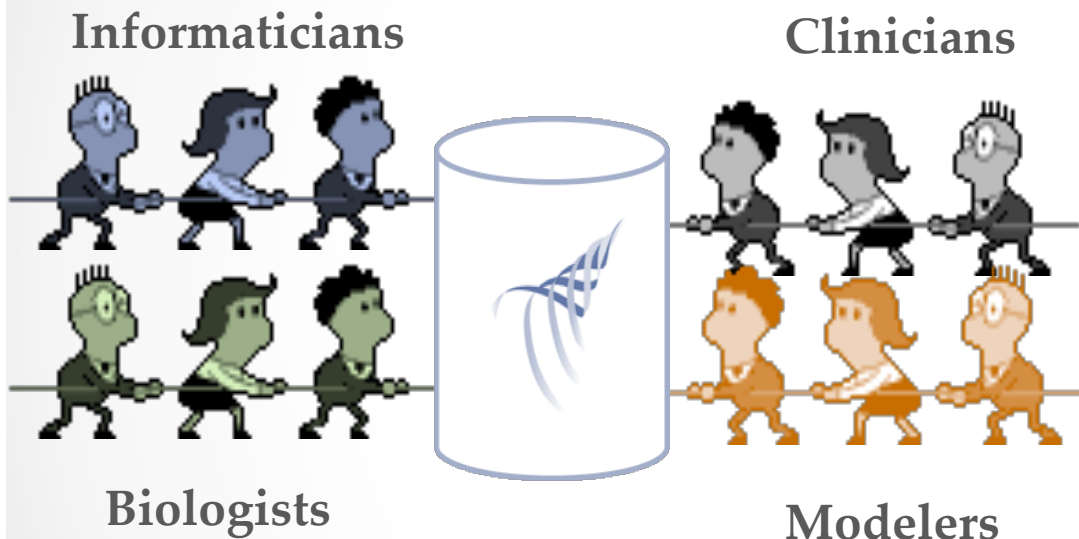


Garuda is a divine bird in Hindu mythology who is the mount (*vahana*) of Vishnu – the supreme God of the universe and commander of Churning of the Sea of Milk

A *Hindu* myth in which gods and demons cooperate to churn the primordial ocean, in order to produce amrita, the elixir of immortality

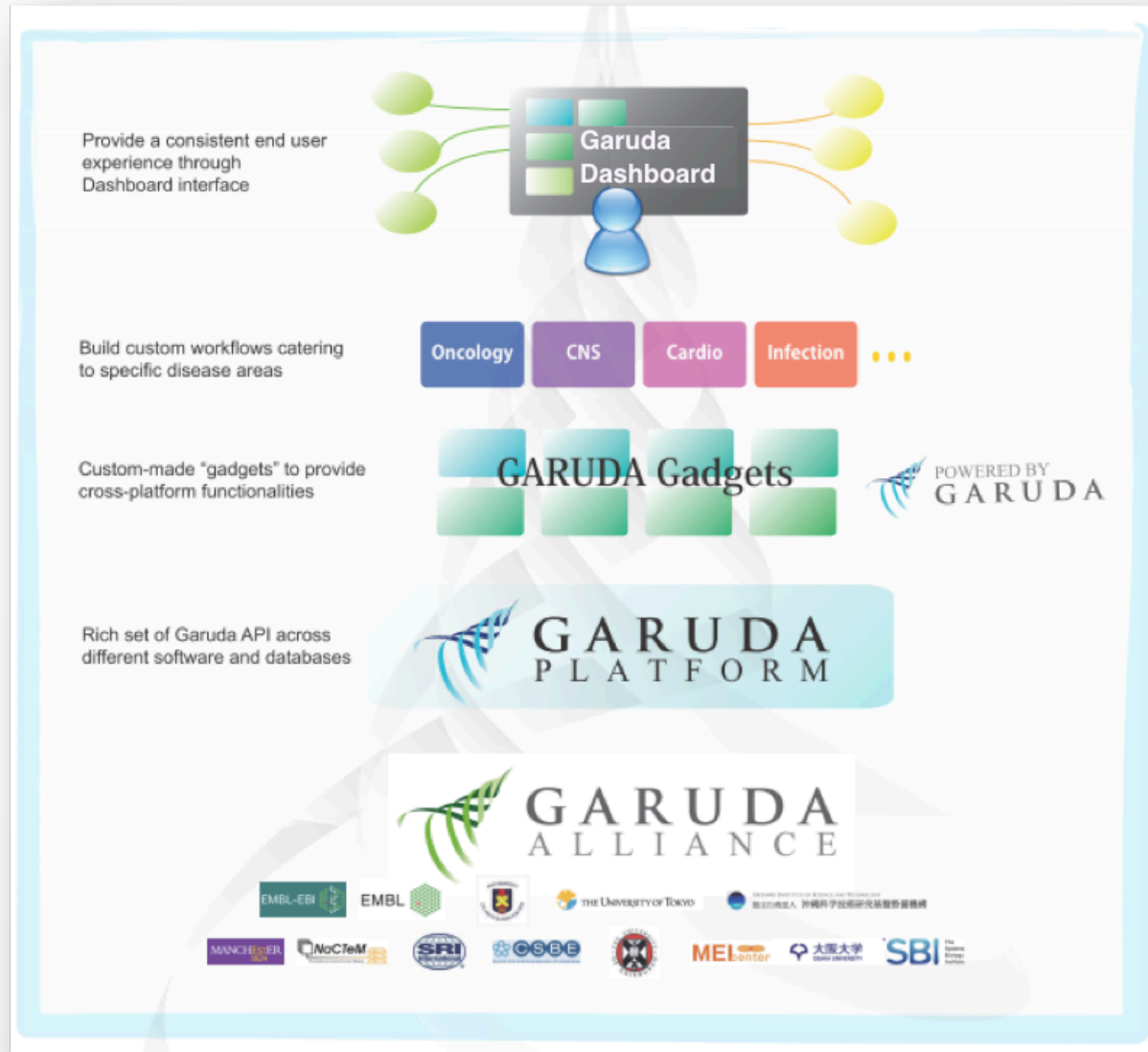
What is Garuda?

The Platform....



Garuda is an open, community-driven, common platform that provides a framework to –
interface,
discover, &
navigate through different applications, databases and services in bio-medical research

What is Garuda?

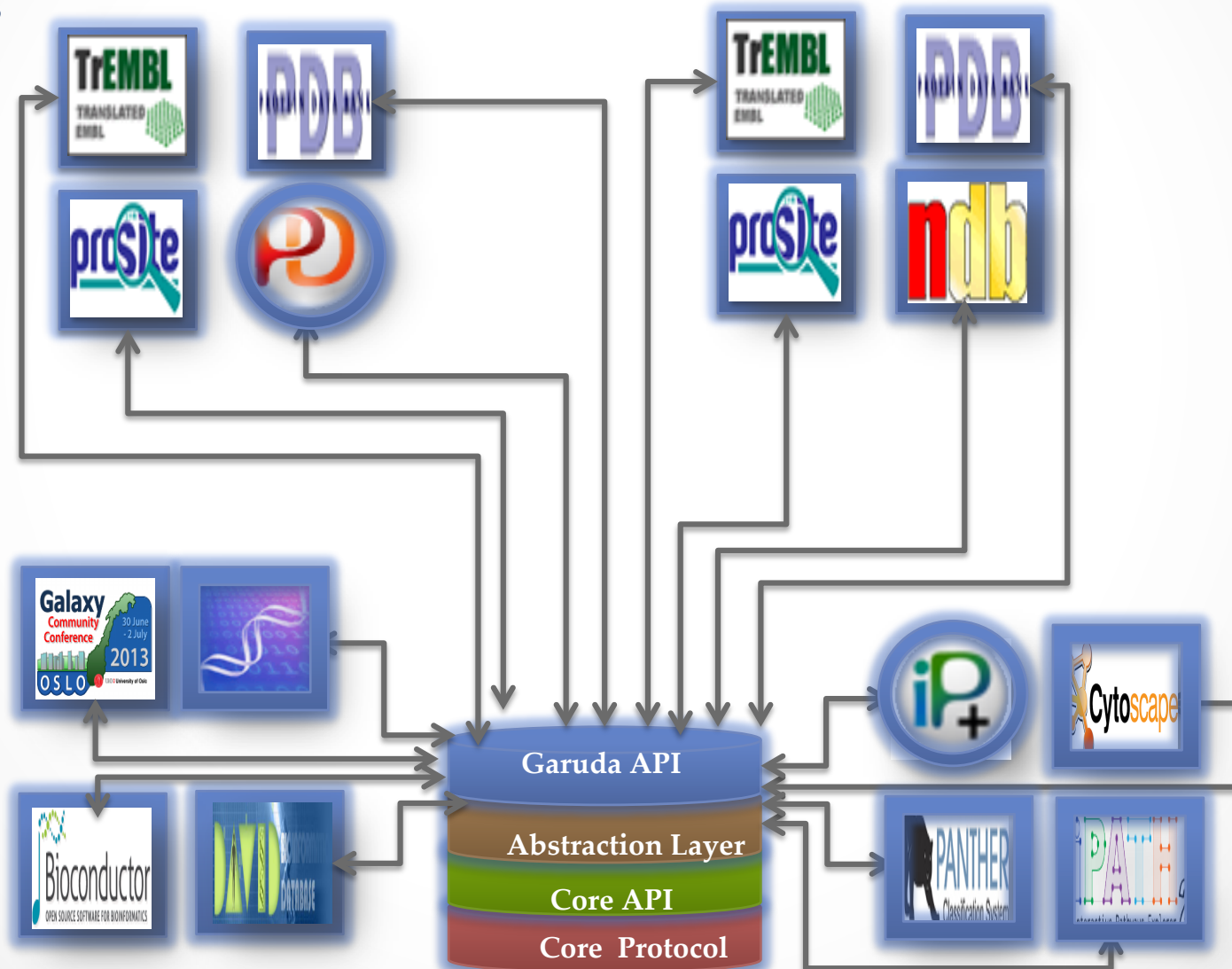


The Gadgets



Garuda Gadgets

Inter-operating universe of Garuda-enabled tools and services



The Dashboard



Garuda Dashboard

Provides the single window desktop interface to access and navigate gadgets

The Garuda Dashboard is a single window desktop interface for accessing and navigating various biological data analysis tools. The interface is organized into several key sections:

- Category List (Left Panel):** A vertical list of categories including: All(33), A Starter Kit, Analytics, Annotation, CellDesigner Plugin, Database, Feedback, Gateway, Help, Installer, Modeling, Pathways, Simulation, Viewer, and Visualization.
- Search Bar (Top Center):** A search field with the placeholder text "Search for a gadget".
- Gadget Grid (Center):** A collection of 33 individual gadget icons, each representing a different tool or service. Some visible icons include: Getting Started, About GARUDA, Network CONTROL, Cytoscape Installer, Gadgets Social, GARUDA Feedback, Gadgets Trace, GARUDA Wishlist, Get Gadgets, GENES, DB, PANTHER, TimeXNet, XM, iPAVS, iP₂, and iP₊.
- Gadget Details (Right Panel):** A panel for viewing the details of a selected gadget. It includes fields for Name, Gateway, Category, Provider (SBI, Tokyo), and Description. The description for the "Garuda" gadget reads: "Your window to the Garuda gadgets universe online. Request an account and explore gadgets to download on your dashboard".
- Preview (Bottom Right):** A small window showing a preview of the Garuda dashboard interface.
- Logo (Bottom Left):** The Garuda logo with the tagline "THE WAY BIOLOGY CONNECTS".

The Gateway



Invited
Access

Garuda Gateway

Web-based interface to access and discover gadgets

CellDesigner™ for Windows
CellDesigner is a structured diagram editor for drawing gene-regulatory and biochemical networks.

New Gadgets View All

- PhysioDesigner Installer for Mac**
by PhysioDesigner projects
Thu, 11/28/2013 - 15:42 UPDATE
Installer of PhysioDesigner.
[Free Download](#)
- Flint for Mac**
by Flint project
Thu, 11/28/2013 - 15:30 UPDATE
A simulator for physiological models
Data Analysis | [Mac](#)
[Free Download](#)
- Ortho Survey for Mac**
by Monash University
Wed, 11/27/2013 - 12:33 UPDATE
Survey for layout of biological pathways
[Free Download](#)
- CellDesigner for Mac**
by SBI
Tue, 11/19/2013 - 15:43 UPDATE
CellDesigner: A Modeling Tool for Biochemical Networks
Visualization | [Mac](#)
[Free Download](#)
- Gadget Social for Mac**
by SBI
Fri, 11/15/2013 - 15:23 UPDATE
The gadget "social network"
Visualization | [Mac](#)
[Free Download](#)

Home » CellDesigner for Mac back to list

CellDesigner for Mac

CellDesigner: A Modeling Tool for Biochemical Networks
by SBI

Description

CellDesigner: A Modeling Tool for Biochemical Networks More >>

Screen Shot

0 Use Reviews

[Free Download](#)

Share [Twitter](#) [Facebook](#)

Category: [Visualization](#)

OS: [Mac](#)

Release: 11/19/2013

Version: 1.0 beta

File size: 52.7MB

Email: [Mail Author](#)

Website: [Author Website](#)

Review

[let's write review](#)

Related Gadgets back to list

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<http://gateway.garuda-alliance.org>

The Alliance



Round the World



Circle Asia



Circle North Asia



Circle Pacific



Round the World. Add destinations to your itinerary.

Your Round the World Itinerary

Add city to itinerary +

1. Tokyo (JP)			
2. Frankfurt (DE)			
3. New York (US)			
4. Honolulu (US)			
5. Tokyo (JP)			

Itinerary status: Complete, please choose flights

■ Direct flights □ Single connections ▣ Multiple connections ○ Not Selectable

Segments: 4 (max 16) Stopovers: 3 (max 15) Mileage: 18,576 39,000

Previous

Save

Email

Download PDF

Print

Help

Next

Garuda Alliance

A global consortium of key leaders in informatics and analytics



Garuda Alliance



Garuda One, Okinawa 2010



Garuda Three, Edinburgh 2010



Garuda Nine, Okinawa 2013

How does it work?



Bit of History....

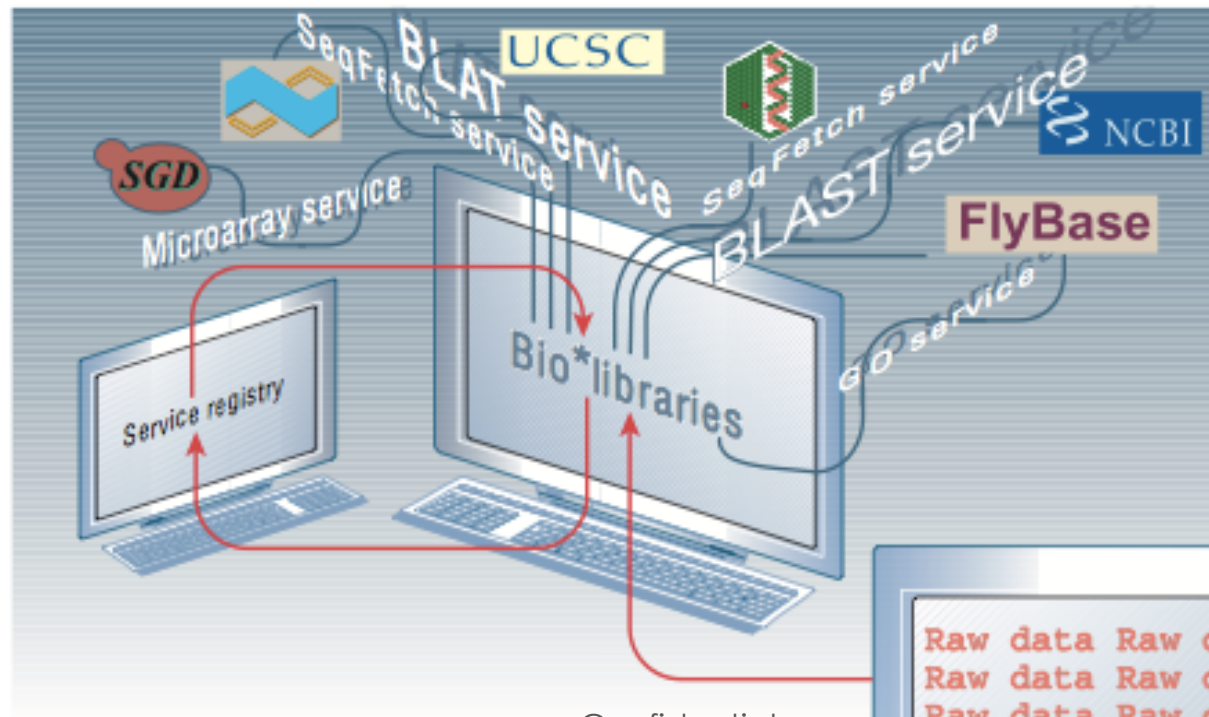
commentary

Creating a bioinformatics nation

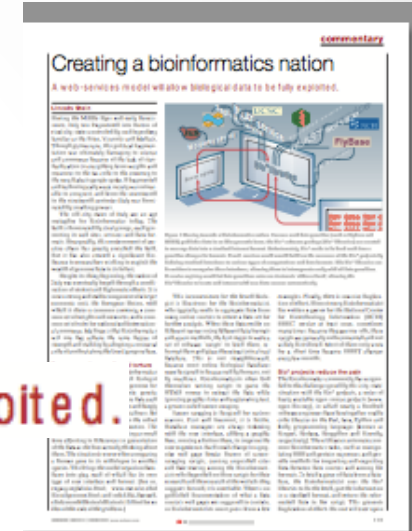
A web-services model will allow biological data to be fully exploited.

Lincoln Stein NATURE | VOL 417 | 9 MAY 2002 | www.nature.com

A web-services model will allow biological data to be fully exploited.



Confidential



Planet of APIs

Power of Open APIs!!!

NOISE TO SIGNAL
Rob Cottingham



Apparently our open API is giving our customers unprecedented control over their own lives and allowing them to seize control of their destinies. So please shut it down.

Confidential

Key Concepts

Dashboard

Provides the single window desktop interface to the end users for all things Garuda!

GCore

The engine driving the Garuda Platform. Provides the implementation of the Garuda Protocol and does all the heavy lifting!

Gadgets

The “Garuda-enabled” software driving Garuda! Software which implement the Garuda Protocol APIs

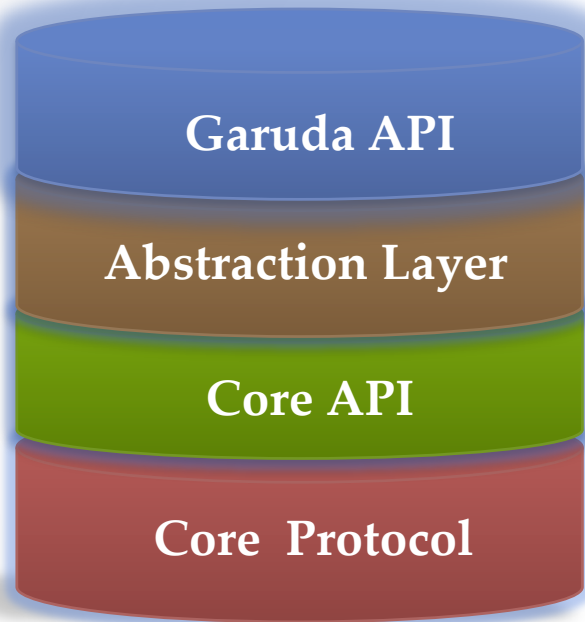
Gateway

The web interface to Garuda Platform.
Provides gadget management and related functionalities

The Core Engine



Garuda Core



Core Protocol: A communication framework on existing networking protocols

Core API: Core engine interface to the protocol

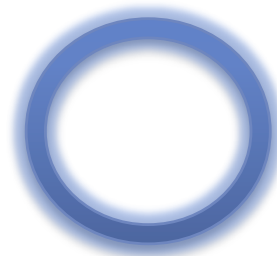
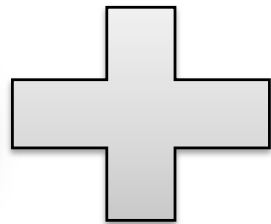
Abstraction Layer: A language and system agnostic interface to Core

Garuda API: Set of application programming interfaces to interact with Garuda Core over the Garuda Protocol (multi-language bindings)



Garuda Gadgets

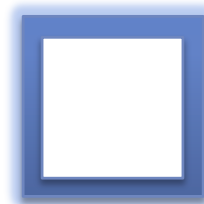
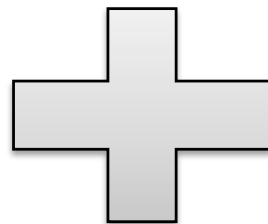
A software or service which implements the Garuda API to enable its functions on Garuda Platform



PhysioDesigner
Application

Garuda API

PhysioDesigner
Garuda Gadget



Reactome
Web Service

Garuda API

Reactome
Garuda Gadget

Core Principles

Single platform for end users

Plug and Play (PnP) for users

Dynamic inter-operability
and discovery

Zero end-user configurations

Open APIs for developers

Language independent protocols

Standardized UX

Multi-language bindings

History of Garuda





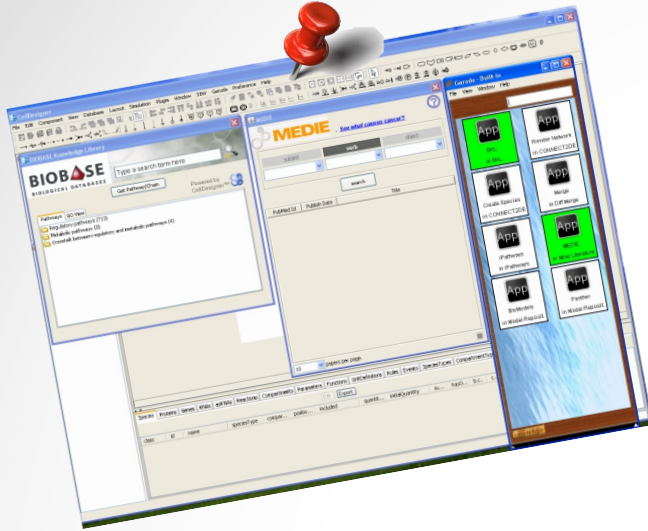
Our journey so far!





Garuda One, Okinawa, Japan 2010

- ✓ Concept of a common platform
- ✓ Motivation
- ✓ Guiding principles
- ✓ Core members



Garuda Two, Manchester, UK 2010

- ✓ First seeds of Alliance
- ✓ Need of APIs
- ✓ Need of services

Garuda Three, Edinburgh, UK 2010

- ✓ First demo of dashboard
- ✓ Concept of Gadgets
- ✓ Concept of Garuda Core
- ✓ Garuda API (GAPI)



Garuda Four, Okinawa, Japan 2011

- ✓ Garuda platform architecture
- ✓ Formalization of services
- ✓ Formalization of APIs
- ✓ Scrap-built demo
- ✓ Garuda Logo conception



Garuda Five, Heidelberg, Germany 2011

- ✓ Review of new architecture
- ✓ Beta version www.garuda-alliance.org
- ✓ Garuda Logo launch

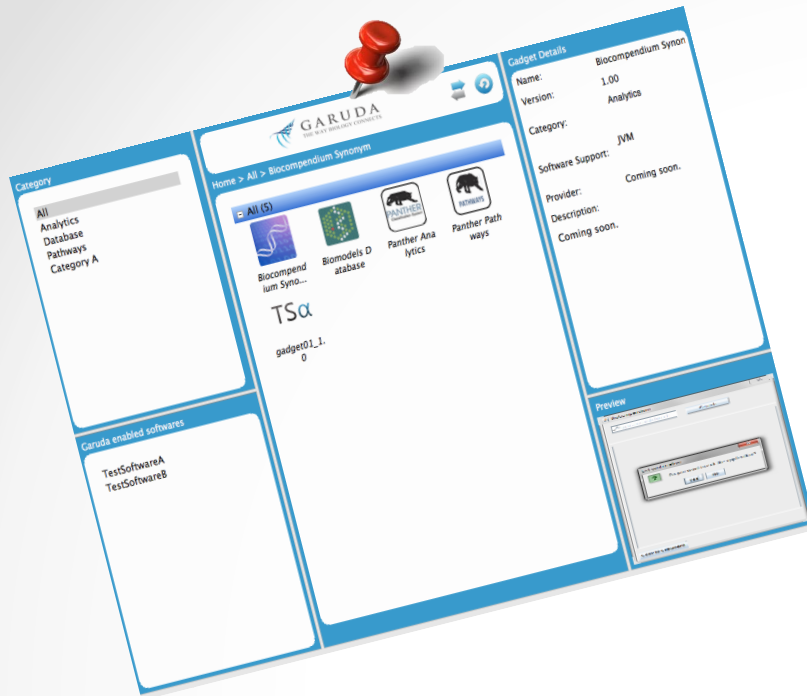


Garuda Six, LCSB, Luxembourg, 2011

- ✓ Internal release of Alliance website
- ✓ Draft specification of service & core APIs
- ✓ Sample Garuda gadgets development
- ✓ Sample Garuda enabled software

Garuda Seven, Okinawa, 2012

- ✓ Final specification of Core and API
- ✓ First version of Java SDK
- ✓ New Dashboard design



Garuda 7.5, Long Beach, CA, 2012

- ✓ Garuda 1.0 Community alpha1
- ✓ Beta version of Java SDK
- ✓ C++ and Python bindings samples

Garuda 8, Toronto, Canada, 2012

- ✓ Garuda 1.0 Community alpha2
- ✓ Beta2 version of Java SDK
- ✓ Concept of Garuda Gateway

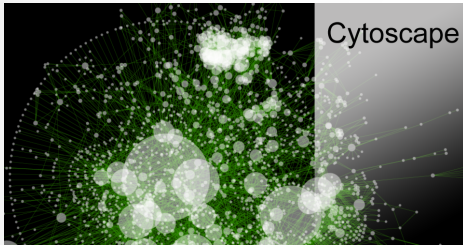
Garuda 9, Okinawa, 2013

Goals

- ✓ Hackathon – Enable gadgets on the dashboard
- ✓ Community expansion and outreach
- ✓ Roadmap for public beta
- ✓ Community beta release



Flint



Cytoscape



Garuda 10, Copenhagen, 2013

First public workshop on Garuda!

- ✓ Introduction to Garuda
- ✓ Public beta users
- ✓ Comments and Feedback
- ✓ Sign-up for public beta
- ✓ Help us spread and improve Garuda



Garuda 2014

First public release of
Garuda!



Discover and Navigate

Controllability

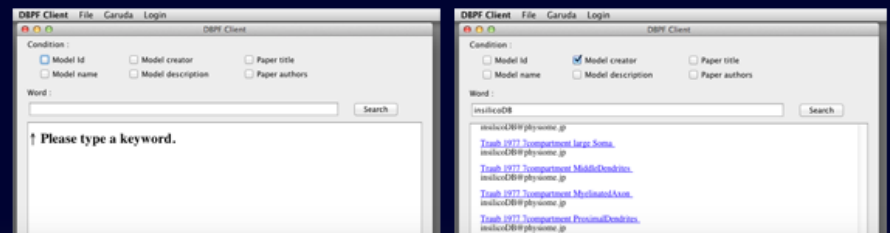


Anal
entit



DBPF Client

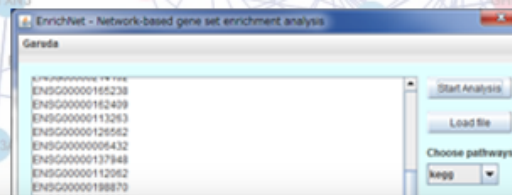
Dynamic Brain Platform client



EnrichNet

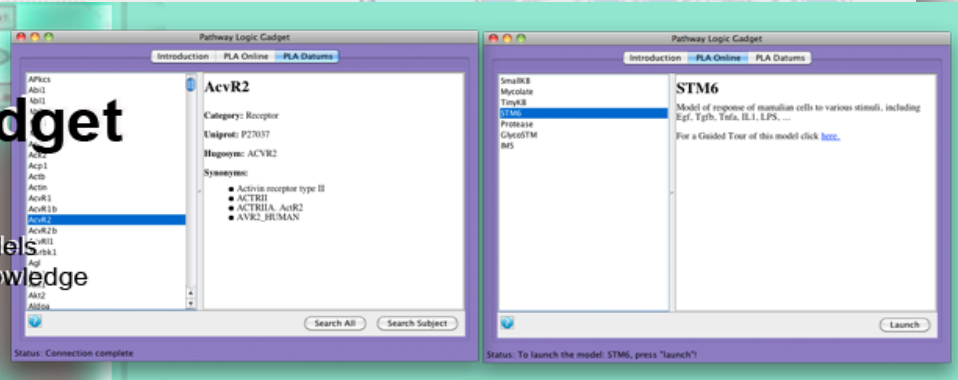
EnrichNet computes a network-based

pathway
the in
pathway
molec



Pathway Logic Gadget

Pathway Logic models cellular processes using formal executable specifications. The gadget provides access to curated models and an experimental evidence (datums) knowledge



Garuda Alliance

www.garuda-alliance.org

The screenshot shows the Garuda Alliance website homepage. At the top left is the logo with the text "GARUDA THE WAY BIOLOGY CONNECTS". A navigation bar contains links for Home, Overview, Garuda Alliance Members, Garuda Resources, User Stories, News/Topics, Events, and Developer Center. A search bar is located in the top right. Below the navigation bar is a large banner titled "About Garuda Alliance" with a "More" button. To the right of the banner is a "Developer Center Log in" section with buttons for "Garuda Alliance Member Center Log in", "Garuda Developer Center Log in", and "Create an account". Below this is a green box stating "Developers Center will open in 2012" with an upward arrow. The main content area features two "User Stories" cards. The first card, "To understand mechanisms of drug resistance", includes a flowchart and is dated 7 November, 2011. The second card, "Distributed pathway curation", includes a flowchart and is dated 7 November, 2011. On the right side, there are sections for "News/Topics" and "Events". The "News/Topics" section includes "Introducing Garuda" (7 November, 2011) and "New Garuda-Alliance.org site open for preview!" (29 September, 2011). The "Events" section includes "Garuda Seven in Okinawa" (29 September, 2011) and "Garuda Six in Luxembourg" (28 September, 2011).

Explore new user stories, Resources and Events!

Join the Community!




Community

Community is key to Garuda

Join the Garuda community and –

- Use gadgets in your projects
- Suggest new gadgets and pipelines
- Develop your own gadgets



Garuda
Science In Style

Thank you!

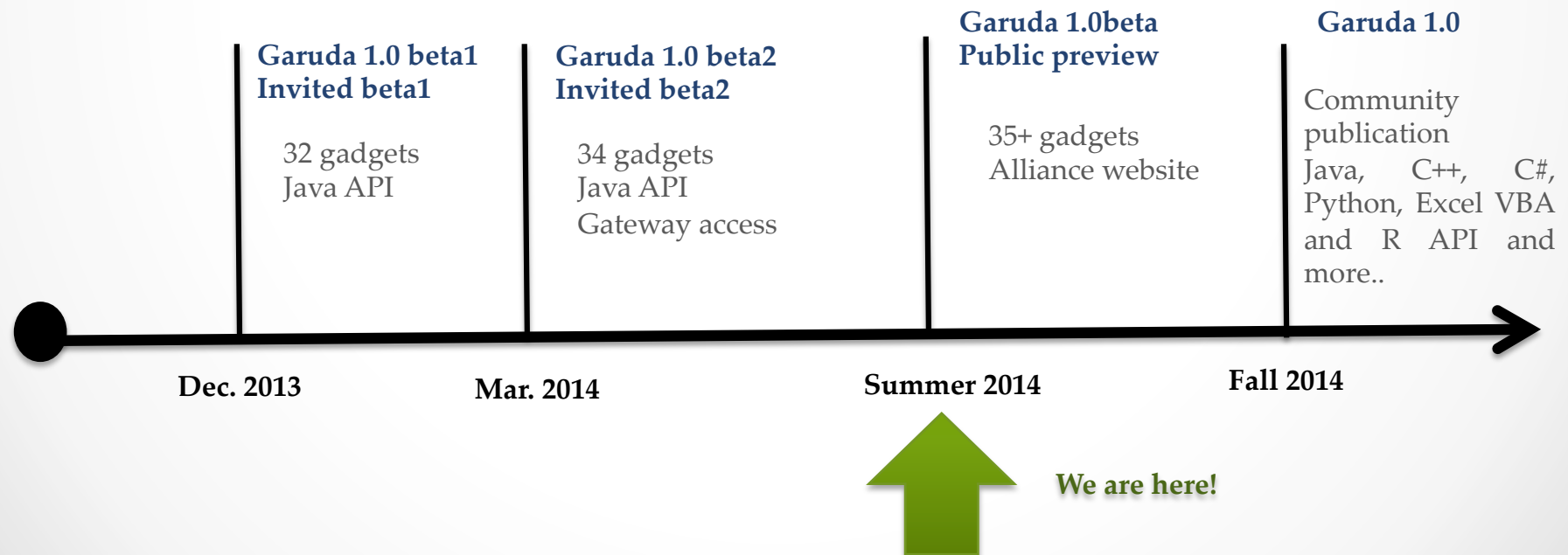
Garuda 1.0 beta – A Preview



Release Roadmap

Garuda Platform 1.0 beta public preview :

- Over 30 gadgets from 20 academic partners covering modeling, simulation, visualization, analytics and more.
- Invited access to gadgets from gateway
- Invited access to APIs in Java, C++, C#, Python, R and Excel Macro and more...



Release Notes: 1.0 beta

New

35

Gadgets available in 1.0 beta
(33 gadgets with 2 installers)



Available on **OSX** and **Windows**

New



GARUDA GATEWAY

Access to **Garuda Gateway**
for download of gadgets on
request

Release Notes: 1.0 beta

Integrated access to **Garuda Gateway**
from dashboard

Updated dashboard, 2 Installer

Lite : Dashboard with core gadgets

Pack: Dashboard with all gadgets

Free Download!

<http://gateway.garuda-alliance.org>

Garuda 1.0 Walkthrough



Getting Started



Garuda Dashboard

On launching Garuda, the Dashboard provides the window to the world of Garuda gadgets

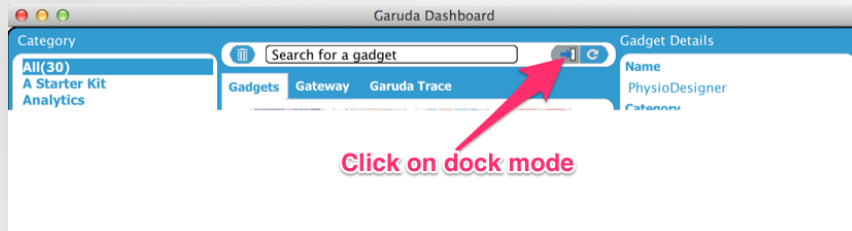
The screenshot shows the Garuda Dashboard interface with several annotated features:

- Delete selected gadget:** A red arrow points to a trash icon in the top navigation bar.
- Dock mode:** A red arrow points to a square icon with a refresh symbol in the top navigation bar.
- Categories:** A red arrow points to a list of categories on the left sidebar, including 'All (27)', 'A Starter Kit', 'Analytics', 'CellDesigner Plugin', 'Database', 'Gateway', 'Help', 'Modeling', 'Pathways', 'Simulation', and 'Visualization'.
- Search for a gadget:** A red arrow points to a search input field in the top navigation bar.
- Refresh:** A red arrow points to a refresh icon in the 'Gadget Details' panel on the right.
- Gadgets - Double click to launch:** A red arrow points to a grid of gadget icons in the center.
- Info Panel:** A red arrow points to the 'Gadget Details' panel on the right, which displays information for a selected gadget, including its name, category, provider (SBI and LCSB), and description.
- Preview Panel (double click to view):** A red arrow points to a 'Preview' window at the bottom right, which shows a small window of the gadget's output.

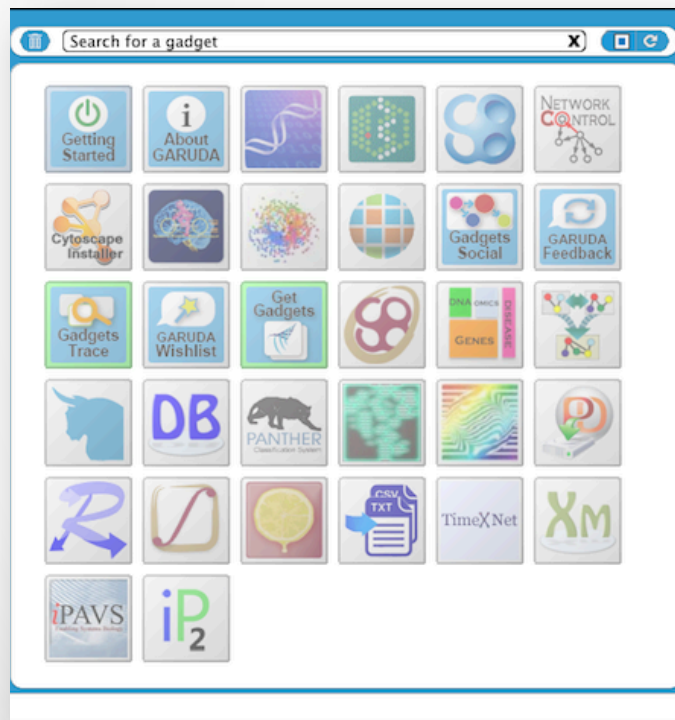
The Garuda logo and tagline 'THE WAY BIOLOGY CONNECTS' are visible at the bottom left of the dashboard.



Usability Tips



Click on *dock mode* to “dock” the dashboard



In Dock Mode, re-size the window to your desired size. This will hide the category and Information Panels!



Where to start?

A good place to start is the “**Starter Kit**” category which has **four** gadgets:



GadgetSocial

Find the social network of gadgets on your dashboard (who can exchange data with whom)



Nandi

The discovery gadget to load data and find gadgets for your workflow



Garuda Trace

Monitor activities between gadgets as you work on Garuda



Gateway

Opens the gateway of new gadgets

How “social” is your gadget?

Pipelines of gadgets in Garuda are built dynamically depending on the data and analytics workflow

- Build your own pipeline of gadget starting with your own files
- How can I know which gadgets can “talk” with other gadgets ?



GadgetSocial:

Builds dynamically the “social network” of gadgets based on their connectivity



Gadget Social

The gadget "social network"
Find how gadgets on your dashboard
"talk" to each other



CellDesigner

by (c) 2002-2013 The Systems Biology Institute. All rights reserved.



Upstream & downstream

Label

CellDesigner: A Modeling Tool for Biochemical Networks



Filter network on data type

Gadget Social: The gadget "social network". Find how gadgets on your dashboard "talk" to each other

Click or hover on a gadget node to get more information

Click or hover on an edge to see how two gadgets can exchange data

Connectivity matrix view

SBI Created by The Systems Biology Institute

Rearrange by name, number of connection, etc

Connectivity matrix shows which gadgets can talk with each other

Shows number of common formats between two gadgets (click to get details)

SBI Created by The Systems Biology Institute

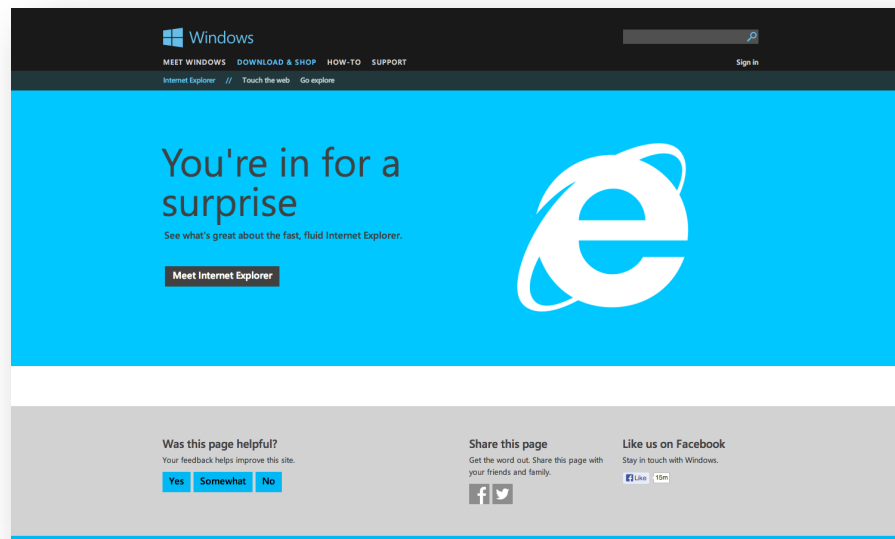


Usability Tips

If you are running a Windows machine (Windows 7, 8 or 8.1),

Please ensure that your Internet Explorer (IE) version is 9.0 or above (the latest version is 11.0)

GadgetSocial does not work if the IE browser version is less than 9.0





Monitor activities between gadgets as you work on Garuda

Gadgets Gateway Garuda Trace

11/28/2013 17:03:14.0517
Core sent a connection response. Connection succesful. GadgetSocial

11/28/2013 17:03:14.0516
GadgetSocial sent an activate gadget request to Core

11/28/2013 17:03:12.0018
Core is attempting to launch GadgetSocial

11/28/2013 17:01:37.0343
Core sent a connection response. Connection succesful. GadgetSocial

11/28/2013 17:01:37.0341
GadgetSocial sent an activate gadget request to Core

11/28/2013 17:01:34.0134
Core is attempting to launch GadgetSocial

11/28/2013 16:46:37.0117
Core sent a LoadGadget request for gadget open "gadgets/ba528141-245c-4358-b1c4-f1713c1e5ca4/GarudaDashboard.jar" to Dashboard

11/28/2013 16:46:37.0116
Core sent a LoadGadget request for gadget ./gadgets/cad84b2b-1289-4d43-9008-db855f459167/GLauncher.sh to Gateway

11/28/2013 16:46:33.0565
Core sent a connection response. Connection succesful. Dashboard

Source gadget **Communication message and data** **Destination gadget**



An entry point gadget
for the rest of the Garuda gadgets



1 Choose your question or "Show all" if you want to explore

2 Load your data file

3 Select file content or format

4 Press Discover to find gadgets to analyse your data

5 Garuda shows gadgets here. Double click on a gadget to send your data and begin analyze.

Change your question and click discover to view new gadgets for your data

1. Choose a question or "show all gadgets"
2. Load your data or choose from sample files
3. Select file content or unknown if not sure
4. Press "discover"
5. Double click on discovered gadgets to start



An entry point gadget
for the rest of the Garuda gadgets



Spotlight Feature

After discovering gadgets for a selected file and file content, select your question from the drop-down to automatically highlight recommended gadgets for the question!



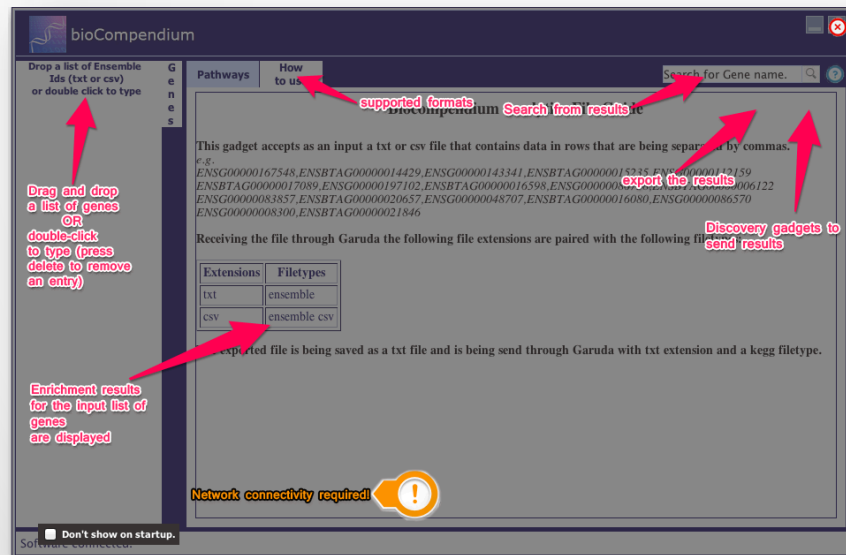
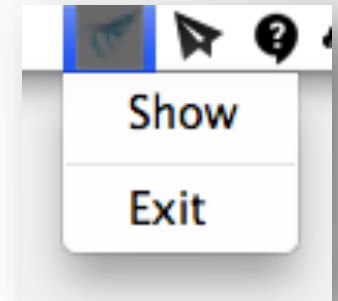


Productivity Tips

Closing the Dashboard window does not close Garuda Core.

To Close Garuda,

1. Locate the Garuda icon on your taskbar and
2. click to show Dashboard to **Exit** Garuda Core.



Alt + H also brings the Help



Clicking the **help icon** on most gadgets bring the help view.



Click on red cross to **close help**.

Check “Don't show on startup” to prevent auto launch of help view.

What can I do?

Garuda does not refine any specific analytics workflows. It is an “open” platform where you *discover* and *navigate* through different gadgets depending on your question

The image displays several overlapping screenshots of the Garuda platform interface, illustrating its capabilities:

- NANDI FILE GATEWAY:** A window for loading and analyzing data. It features a "Load Your Data" section with a "File List" table containing files like "Chicago_2003_pancreatic_beta-cell_with_SBML.xml" and "EGFR.xml". Below the list is the "Garuda Discovery Engine" which has discovered gadgets for the selected files.
- Garuda Dashboard:** A central hub displaying a grid of various analytical gadgets such as GARUDA TRACE, PAVS, GENES, and XM i₂.
- Gadget Social:** A network visualization tool showing a complex graph of interconnected nodes and edges, representing relationships between data points.
- bioCompendium:** A window titled "Biocompendium Analytics File Guide" that provides instructions on how to use the platform. It includes a table for file extensions and filetypes:

Extensions	Filetypes
txt	ensemble
csv	ensemble.csv

The bioCompendium window also shows a list of gene accessions and names, such as ENSG00000167548 and ENSBTAG00000014429.

- PANTHER Classification System:** A window for gene classification, showing a table with columns for Gene, Family, Pathway, and Category.
- Percellome Project:** A window for data analysis, featuring a "Group average Data" section with a list of data types (Group average Data, Group SD Data, Group Median Data, Individual Data, Graph) and a "Species" dropdown menu set to "Mouse".

What can I do?

Nandi as the gate-keeper gadget can provide a starting point with a pre-defined set of analytics



The screenshot displays the Nandi File Gateway interface. At the top left is the Nandi logo (a blue bull head) and the text "NANDI FILE GATEWAY". A search bar contains the text "What do you want to do?". A dropdown menu is open, listing several analytics options: "Show All gadgets", "Analyze a list of Ensemble gene symbols", "Simulate dynamic models", "Analyze a list of Genes symbols", "View and Analyze pathways", "Simulate Physiology Models", "View and analyze KEGG pathways", "Show All gadgets", and "View experimental data for a list of genes". Below the dropdown is a "Garuda Discovery Engine" section with a message: "Garuda has not discovered any Gadgets yet. Please load a file, choose a content and click Discover." A "Discover on GARUDA" button is visible in the bottom right of the interface.



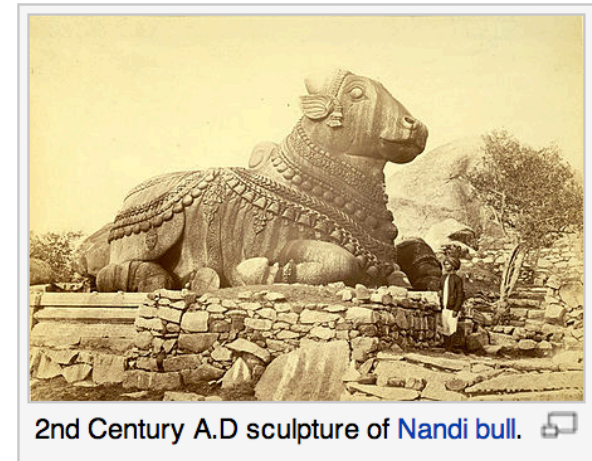
Myth Tip: Nandi

Nandi (bull)

From Wikipedia, the free encyclopedia

Nandi (**Sanskrit**: नन्दी, **Tamil**: நந்தி, **Telugu**: నంది) is the name for the **bull** which serves as the mount (**Sanskrit**: *Vahana*) of the god **Shiva** and as the gate keeper of Shiva and **Parvati**. In **Hindu** mythology, he is the chief guru of eighteen masters (18 siddhas) including **Patanjali** and **Thirumular**.^[1] Temples venerating Shiva display stone images of a seated Nandi, generally facing the main shrine. There are also a number of temples dedicated solely to Nandi.

The application of the name Nandi to the bull (**Sanskrit**: *vṛṣabha*) is in fact a development of recent centuries, as Gouriswar Bhattacharya has documented in an illustrated article entitled "Nandin and Vṛṣabha".^[2] The name Nandi was earlier widely used instead for an anthropomorphic deity who was one of Shiva's two door-keepers, the other being **Mahākāla**. The doorways of pre-tenth-century North Indian temples are frequently flanked by images of Mahākāla and Nandi, and it is in this role of Shiva's watchman that Nandi figures in **Kālidāsa**'s poem the *Kumārasambhava*.



2nd Century A.D sculpture of **Nandi bull**. 

What can I do?

Perform enrichment analysis
on a list of Ensemble gene identifiers

NANDI FILE GATEWAY

What do you want to do? ?

Analyze a list of Genes

Load Your Data

Load Sample Files File Content

File List

ensemble

EGFR.xml

EnsembleGenelist.csv

EnsembleGenelist.txt

Expression_reacome.txt

GeneSymbols.txt

HodgkinHuxley_1952_neuron_model.xml

M-Phase.xml

MAPK.xml

TLR.xml

Garuda Discovery Engine

Biocompendium A...

Garuda discovered 1 gadgets which can process the selected data file.
Double click to send file to a gadget and launch it.

bioCompendium

Drop a list of Ensemble Ids (txt or csv) or double click to type

Search for Gene name.

Garuda

Ensemb Gene Id	KEGG Pathway ID	KEGG Pathway Name	Adjusted P-Value	Gene Name	KEGG Gene Id
ENSG00000103653	hsa03040	Spliceosome	5.1746e15	DHX8	hsa:1659
ENSG00000174021	hsa03040	Spliceosome	5.1746e15	EFTUD2	hsa:9343
ENSG00000124939	hsa03040	Spliceosome	5.1746e15	SF3B1	hsa:23451
ENSG00000110347	hsa03040	Spliceosome	5.1746e15	SNRPA1	hsa:6627
ENSG00000005483	hsa03040	Spliceosome	5.1746e15	SNRPF	hsa:6636
ENSG00000142168	hsa03040	Spliceosome	5.1746e15	CWC15	hsa:51503
ENSG00000086062	hsa03040	Spliceosome	5.1746e15	U2AF1	hsa:7307
ENSG0000004897	hsa03040	Spliceosome	5.1746e15	SLU7	hsa:10569
ENSG00000102189	hsa03040	Spliceosome	5.1746e15	HNRNPK	hsa:3190
ENSG00000119820	hsa03040	Spliceosome	5.1746e15	PLRG1	hsa:5356
ENSG00000167272	hsa03040	Spliceosome	5.1746e15	PRPF8	hsa:10594
ENSG00000163806	hsa03040	Spliceosome	5.1746e15	PRPF8	hsa:10594
ENSG00000178667	hsa03040	Spliceosome	5.1746e15	PRPF8	hsa:10594
ENSG00000171566	hsa03040	Spliceosome	5.1746e15	PRPF8	hsa:10594
ENSG00000147180	hsa03040	Spliceosome	5.1746e15	PRPF8	hsa:10594
ENSG00000198399	hsa03040	Spliceosome	5.1746e15	PRPF8	hsa:10594
ENSG00000053524	hsa03040	Spliceosome	5.1746e15	PRPF8	hsa:10594
ENSG00000087086	hsa03040	Spliceosome	5.1746e15	PRPF8	hsa:10594
ENSG00000103546	hsa03040	Spliceosome	5.1746e15	PRPF8	hsa:10594
ENSG00000135476	hsa03040	Spliceosome	5.1746e15	PRPF8	hsa:10594
ENSG00000060491	hsa03040	Spliceosome	5.1746e15	PRPF8	hsa:10594
ENSG00000171067	hsa03040	Spliceosome	5.1746e15	PRPF8	hsa:10594
ENSG00000112493	hsa03040	Spliceosome	5.1746e15	PRPF8	hsa:10594
ENSG00000151576	hsa03040	Spliceosome	5.1746e15	PRPF8	hsa:10594
ENSG00000166226	hsa04114	Oocyte meiosis	6.2973e07	CDC27	hsa:996
ENSG00000166851	hsa04114	Oocyte meiosis	6.2973e07	AURKA	hsa:6790
ENSG00000141540	hsa04114	Oocyte meiosis	6.2973e07	FBX05	hsa:26271

Search

All queries finished.

1. Choose Ensemble gene from sample data and discover **BioCompendium** gadget
2. Click **Search** to perform enrichment analysis on BioCompendium

What can I do?

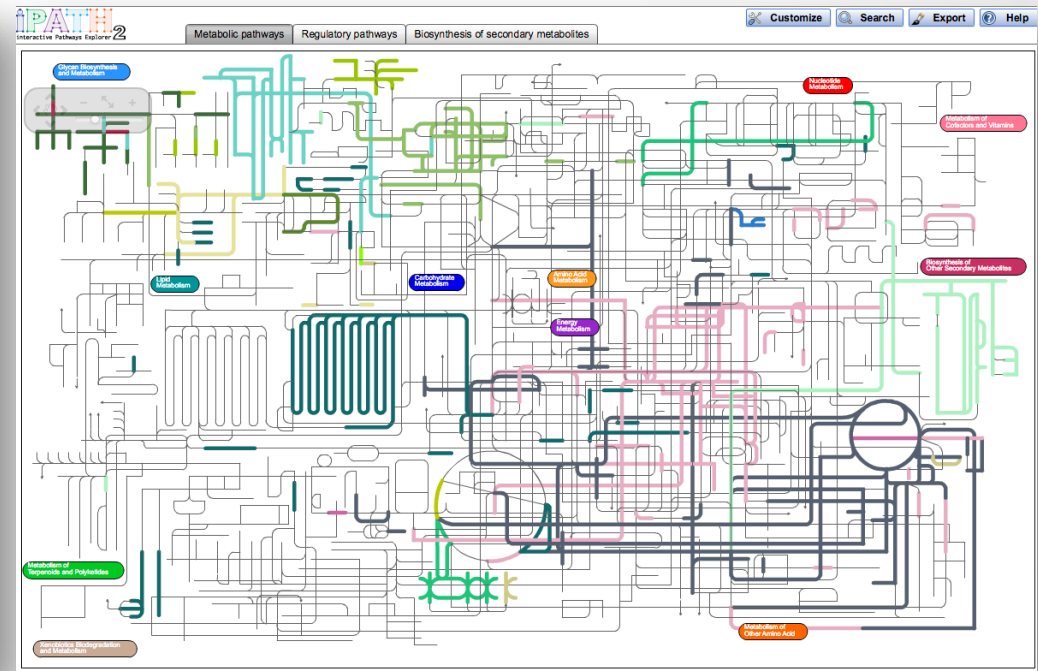
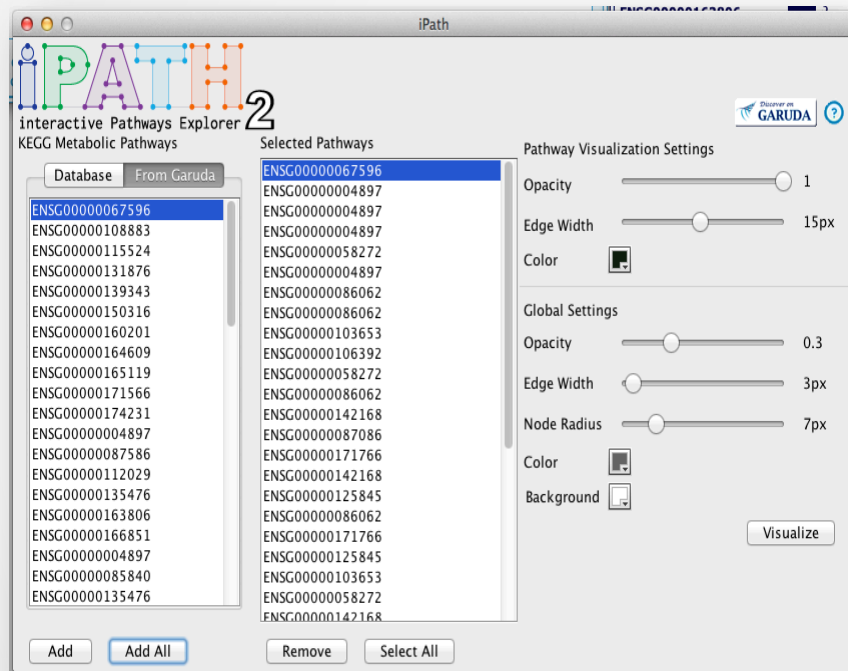
Continue the analysis for pathway enrichment by clicking on **Garuda Discover** and selecting **iPath gadget**

The screenshot shows the bioCompendium interface. On the left, there is a list of genes with IDs such as ENSG00000103653, ENSG00000174021, etc. Below the list is a 'Search' button. The main area displays a table of pathways with columns for 'Ensemb Gene Id', 'KEGG Pathway ID', 'KEGG Pathway Name', and 'Adjusted P-Value'. The table lists several 'Spliceosome' pathways with a p-value of 5.1746e15 and 'Oocyte meiosis' pathways with a p-value of 6.2973e07. On the right, a sidebar contains the GARUDA logo and a 'Gadgets' section with 'Nandi File Gateway' and 'iPath' options. A 'Close on Disconnect' checkbox is checked at the bottom of the sidebar. At the bottom of the main window, it says 'All queries finished.'

Ensemb Gene Id	KEGG Pathway ID	KEGG Pathway Name	Adjusted P-Value
ENSG0000006759	hsa03040	Spliceosome	5.1746e15
ENSG0000010888	hsa03040	Spliceosome	5.1746e15
ENSG0000011552	hsa03040	Spliceosome	5.1746e15
ENSG0000013187	hsa03040	Spliceosome	5.1746e15
ENSG0000013934	hsa03040	Spliceosome	5.1746e15
ENSG0000015031	hsa03040	Spliceosome	5.1746e15
ENSG0000016020	hsa03040	Spliceosome	5.1746e15
ENSG0000016460	hsa03040	Spliceosome	5.1746e15
ENSG0000016511	hsa03040	Spliceosome	5.1746e15
ENSG0000017156	hsa03040	Spliceosome	5.1746e15
ENSG0000017423	hsa03040	Spliceosome	5.1746e15
ENSG0000000489	hsa04114	Oocyte meiosis	6.2973e07
ENSG0000008758	hsa04114	Oocyte meiosis	6.2973e07
ENSG0000011202	hsa04114	Oocyte meiosis	6.2973e07

What can I do?

Continue the analysis for pathway enrichment by clicking on **Garuda Discover** and selecting **iPath gadget**



1. Configure KEGG pathways on iPath gadget

2. Click **Visualize** to view on browser



Navigability Tip

To navigate from one gadget to next, locate the “Discover on Garuda” button and click to show Garuda Panel

The screenshot shows the Biomodels Database interface. The 'Models' table is visible on the left, and the 'Details' panel is on the right. A red circle highlights the 'Discover on Garuda' button in the top right corner of the interface.

The screenshot shows the Biomodels Database interface with the Garuda Panel open on the right side. The panel contains a list of gadgets: Flint, Nandi File Gateway, SBMLsimulator, CellDesigner, SBMLsqueezer, and Cytoscape 3.0.0. A red arrow points to the 'Discover on Garuda' button, and another red arrow points to the Garuda Panel. A red box contains the text: "Double click on a gadget to send data and continue your work flow". A red arrow points to the Garuda Panel with the text: "Garuda panel". A red box contains the text: "Ctrl-alt-G will bring up the Garuda Panel".

Cntrl + Alt + G also brings the Garuda Panel
Click anywhere outside the panel to hide it

What can I do?

I have a list of Gene Symbols.
What kind of analytics can I perform?

NANDI FILE GATEWAY

What do you want to do? **Analyze a list of Genes symbols**

Load Your Data

Load Sample Files File Content

File List toggle to view contents of selected file

EGFR.xml
EnsembleGenelist.csv
EnsembleGenelist.txt
GeneSymbols.txt
PhysiologyModel_HodgkinHuxley_1952_neuron_model.xml
SimulationModel.xml
TLR.xml

genelist

Garuda Discovery Engine

PANTHER Classification System

DNA OMICS DISEASE GENES

Discover on GARUDA

Panther Database Knowledge Integrat...Pathway Logic Gad...

Garuda discovered 3 gadgets which can process the selected data file. Double click to send file to a gadget and launch it.

1. Choose this question

2. Choose sample file or load your own gene symbols

3. Choose gene list from dropdown

4. Choose this question



Perform enrichment analysis



Explore semantic enrichment



Explore literature mining

Tip: If no results are found, choose "Show All gadgets" from question list and click Discover again!

What can I do?



Panther gadget performs enrichment across genes, families, pathways and GO category

The screenshot displays the PANTHER Classification System interface. On the left, a vertical list of gene symbols is shown, with 'CRH' selected. The main area displays a table of results for the selected gene, showing Gene Accession, Gene Name, and Gene Symbol. The table is as follows:

Gene Accession	Gene Name	Gene Symbol
DICDI dictyBase=DDB_G0289067 U niProtKB=Q54I18	Suppressor of Mek1	SMEK
DICDI dictyBase=DDB_G0281649 U niProtKB=Q54TN4	Probable serine/threonine-protein	MKCE
DICDI dictyBase=DDB_G0273399 U niProtKB=Q557I6	MEK1 interacting protein 1	Q557I6
RAT RGD=61888 UniProtKB=F1LMI4	Dual-specificity mitogen-activated protein	F1LMI4
DICDI dictyBase=DDB_G0269152 U niProtKB=Q55CL6	Dual specificity mitogen-activated protein	MP2K1
RAT RGD=70495 UniProtKB=Q0198 6	Dual specificity mitogen-activated protein	MP2K1
CHLRE ENTREZ=5726354 UniProtKB =A8I6E0	Predicted protein	A8I6E0
CHLRE ENTREZ=5718079 UniProtKB =A8IUA4	Predicted protein	A8IUA4
DICDI dictyBase=DDB_G0268550 U niProtKB=Q55FV5	Probable serine/threonine-protein	Y8550
CIOIN ENSEMBL=ENSCING00000023 510 UniProtKB=H2Y2V1	Uncharacterized protein	H2Y2V1
RAT RGD=1307318 UniProtKB=D3Z A65	Protein Stk36	D3ZA65
CHLRE ENTREZ=5722233 UniProtKB =A8HYY7	Mitogen-activated protein kinase kinase 1	A8HYY7
CHLRE ENTREZ=5722831 UniProtKB =A8J6U8	Predicted protein	A8J6U8
CHLRE ENTREZ=5722315 UniProtKB =A8J4U2	Predicted protein	A8J4U2

At the bottom of the interface, a status bar indicates: "Retrieving results for CRH . 40 item(s) left in queue." with a progress indicator.

What can I do?



Knowledge Integration uses the Wolfram Alpha semantic engine API to retrieve enriched information on genes

A screenshot of the Wolfram Alpha Knowledge Integration interface. The search bar contains 'MEK1'. Below the search bar is a list of search terms, with 'MEK1' selected. To the right, the search results are displayed in a structured format. The first section is 'Location', followed by 'Reference sequence' which shows the DNA sequence: 'AGGCGAGGCTTCCCCTTCCCGGCCCTCCCGGGCCTCCA ... AAATATACTATGAAATAAAAAAAAAAAGGATGAAAGCTA'. Below this is 'Reference sequence length', 'Nearby genes' which shows a diagram of the MAP2K1 gene and its neighbors RPL9P25 and SNAPC5, and 'Gene splicing structure'. The interface is titled 'Knowledge Integration' and includes the Wolfram Alpha logo and a 'GARUDA Discover on Gateway' button.

Note: Knowledge Integration requires an API key registration to work
It will not launch on Mac OSX 10.6 or below

What can I do?



Pathway Logic performs specific search on curated literature and logical connections derived from the data

The image displays two screenshots of the Pathway Logic Gadget software interface. The left screenshot shows the main window with a list of proteins on the left and details for 'Asap1' on the right. The right screenshot shows a search results window for 'Asap1 all'.

Pathway Logic Gadget - Main Window

Introduction | PLA Online | PLA Datums | Search all for Asap1

ArhGef7
Arl1
Arl2
Arnt
Arrb1
Arrb2
Artemis
Asap1
Asap2
Ask1
Atf1
Atf2
Atf3
Atg10
Atg12
Atg3
Atg5
Atg7
Atm
Atp1a1
Atp6V0c
Atp6V0d1

Asap1

Uniprot: Q9ULH1
Hugosym: ASAP1
Synonyms:

- Arf-GAP with domain-conta
- 130-kDa pho
- ARF1 GAP
- PIP2-depende
- ADP-ribosyla
- protein 1
- ARF GTPase
- Development
- Paxillin-assoc
- PAG2
- ASAP1
- KIAA1249
- PAPalpha
- ASAP1_HUM

Status: Select one of the 1204 proteins to proceed.

Pathway Logic Gadget - Search Results Window

Introduction | PLA Online | PLA Datums | Search all for Asap1

Asap1 all

1. Asap1[Ab] copptby[WB] Reps2[Ab] is detectable
cells: CHO in BMS
Source: [12149250-Fig-2a](#)
2. xAsap1[tAb] copptby[WB] xPxn[GST] is detectable
cells: CHO in BMS
unaffected by: xReps2 [addition]
Source: [12149250-Fig-6a](#)
3. xAsap1[tAb] copptby[WB] xRalbp1[tAb] is detectable
cells: CHO in BMS
enhanced by: xReps2 [addition]
inhibited by: xReps2(P423A/P426A) [addition]
Source: [12149250-Fig-5b](#)
4. xAsap1[tAb] copptby[WB] xReps2[tAb] is detectable
cells: CHO in BMS
inhibited by: xReps2(P423A/P426A) [substitution]
Source: [12149250-Fig-4c](#)
5. xReps2[Ab] copptby[WB] xAsap1[Ab] is detectable

Dismiss

Status: Select one of the 1204 proteins to proceed.

What can I do?

Simulate biochemical models based on Ordinary Differential Equations to study molecular dynamics

The screenshot displays the NANDI FILE GATEWAY interface. At the top left is the NANDI logo (a blue bull) and the text "NANDI FILE GATEWAY". Below the logo is a search bar with the text "What do you want to do?" and a question mark icon. A blue bar below the search bar contains the text "Simulate dynamic models".

Below the blue bar, there are two buttons: "Load Your Data" and "Load Sample Files". To the right of "Load Your Data" is a "File Content" dropdown menu showing "sbml".

The main area is a "File List" table with a plus icon on the left and a list icon on the right. The table contains the following files:

File List
EGFR.xml
EnsembleGenelist.csv
EnsembleGenelist.txt
GeneSymbols.txt
KEGGList.txt
M-Phase.xml
PhysiologyModel_HodgkinHuxley_1952_neuron_model.xml
SimulationModel.xml
TLR.xml

Below the file list is a "Garuda Discovery Engine" section. It features a row of six icons representing different simulation tools:

- Flint
- SBMLsimulator
- PhysioDesigner
- CellDesigner
- SBMLsqueezer
- Cytoscape 3.0.0

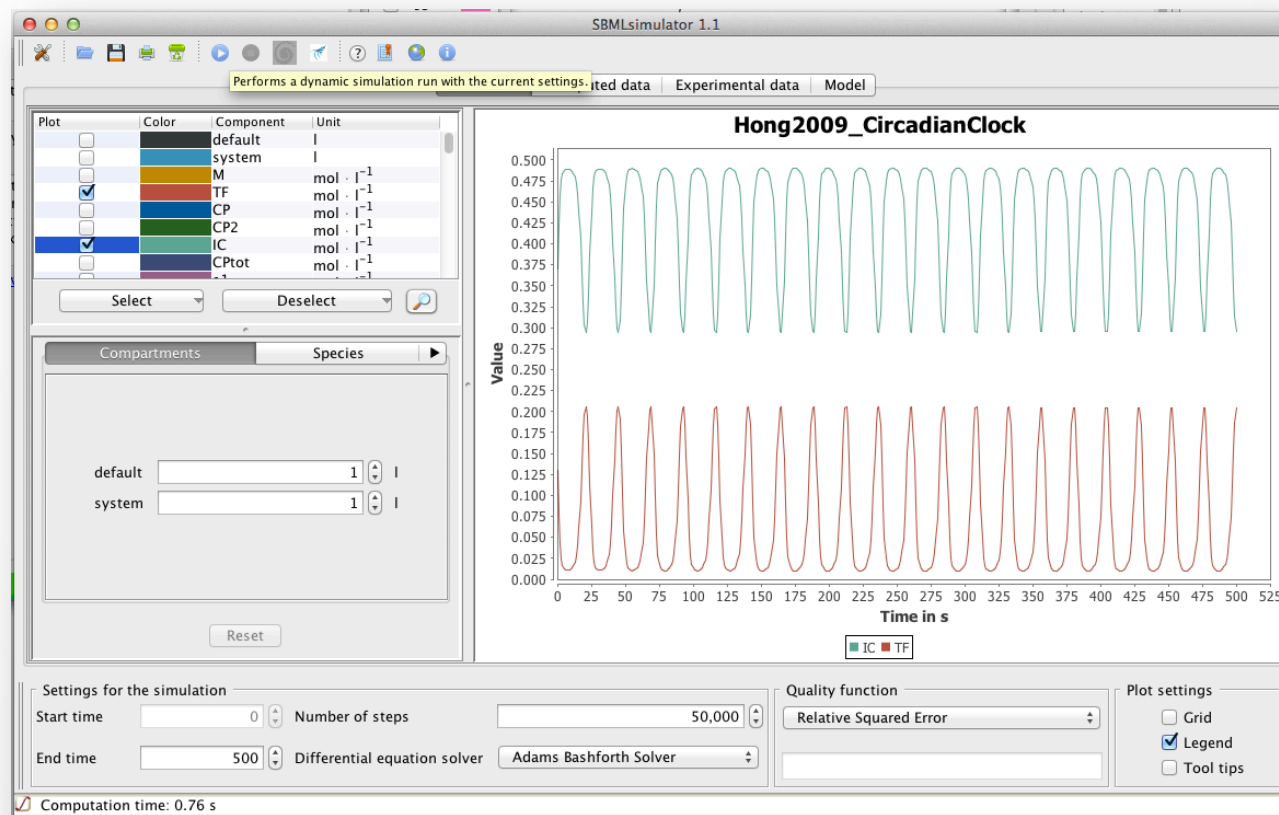
At the bottom of the interface, a message states: "Garuda discovered 6 gadgets which can process the selected data file. Double click to send file to a gadget and launch it."

What can I do?

Compare simulation results for a single biochemical model across different engines by using the different gadgets



Simulate the model using **SBML Simulator**

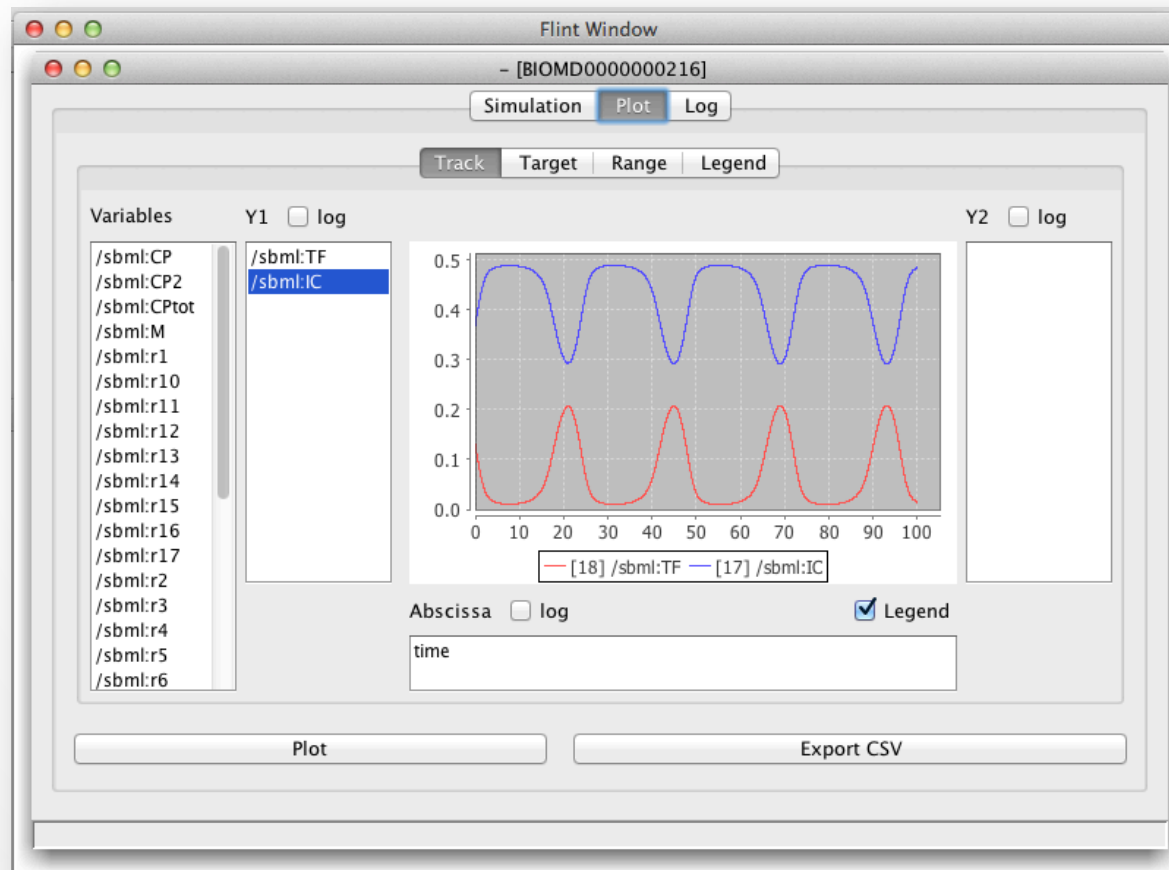


What can I do?

Compare simulation results for a single biochemical model across different engines by using the different gadgets



Simulate the model using **Flint**

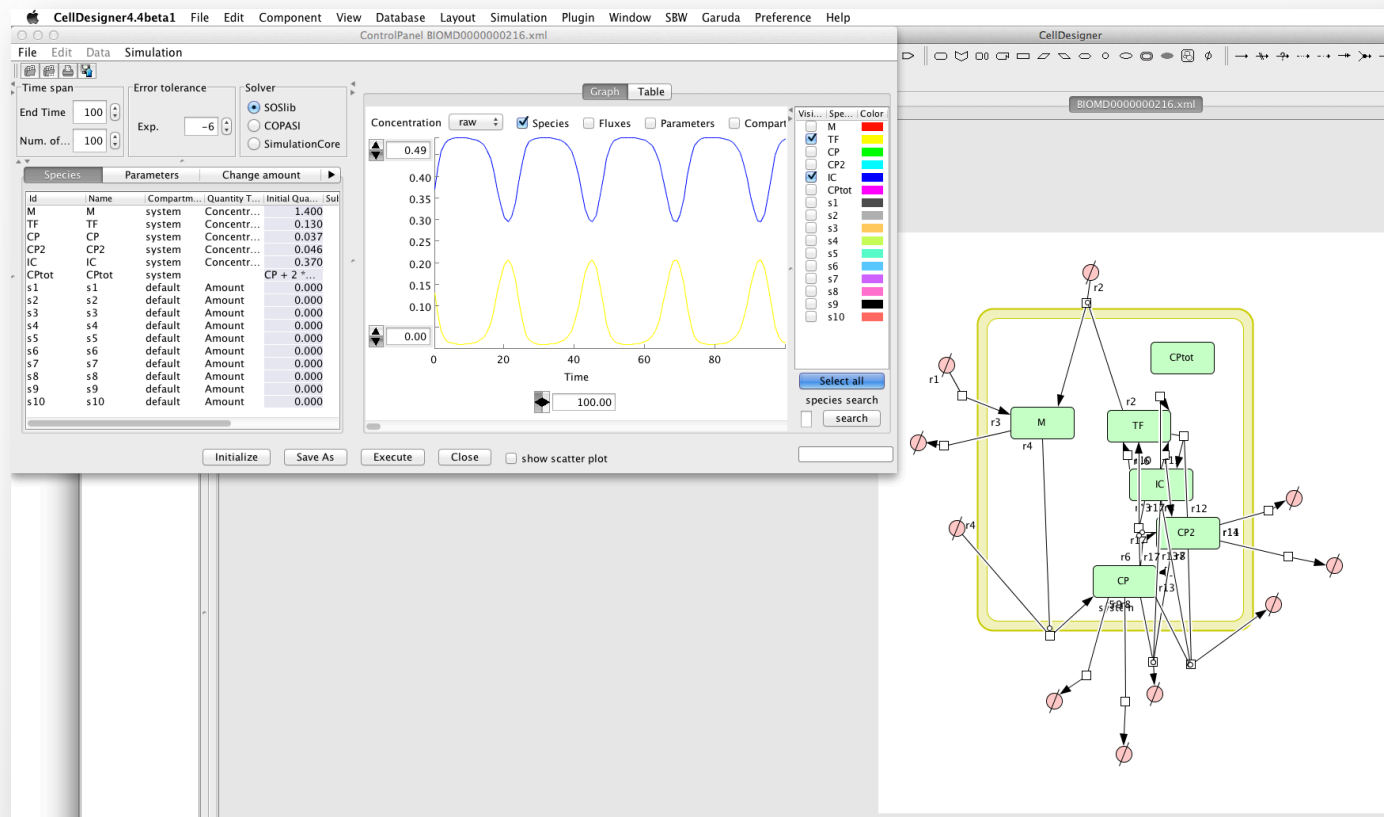


What can I do?

Compare simulation results for a single biochemical model across different engines by using the different gadgets



Visualize the model in **CellDesigner** and simulate using the **in-built simulators**



What can I do?

How can I simulate Physiological Models?

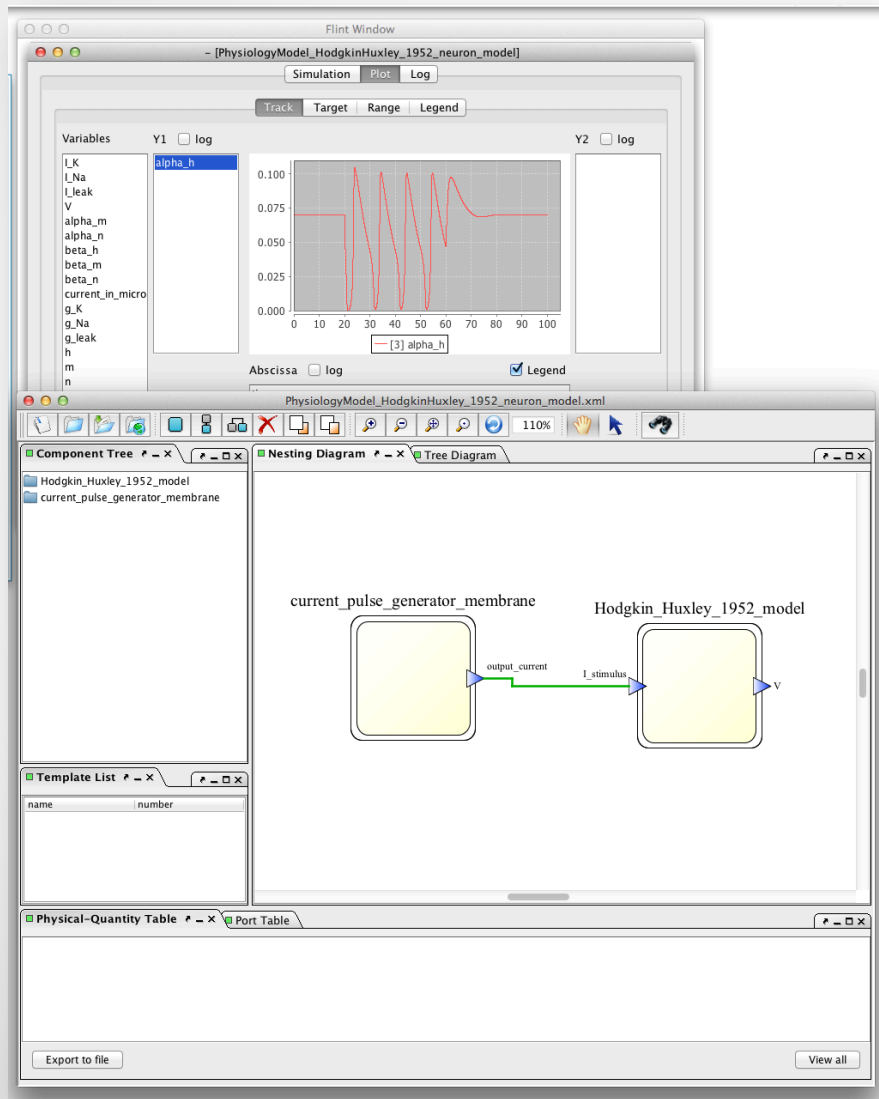


1. Load your own model (e.g. PHML file) or choose *Hodgkin Huxley model* from Sample data.
2. Choose “**Simulate Physiology Models**” from question list
3. Click **Discover** button to discover **Physiodesigner** and **Flint** gadgets



What can I do?

How can I simulate Physiological Models?



- Launch **PhysioDesigner** to view, edit the model
- **Flint** can be launched from PhysioDesigner

* For simulation only, choose Flint



Garuda Pipeline

Garuda Pipeline

Pipelines of gadgets in Garuda are built dynamically depending on the data and analytics workflow

I have a gene list and I want to -

Find information on genes



Gene list



Knowledge Xplorer

Gene exploration pipe

View expression patterns



Gene list



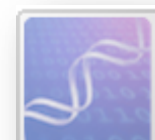
Percellome

Gene expression analysis pipe

Perform gene and pathway enrichment



Gene list



BioCompendium



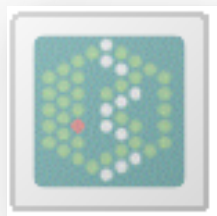
iPath

Enrichment pipe

Garuda Pipeline

Build and explore complex analytics pipelines

I want to view a published mathematical model, visualize and simulate its dynamics, then analyze network properties



BioModels



CellDesigner



Cytoscape

Model ID: BIOMD000000391, BIOMD000000385, BIOMD000000386, BIOMD000000393, BIOMD000000388, BIOMD000000054, BIOMD000000401, BIOMD000000402, BIOMD000000403, BIOMD000000347, BIOMD000000242, BIOMD000000071, BIOMD000000296, BIOMD000000413, BIOMD000000414, BIOMD000000197, BIOMD000000272, BIOMD000000271, BIOMD000000368, BIOMD000000369, BIOMD000000374, BIOMD000000377, BIOMD000000373, BIOMD000000128, BIOMD000000376, BIOMD000000062, BIOMD000000254, BIOMD000000058, BIOMD000000375, BIOMD000000077, BIOMD000000043, BIOMD000000044, BIOMD000000045, BIOMD000000223, BIOMD000000086, BIOMD000000052, BIOMD000000343, BIOMD000000404, BIOMD000000200, BIOMD000000033, BIOMD000000217, BIOMD000000332

Model Name: Arnold2011_Poolman2000_Calvin..., Arnold2011_Schultz2003_Rubisco..., Arnold2011_Sharky2007_Rubisco..., Arnold2011_Zhu2007_CalvinCycle..., Arnold2011_Zhu2009_CalvinCycle..., Ataulhkhani1996_Adenylate..., Ayatz2010_BoneRemodelingDynam..., Ayatz2010_BoneRemodelingDynam..., Ayatz2010_BoneRemodelingDynam..., Bachmann2011_LJAK2-STAT5_See..., Bal2003_C1ghaseRegulation..., Bakker2001_Clycolysis..., Balagadda2008_E_coli_Predator_P..., Rand2012_Dll-Venus_FullModel..., Rand2012_Dll-Venus_ReducedMo..., Bartholome2007_MDCkII..., Becker2010_EpR_AuxiliaryModel..., Becker2010_EpR_CoreModel..., Beltrami1995_Thrombogenesis..., Beltrami1995_Thrombogenesis..., Bertram1995_PancreaticBetaCell_C..., Bertram2000_PancreaticBetaCell..., Bertram2004_PancreaticBetaCell..., Bertram2006_Endothelin..., Bertram2007_JuxtCell_Oscillations..., Bharava2003_Tryptophan_operon..., Bier2000_GlycolyticOscillation..., Bindshchaler2001_coupled_Ca_os..., Birnstiel2007_ErbB_Signalling..., Blum2000_Interaction_1..., Borghans1997_CaOscillation_model1..., Borghans1997_CaOscillation_model2..., Borghans1997_CaOscillation_model3..., Borsovsz2009_EGF_insulin_Crosstalk..., Bornheim2004_CTPaseCycle..., Brands2002_MonosaccharideCasein..., Brannmar2010_InsulinSignalling..., Bray1993_chemotaxis..., Bray1995_chemotaxis_receptor..., Brown2004_MCF_EGF_signaling..., Bruggeman2005_AminonutrientAssim..., Bruggeman2005_AminonutrientAssim...

PubMed ID: 18004277
Model Name: Birnstiel2007_ErbB_Signalling
Last Modified: 21 Apr 2009 20:13:48 UTC
Title: Ligand-dependent responses of the ErbB signaling network: experimental and modeling analyses.
Authors: Birnstiel MR, Hatakeyama M, Yumoto N
Journal: Molecular systems biology
Date: 2007
Abstract: Deregulation of ErbB signaling plays a key role in the progression of multiple human cancers. To help understand ErbB signaling quantitatively, in this work we combine traditional experiments with computational modeling, building a model that describes how stimulation of all four ErbB
URL: <http://www.ncbi.nlm.nih.gov/pubmed/18004277>

Compatible softwares
Please select software to send to.
Flint
Demo Gadget A
PhysioDesigner
CellDesigner
Dunnart
Demo Gadget B
Demo Gadget C
Arena3D

CellDesigner4.3Garuda1 File Edit Component View Database Layout Simulation Plugin Window SWW Control Preference Help

Model: BIOMD000000175.xml
Send SBML to: Flint, Demo Gadget A, PhysioDesigner, Dunnart, Demo Gadget B, Demo Gadget C, Arena3D, Cytoscape 3.8.0

Model: BIOMD000000175.xml
Layer: base

Simulation
Time span: 100.00
End Time: 100.00
Exp. #: 4
Error tolerance: 1e-06
Num. of: 100.00
Simulation Core

Parameters
Change amount

ID	Name	Component	Quantity	Initial Value
E1	ErbB	membrane	Amount	274.0
E2	ErbB	membrane	Amount	134.0
E3	ErbB	membrane	Amount	294.0
E4	ErbB	membrane	Amount	398.0
E11	EGF	membrane	Amount	0.0
E12	EGF	membrane	Amount	0.0
E13	EGF	membrane	Amount	0.0
E14	EGF	membrane	Amount	0.0
E15	EGF	membrane	Amount	0.0
E16	EGF	membrane	Amount	0.0
E17	EGF	membrane	Amount	0.0
E18	EGF	membrane	Amount	0.0
E19	EGF	membrane	Amount	0.0
E20	EGF	membrane	Amount	0.0
E21	EGF	membrane	Amount	0.0
E22	EGF	membrane	Amount	0.0
E23	EGF	membrane	Amount	0.0
E24	EGF	membrane	Amount	0.0
E25	EGF	membrane	Amount	0.0
E26	EGF	membrane	Amount	0.0
E27	EGF	membrane	Amount	0.0
E28	EGF	membrane	Amount	0.0
E29	EGF	membrane	Amount	0.0
E30	EGF	membrane	Amount	0.0
E31	EGF	membrane	Amount	0.0
E32	EGF	membrane	Amount	0.0
E33	EGF	membrane	Amount	0.0
E34	EGF	membrane	Amount	0.0
E35	EGF	membrane	Amount	0.0
E36	EGF	membrane	Amount	0.0
E37	EGF	membrane	Amount	0.0
E38	EGF	membrane	Amount	0.0
E39	EGF	membrane	Amount	0.0
E40	EGF	membrane	Amount	0.0

Concentration (µM) vs Time (min)

Species search

Session: New Session

Control Panel: Network, VizMapper, Filters

Network: BIOMD000000175.xml
Nodes: 222(0)
Edges: 463(0)

Results Panel: Network Statistics of BIOMD000000175.xml

Shortest Path Length Distribution

Path length	Frequency
1	2.0
2	3.0
3	6.0
4	9.0
5	10.0
6	8.0
7	5.0
8	3.0
9	2.0
10	1.0
11	1.0
12	1.0

Shared Neighbors Distribution

Chart Settings: Enlarge Chart, Change Range, Export Chart, Export Data, Help

Table Panel: BIOMD000000175.xml

Node Table

Backup



Garuda Architecture



Garuda Concepts

Provide a consistent end user experience through Dashboard interface



Build custom workflows catering to specific disease areas



Custom-made "gadgets" to provide cross-platform functionalities



Rich set of Garuda API across different software and databases



Platform Principles

1. Provide **end-users** with a **single platform** for implementing their varied biological workflows
 1. Each workflow constitutes different **software modules** to implement specific functions
 2. Users can download, install and use the modules from the single platform interface
 3. The platform should support **inter-operability** of Garuda powered software tools and services
2. Provide **developer community** with a set of APIs, UX guidelines and manuals to develop their own Garuda Apps by leveraging the APIs to access multiple functions of the Garuda Alliance tools and services
 1. Provide Garuda APIs
 2. Provide Garuda UX design guidelines
 3. Provide ease of testing Apps and enabling them on the Garuda Platform for the end-users

Platform Principles

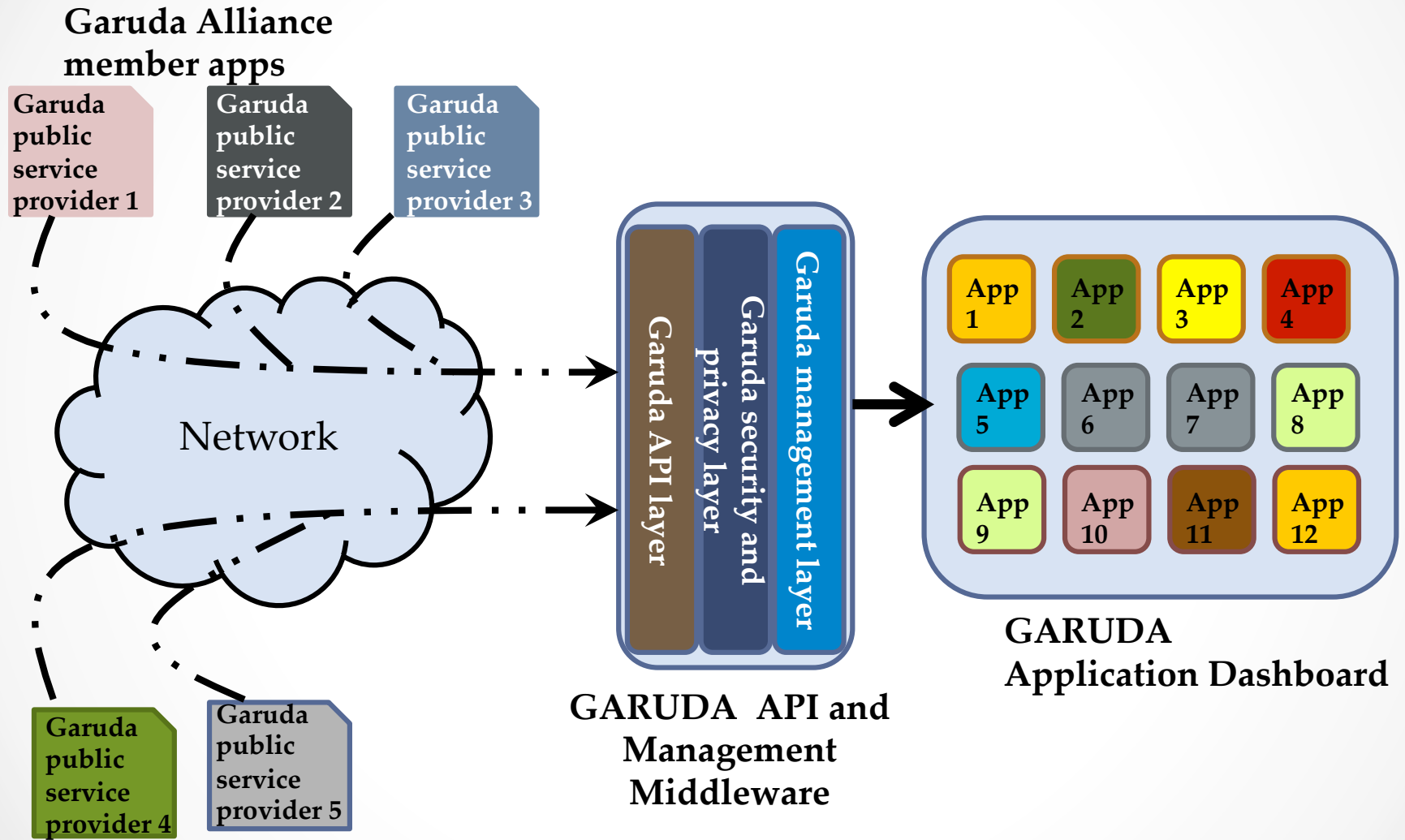
End-Users

1. **Plug and Play (PnP)** architecture for the deployment of Apps
2. **Zero Configuration** (ZeroConf) installation, maintenance and updates for the end-users

Developers

3. Provide a **secure management and configuration layer** (Garuda Service Layer) to all Garuda powered tools and services to facilitate deployment and use of Garuda gadgets
4. Free the developer of book-keeping and management layer functionalities for enabling their gadgets on the Garuda Platform

Platform Architecture



- Garuda Alliance member apps

Platform Stack

Core Components

1. API

1. The Garuda API should provide a clean and consistent interface to the functionalities of the Alliance software and services
3. It should also provide the interface to the Alliance members to enable their software and services to comply and use the Garuda Platform

2. Management Services Architecture (GSL)

1. Provide the ability to register, manage and maintain Garuda Apps
2. Provide zero-conf broker services to the various Garuda Alliance software for inter-operability and inter-tool communication