Develop an integrated and reliable bioinformatics infrastructure:
Interoperable web services and database resources
Workflow platforms for genome annotation
Visualization of the large scale data sets
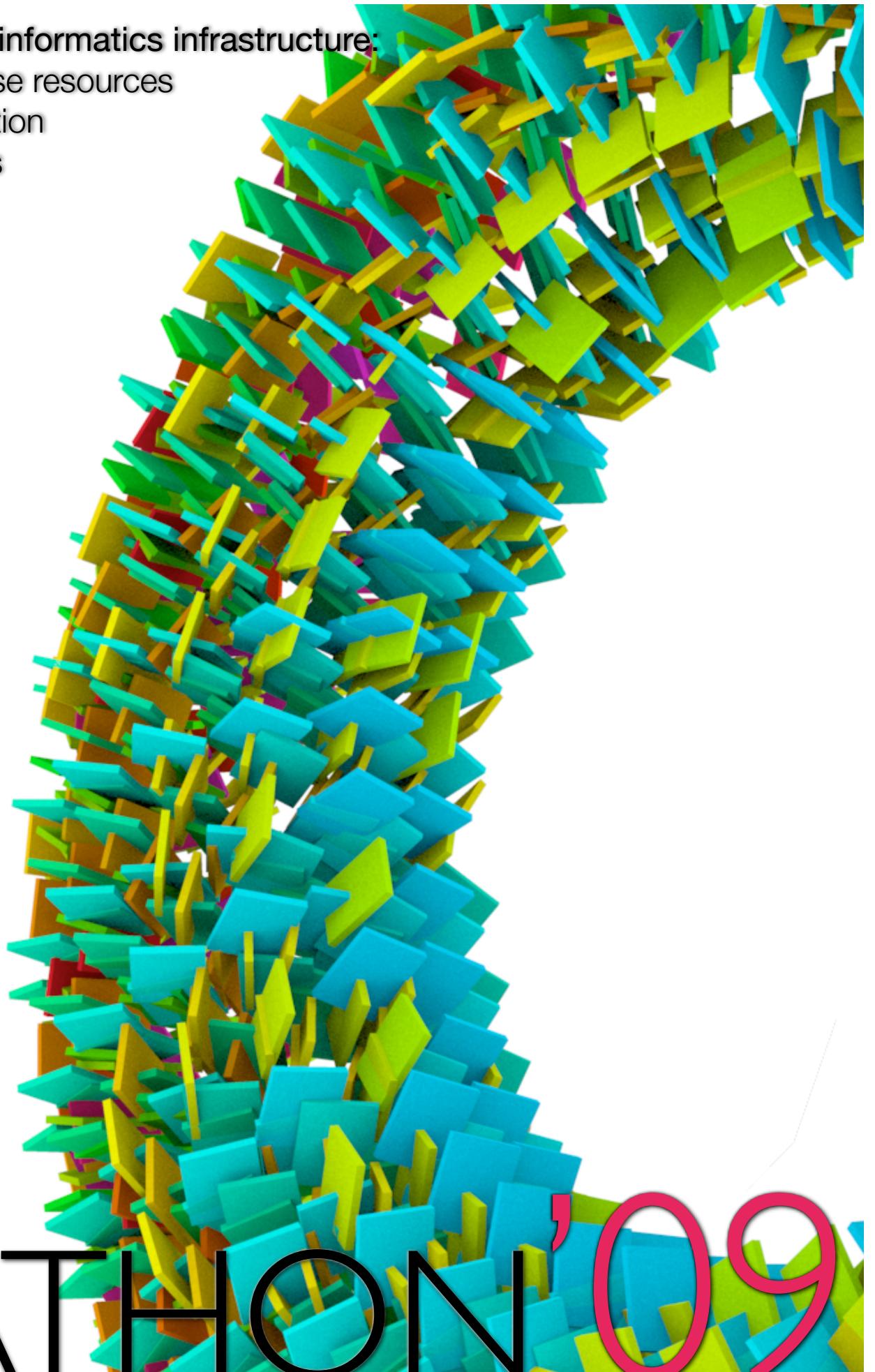
BIO HACKATHON '09

15-21 Mar. 2009
DBCLS Tokyo / OIST Okinawa, Japan

International symposium
Takeda frontier science hall, 9:00 - 12:00 16 Mar. 2009
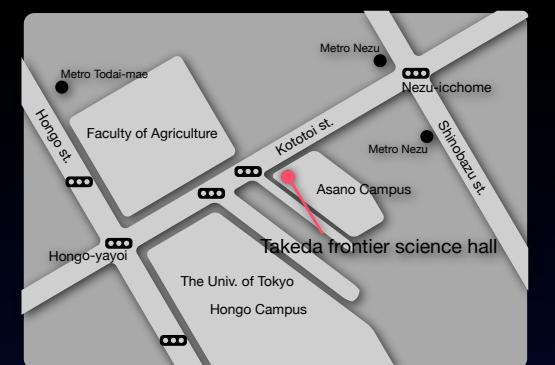
James Taylor	9:20	*Integrated reproducible analysis with Galaxy*
Tobias Gattermayer	9:40	*Biomolecular Function Discovery with the ANNOTATOR*
Jessica Severin	10:00	*Accelerating experimentation and biological discovery within RIKEN OSC LifeScienceAccelerator -- eeDB gLyphs*
Arek Kasprzyk	10:20	*BioMart and third party applications: Working towards better interoperability*
Tom Oinn	10:40	*The Taverna 2 Workflow Engine API : Extensible, High Performance and Easy to Integrate*
Oswaldo Trelles	11:00	*Multi-repository architecture for service integration*
Alberto Labarga	11:20	*Integrating literature and annotation resources: the Elsevier Grand Challenge experience*
Hideaki Sugawara	11:40	*Looking back on a WABI life for tomorrow*

http://hackathon2.dbcls.jp

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