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Automated visualization of multiomics (metabolomics, proteomics, fluxomics and transcriptomics) data on Garuda, a connectivity platform for biological analytics

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Overview

- The purpose of this study is to quickly look the many measurement results obtained and to create new knowledge and hypotheses.
- We developed a pipeline for automated visualization of the multiomics data (metabolomics, proteomics, fluxomics and transcriptomics) on the Garuda platform[1].
- By utilizing the Garuda platform, we succeeded in an easy visualization the four omics data on the metabolic map.

Introduction

Objective

In order to understand biological systems, it has become common to analyze over 100 metabolites. In particular, multiomics analysis which attempts to understand biological systems from multiomics data, has been utilized. With the increase in the number of metabolites and the number of proteins to be analyzed, there is now a big need for a tool to quickly look the many measurement results obtained and to create new knowledge and hypotheses.

We previously reported that we developed a pipeline for automated visualization of the multiomics data combining protein, metabolite and metabolic flux on the Garuda platform that provides the framework to connect, discover, and navigate through different software called "gadgets". This study has made it possible to handle transcriptome data.

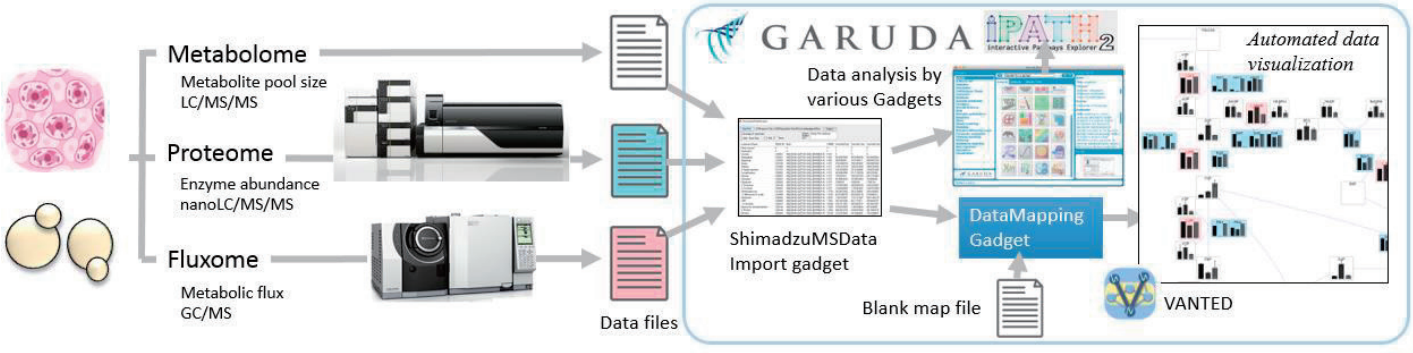

Figure 1 Automated visualization of multiomics data on Garuda

Garuda platform

Garuda is an open, community-driven, and common platform for systems biology, healthcare and beyond.Garuda provides a framework to connect, discover, and navigate through different analytics applications, databases and services (called "gadgets" available on a dashboard).

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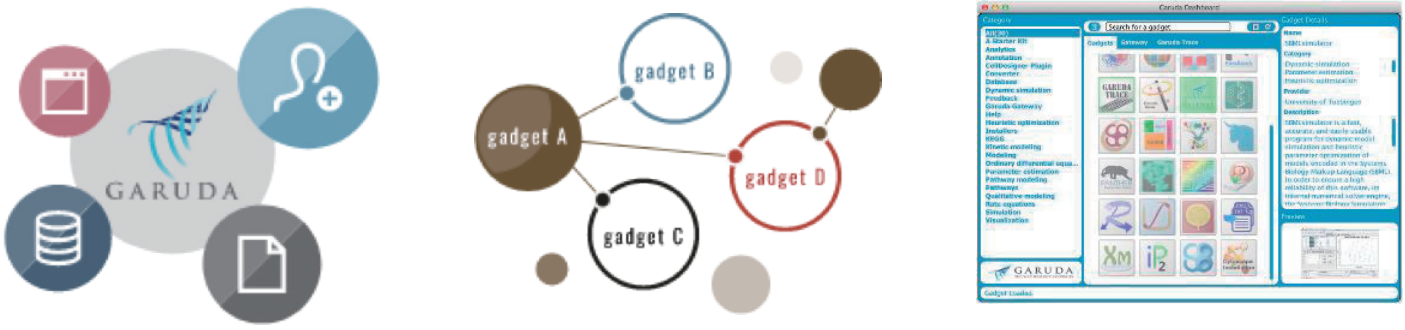


Connections among gadgets

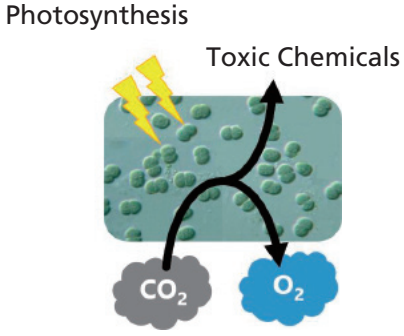
Garuda dashboard

Figure 2 Garuda platform

Methods

Synechocystis sp. PCC 6803

The Synechocystis sp. PCC 6803 strain was cultured under three conditions: 1) the autotorphic condition, 2) the mixotorphic condition and 3) the photoheterotrophic condition (Figure 3). For each condition, the transcriptome, proteome, metabolome and metabolic flux data have been acquired by the Shimizu et al. Group at Osaka University[2,3,4].



Nutritional conditions	photosynthesis	Glucose assimilation
Autotorphic (Auto)	+	-
Mixotorphic (MIxo)	+	+
Photoheterotrophic (Hetero)	-	+

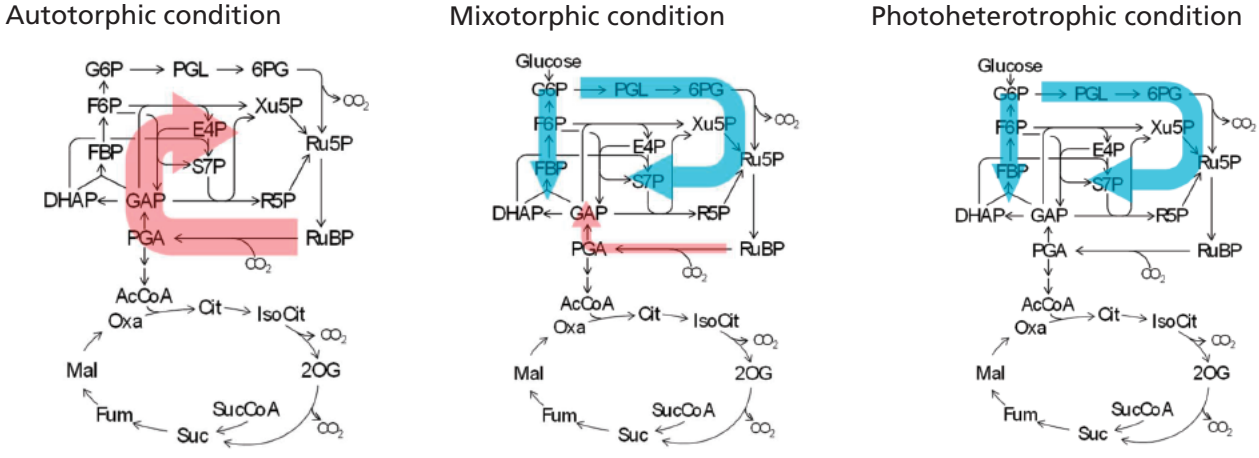


Figure 3 Estimated metabolic flux distribution
(Red arrow : photosynthesis, Blue arrow : glucose assimilation)

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Shimadzu multiomics analysis gadgets

Data import and analytic tools were specifically developed as gadgets on the Garuda platform, namely, the "Shimadzu MS Data Import" and the "Multiomics Data Mapper". Furthermore, these gadgets were connected with downstream gadgets for analysis and visualization by VANTED[5], available freely on the Garuda platform. Similarly, other analysis workflows are realized by connecting iPATH2[6], Cytoscape and Shimadzu multiomics analysis gadgets (Figure 4).

Shimadzu multiomics analysis gadget pack (free version) are now available! Installation guide is available on http://www.garuda-alliance.org/gadgetpack/shimadzu

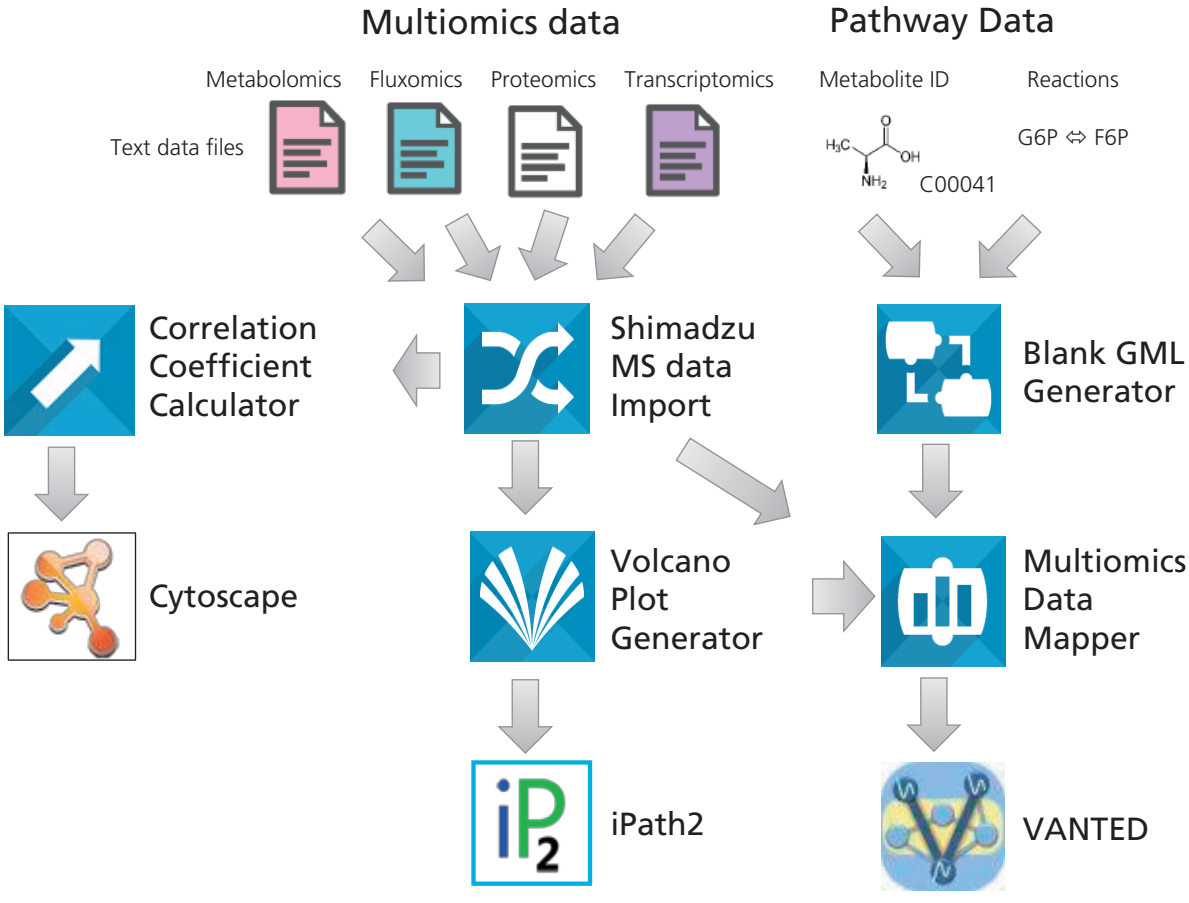

Figure 4 Analysis workflows

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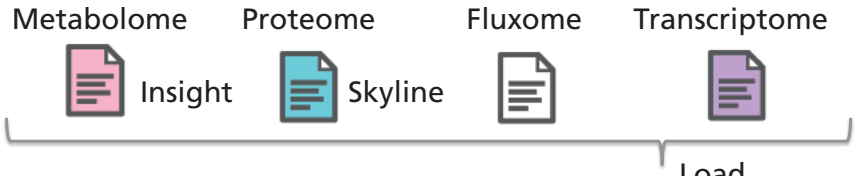
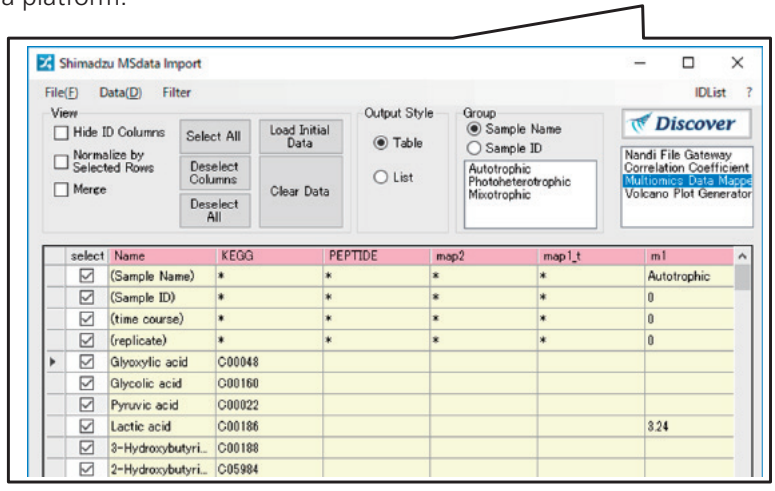
Results

We attempted a visualization of four omics layers using four pieces of data. In addition to the three sets of data (proteome, metabolome and metabolic flux) that could already be visualized, this study has made it possible to handle transcriptome data (Figure 5).



We transformed transcriptome data analyzed by microarray into text format and succeeded in reading with the "Load" function on the "Shimadzu MS Data Import" gadget on the Garuda platform.



The transcriptome, proteome, metabolome and metabolic flux data were read by the "Shimadzu MS Data Import" gadget, respectively, and the integrated data was transferred to the "Multiomics Data Mapper" gadget using the "Discovery" function.

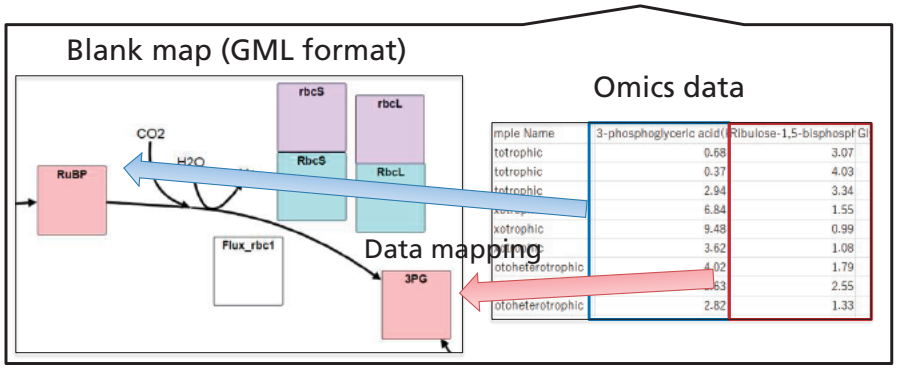


Figure 5 Visualization of four omics layers

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The data was visualized on the metabolic map of the Calvin Benson cycle including the RuBisCO, which is an enzyme involved in the first major step of carbon fixation in terms of photosynthesis (Figure 6).
The carbon fixation catalyzed by RuBisCO (RbcL / RbcS) showed that the metabolic flux (Flux_rbc1) decreased in the order of an autotorphic condition, a mixotorphic condition and a photoheterotrophic condition. The RuBP of the substrate metabolite, the 3PG content of the product and the expression level of the rbcL / rbcS gene encoding the RuBisCO protein did not clearly correlate with the metabolic flux. On the other hand, the change in the expression level of rbcL / rbcS, which is a RuBisCO protein, was similar to the change in metabolic flux.

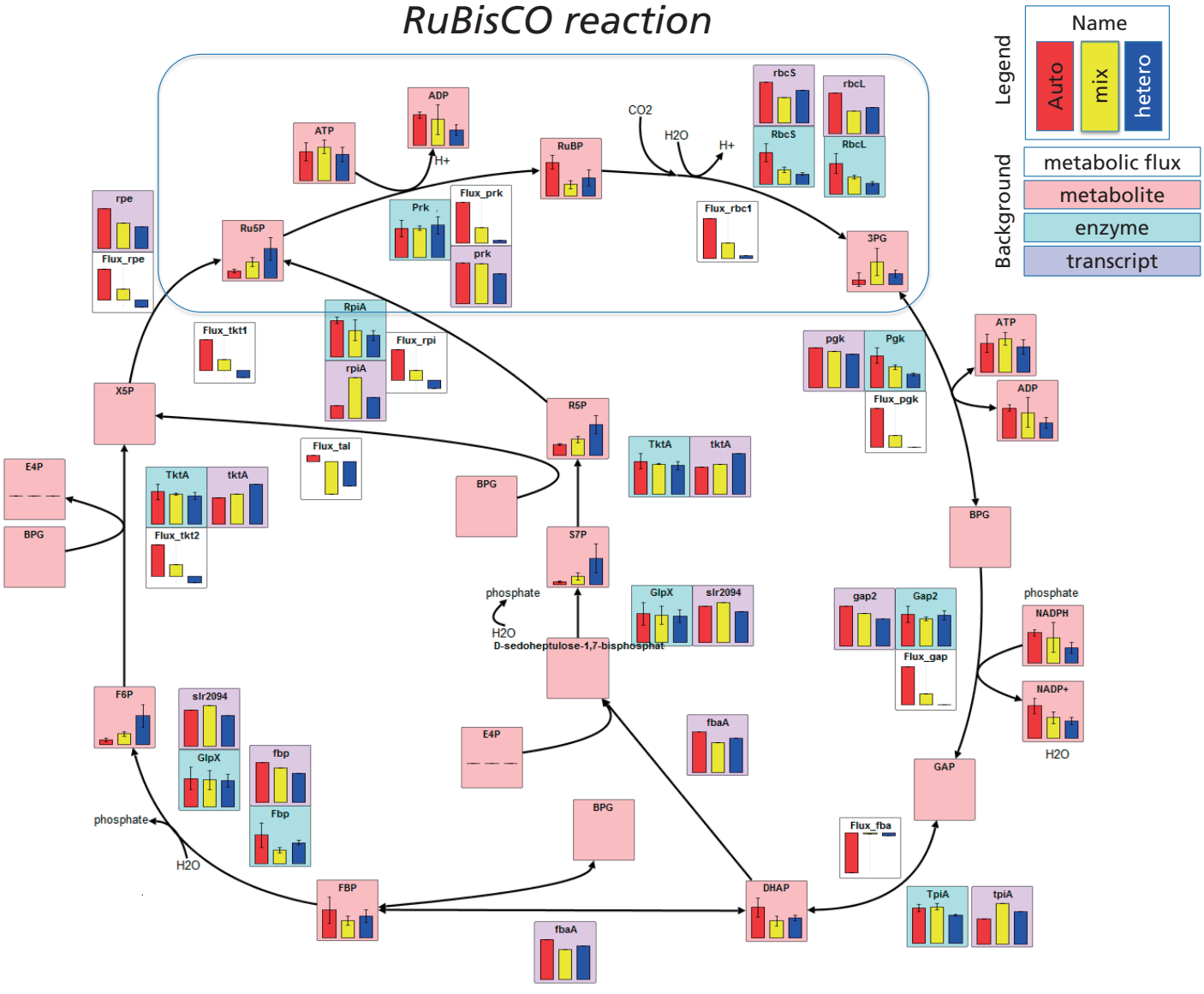

Figure 6 Multiomics changes between conditions

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Conclusions

- By utilizing the Garuda platform, we succeeded in an easy visualization the four omics data on the metabolic map.
- This research can be expected to interpret the data by connecting others gadgets on Garuda platform.

References

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