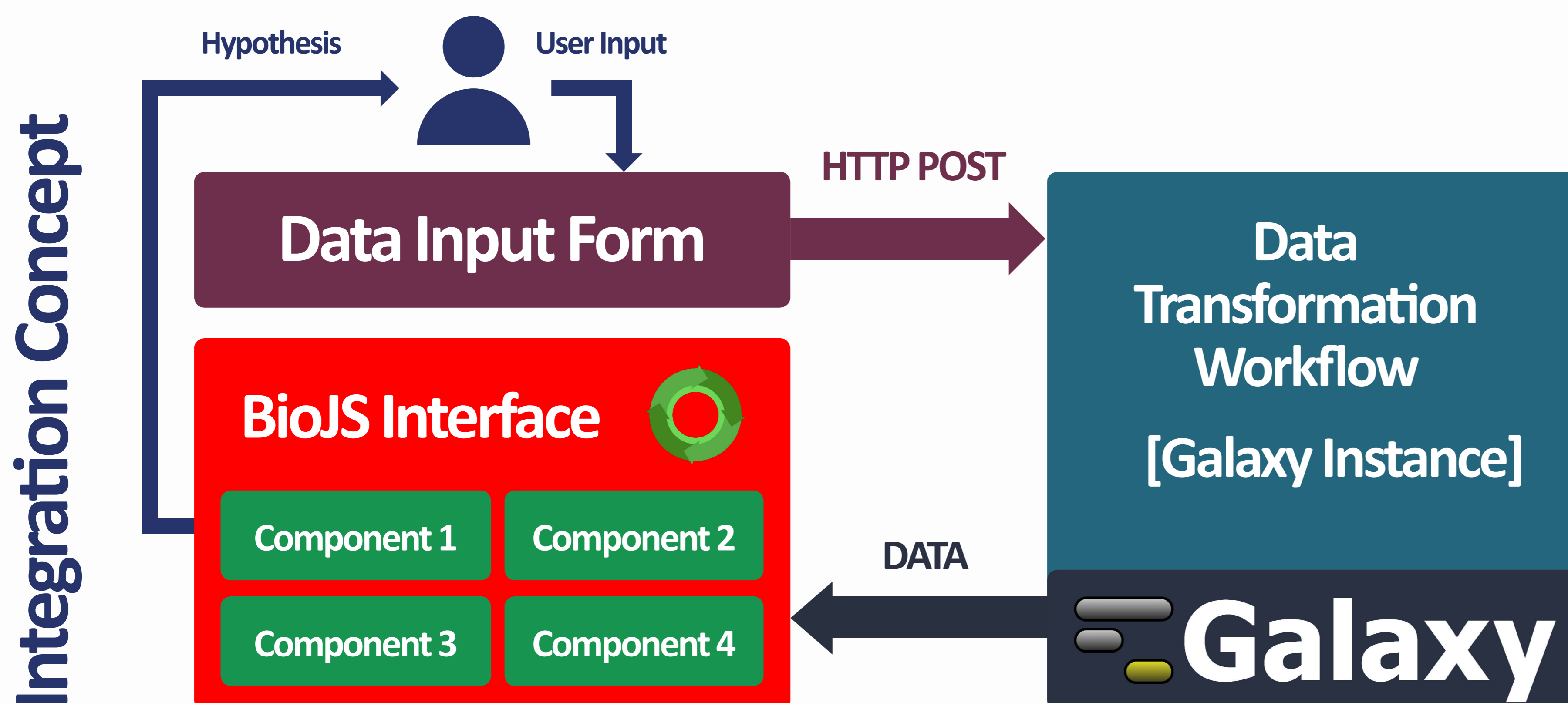# VAPoR: A Visual web pipeline for Annotation of host/pathogen interactions in Plant Resistance

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Introduction

BioJavaScript (BioJS) is an open source bioinformatics project that provides reusable JavaScript components for visualisation of biological data on the web. Multiple BioJS components can be combined to visualise complex sets of data. Each BioJS component requires a different type of data input. Therefore, fast and efficient ways to transform data become extremely important. Galaxy constitutes a very convenient way to automatically generate all the inputs required by the different BioJS components. As such, Galaxy and BioJS can be integrated to very quickly and easily develop web applications to solve specific problems in biology in a visual way. As an example we present VAPoR, a tool for the visual annotation of host/pathogen interactions in plant resistance.

Integration Concept

Hypothesis — User Input

Data Input Form

HTTP POST

BioJS Interface
- Component 1
- Component 2
- Component 3
- Component 4

DATA

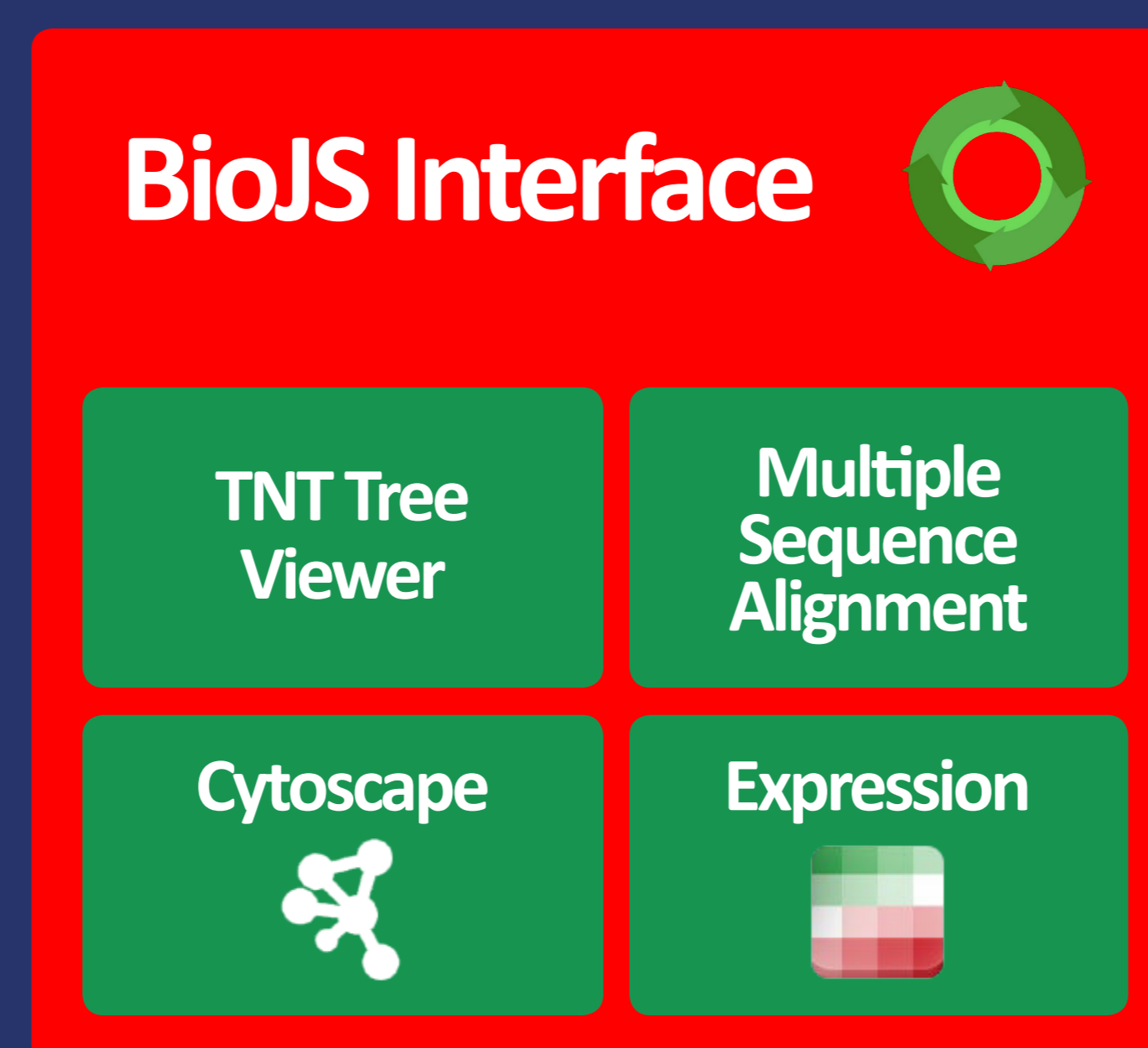Data Transformation Workflow [Galaxy Instance]

Galaxy

Advantages

- Very easy and quick to implement
- As powerful as you want
- A programmer with moderate knowledge of JavaScript and Bioinformatics tools can make it (an intern?)
- Specifically tailored towards a research group's needs
- Every part of it is open-source licensed and available on GitHub
- Web-based, so end users don't have to download/install anything

VAPoR as an example

- Plant scientists may want to know more about a specific protein sequence
- VAPoR collects information about homologues to the protein in *A. thaliana*.
- VAPoR finds homologues, gathers metadata and visualises it via a BioJS interface
- Data transformation and gathering is implemented as Galaxy workflow
- From this new hypotheses can be created.

BioJS Interface
- TNT Tree Viewer
- Multiple Sequence Alignment
- Cytoscape
- Expression

Galaxy Workflow
- Blast+
- Neighbour joining
- T-Coffee

T COFFEE — NCBI BLAST

Galaxy

TAP NFC

Live VAPoR demo!

GitHub

https://github.com/bene200
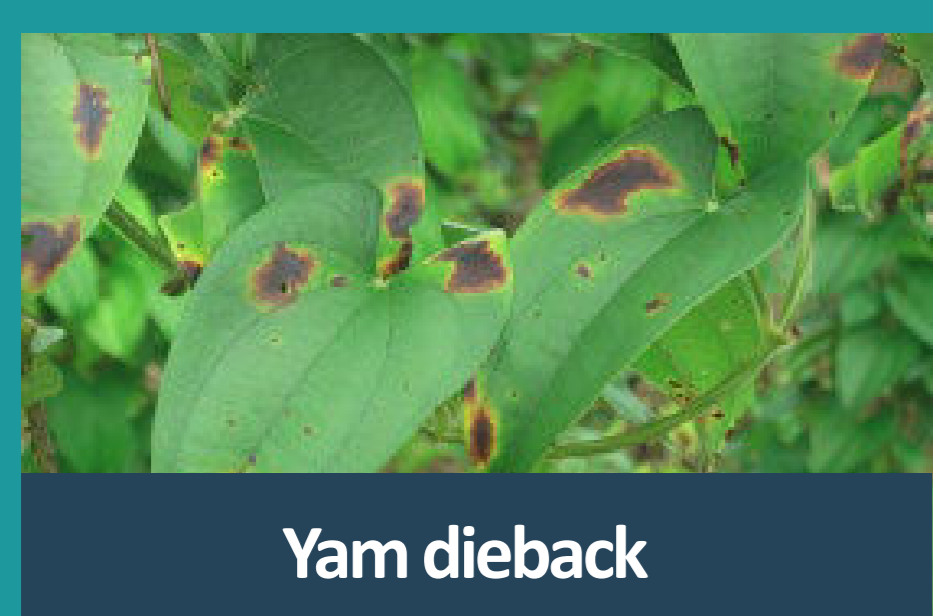
Purple Yam as biological use case

Discorea alata **(Purple Yam)**

Yam dieback

- Yam (*dioscorea alata*) is a staple crop of great significance in several countries
- Production of the purple yam has experienced up to 90% annual yield loss due to anthracnose disease caused by *colletotrichum gloeosporioides*
- Discovery and annotation of R-genes in D. alata would therefore be useful in improving genomic breeding programs

Conclusions

- Galaxy and BioJS frameworks can be integrated to efficiently create powerful web applications serving a specific purpose tailored towards a group's needs.
- Finding genes involved in the resistance of *d. alata* to yam dieback is a biological use case for VAPoR
- VAPoR (Visual Annotation of Plant Resistance) is an example for such an application that facilitates development of hypotheses on the function of unknown plant proteins.
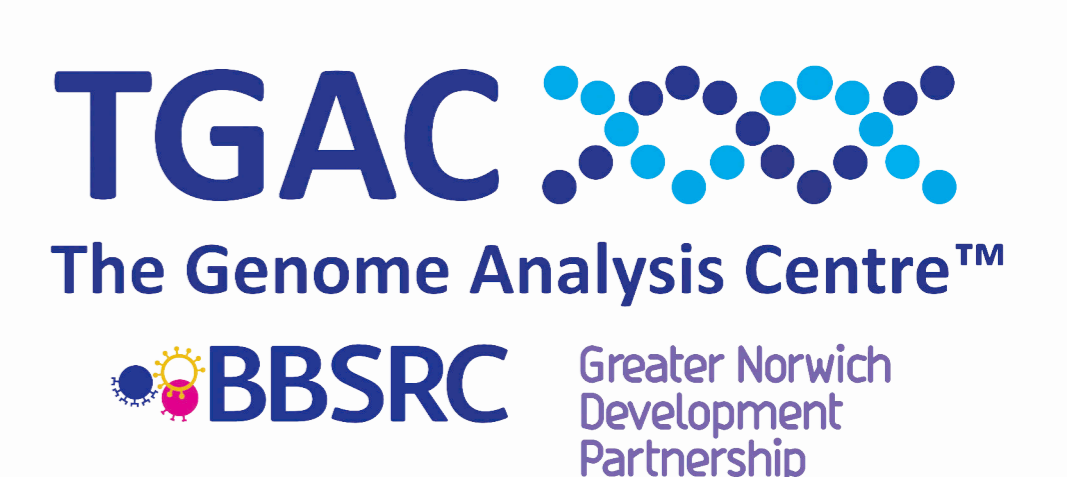
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TGAC The Genome Analysis Centre™

BBSRC — Greater Norwich Development Partnership

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