Tag.bio

Analysis Innovation Platform

https://tag.bio

Microsoft Azure

Life Sciences:

Scientists need to be able to investigate data.

Scientists have vital domain expertise but rarely have the technical skills necessary to ask data questions without help. Tag.bio enables the scientist to ask questions directly and to move through an analytic **workflow** creating a saved and **reproducible** history of their work.
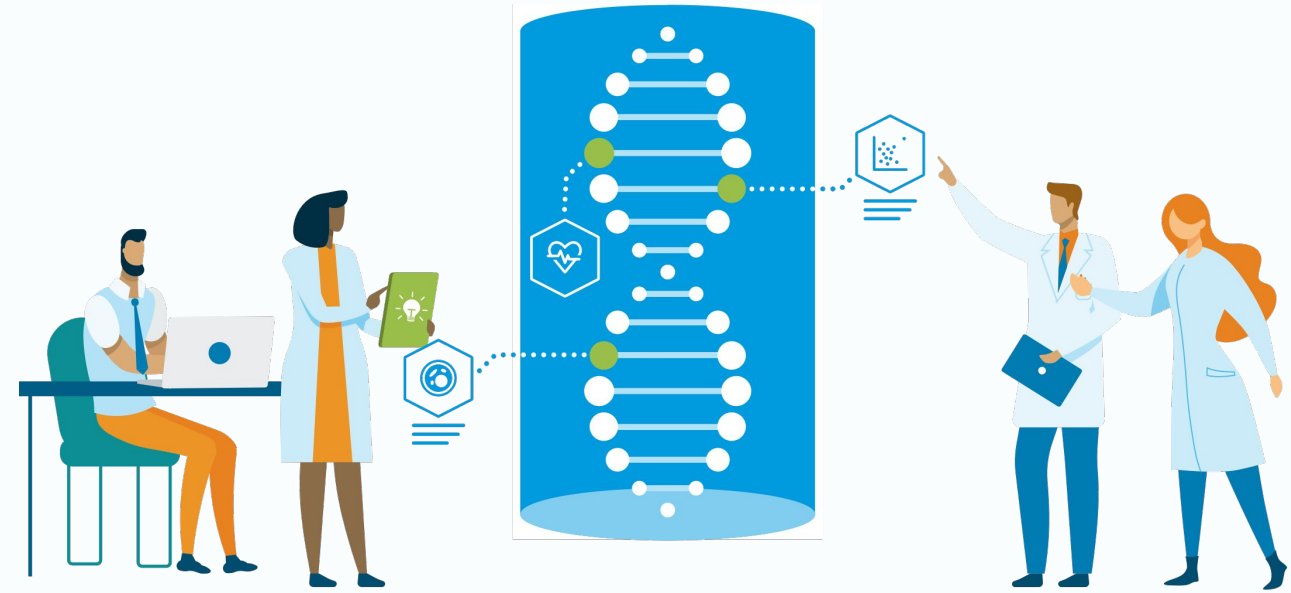
Challenges

The last mile of data analysis is broken. Extracting insights from data takes too long. We join together the data, the algorithms and the user experience into a single data node that enables a researcher to go from question to answer to insight - **on their own.**

Solution

The data scientist takes advantage of the Tag.bio **data mesh** architecture and enterprise environment. They build apps that are specific to the data and the users needs. The researcher runs the apps to investigate data and reach insights. As they do they create a replayable history of their work.

Outcomes

Domain experts ask thousands more questions of data than they previously could.
Data scientists enable their users and concentrate of novel analysis not maintenance.
CIO's and analysts can quantify how data is being used and results are produced. These three elements build a data driven organization.

Tag.bio

A new data experience

A modern, collaborative analysis experience that integrates with your workflow to accelerate discovery in healthcare and life sciences.

Data Nodes

Pick the data you want to be turned into a containerized data node. Create analysis apps which are specific to your data and are written in the language of your users. Enable users to run investigations and share with their team.
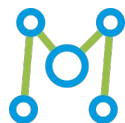
Data Mesh Architecture

The smart API allows data nodes to be connected. This allows the user to move from one data type to another in a single click and to transfer results across datasets. Service Nodes provide single source of annotation and report on how the mesh is being used.

Enterprise Portal

The Enterprise Data Portal provides a personalized experience for each user, allowing them to securely access data nodes and analysis apps. It provides a re-runnable analysis history and the ability to easily share analyses across the organisation.

Tag.bio's platform + Azure

Tag.bio's data innovation platform transforms an organization's relationship with data. Running it on Azure makes the deployment simple, scalable, and secure.


Your VPC, your security

Containerized Tag.bio data nodes are securely deployed into your Azure environment.

Value from day one

Go from data to answers within 24 hours. Select the data you want, map it into the data node within hours, and deploy the node to the analysis site within minutes. Once the node is visible in the site, domain experts can start using the analysis apps to ask and answer their own questions instantly.
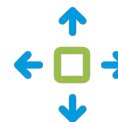
Scale your nodes as your data grows

Azure ensures that as an organization's data grows, the data mesh architecture can scale appropriately.

IUPUI

Iterative analyses, faster discoveries

In the course of one evening in 2019, Dr. Radovich found three significant results from his own dataset in Thymoma (TCGA).

Milan Radovich, PhD,
Assoc. Prof. IU School of Medicine,
IU Health Vice President for Oncology Genomics
Co-Director IUH Precision Genomics
ORIEN Network Scientific Committee Co-Chair

From Months to Minutes

With Tag.bio Dr Radovich was able to re-analyse data he had previously published. The fact that he could rapidly analyse the whole dataset with iterative questions led to three significant insights in one evening of work. There is value hidden in "old" data and rapid analysis lowers the cost of asking questions. Allowing that value to be revealed.

Key Findings

The ability to ask questions iteratively led Dr. Radovich to the following findings in one evening:

- Overexpression of the tumoral muscle-autoantigens: PPARGC1A, NEFM, and NEFL links thymoma to myasthenia gravis
- The FGFR3 oncogene is highly overexpressed in the rare subset of thymomas that metastasize.
- Chromosome 16q loss is a genomic hallmark of thymic carcinomas. The CYLD tumor suppressor on 16q is co-mutated leading to activation of STAT3

AACR Poster

Presented as a poster at the 2019 AACR meeting.

You already have the answer. Let Tag.bio help you find it.

Contact Tag.bio for more information

Ask a question via email: info@tag.bio

Learn more: Tag.bio