
















BrAPI Success Stories

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Abstract

Population growth and climate change require extraordinary efforts to increase efficiency in breeding programs around the world. In the last few years, new phenotyping techniques, genomics technologies, and genetic approaches such as genomic prediction have provided a boost in genetic gain in breeding, but have also created a flood of data that needs careful management to be fully harnessed. In particular, data integration is a challenge due to the multiple types of data being handled by a variety of disparate and dispersed systems. The Breeding API (BrAPI) project is an international, grass-roots effort to enable more efficient data management by enabling interoperability among research databases and tools, using a standardized RESTful web service API specification for exchanging breeding related data. This community driven standard is software agnostic and free to be used by anyone interested in plant breeding, genetics and agronomy data management, including trial, germplasm, phenotyping, and genotyping data management. This manuscript presents the current version of BrAPI, the substantial growth of the project, and a wide variety of open source plant genetics research tools with active BrAPI implementations.

Introduction

To address consequences of climate change and population growth, plant and animal breeding needs to become more efficient and data driven to ensure a healthy, resilient, and sustainable agricultural production system. Modern breeding techniques require large amounts of high quality data to be effective, requiring digital methods for data collection, management, and analysis. They rely on several research disciplines, including plant phenomics, genetics, genomics, and agronomy, involving research institutes, genebanks, and breeding companies. Interoperability between research software tools, systems, and databases can substantially increase the efficiency of a breeding program. The ability to efficiently share data means access to larger and more complete datasets, enabling more accurate computational models, more accurate predictions, and improved selections.

The Breeding API (BrAPI) project is an effort to enable interoperability among breeding tools, systems, and databases. BrAPI is a standardized Representational State Transfer (REST), web service, Application Programming Interface (API), specification for breeding, genetics, phenomics and related agricultural data.¹ By using the BrAPI standard, breeding software can more easily become interoperable, allowing groups to more easily share data and software tools.

Since its first publication¹, BrAPI has seen a significant increase in community services, compatible tools, and participating organizations. The community has organized numerous hackathons to evolve the specifications, resulting in continuous improvements and enhancements. This report includes a short technical description of the standard and a showcase of the applications, services, and tools available in the BrAPI community. BrAPI has become an essential part of the digital infrastructure for breeding, genetics and phenomics applications and related agricultural projects. It is the intention of this manuscript to demonstrate the value of BrAPI to the wider scientific community as an effective and efficient means to collaborate and share resources.

How it works

An API is a technical connection between two pieces of software. Just as a Graphical User Interface (GUI) or a Command Line Interface (CLI) allows a human user to interact with a piece of software, an API allows one software application to interact with another. A GUI or CLI might allow a user to input data, read data, and start processes within an application. An API allows one piece of software (sometimes called a client, user agent, or service consumer) to programmatically input data, read

data, and start process within another piece of software (sometimes called a server or service provider).

A REST style web service is a type of API commonly used in today's web infrastructure. REST is a technical architecture that describes the stateless transmission of data between applications. Typically, RESTful web service APIs are implemented using the standard HTTP protocol that most of the modern internet is built upon. These implementations generally use JavaScript Object Notation (JSON) to represent the data being transferred. Both HTTP and JSON are programming language agnostic, very stable, and very flexible. This means BrAPI can be implemented in almost any piece of software, and can solve a wide range of use cases.

Data repositories and service providers can choose to represent their data as a BrAPI compatible API. By mapping their internal data structures to the standard models, data repositories can easily expose data to the outside world. Similarly, they can accept new data from external sources and automatically map the new data into an existing database. Client application developers can take advantage of this standardization by building tools and connectors that integrate with all BrAPI compatible data repositories. Visualization, reporting, analytics, data collection, and quality control tools can be built once and shared with other organizations following the standards. As the number of BrAPI compatible databases, tools, and organizations grows, so does the value added by implementing the standard into a given application.

Project Updates

Over its lifetime, the BrAPI project has grown and changed substantially. The latest stable version of the specification (v2.1) looks vastly different from the first version (v1.0) released in 2017. The total size of the specification has almost quadrupled in that time, going from 51 endpoints documented in v1.0 to 201 endpoints documented in v2.1. Because of this growth, the specification documents were reorganized into four modules: BrAPI-Core, BrAPI-Germplasm, BrAPI-Genotyping, and BrAPI-Phenotyping. [Figure 1](#) shows a simplified domain map of the whole BrAPI v2.1 data model, divided into the organizational modules. The early versions of the specification focused on read-only phenotype data, with a small consideration to the other domains. Now the specification has a full representation of most of the major concepts applicable to the breeding and research process. The new specification is also internally consistent, easier to navigate, and allows for read, write, and update capabilities. None of those qualities were a guarantee for the earlier versions.

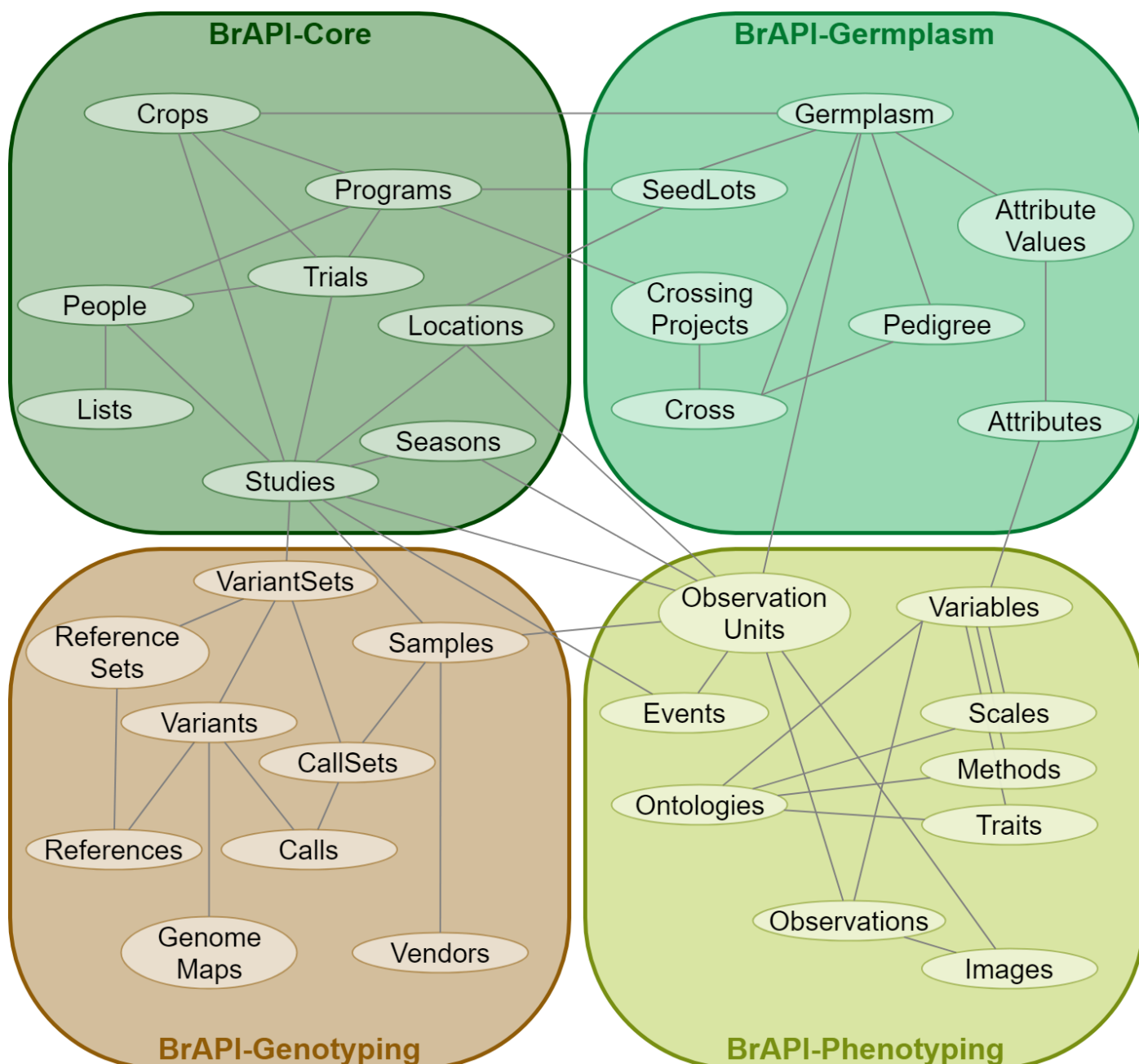


Figure 1: A simplified domain map of the whole BrAPI data model, divided into organizational modules. A more detailed Entity Relationship Diagram (ERD) is available on brapi.org.

As the specification has matured, so have the tools, services, and libraries available to the community to work with the specification. Every version of the specification is now released with a change log to guide developers upgrading from a previous version, an Entity Relationship Diagram (ERD) to describe the whole data model visually, and a JSON Schema data model to be used in some automated development and validation efforts. For groups who are using Java, Java Script, Python, R, or Drupal, there are community maintained libraries available that contain full BrAPI implementations ready to be added to some existing code. The BrAPI Test Server and the BRAVA validation tool are both still available to the community for testing purposes, and they have been maintained to support every version of the specification. Finally, there are three new resource list pages on brapi.org to advertise the BrAPI compatible software available in the community. The BrAPPs list page, servers list page, and compatible software list page showcase many of the BrAPI compatible applications and data resources available in the community.

Community Growth

The international BrAPI Community consists of software developers, biologists, and other scientists working on BrAPI related projects and data sources. This community is what sustains the BrAPI project, builds implementations, maintains development tools, and provides input to enhance the specification. As the project has grown, so has the community. The BrAPI project started in June 2014 with less than ten people coming together to discuss the idea. Over the next ten years, the community has grown to between 200 and 250 members.

The BrAPI Hackathons are a major staple of the BrAPI community. Twice a year, the community gathers to discuss the specification and collaborate on BrAPI related projects. This time is very valuable to the community; for some organizations, the hackathon is the only time during the year when they can collaboratively work on anything related to BrAPI. During the COVID-19 pandemic, virtual hackathons took the place of in-person events. While the virtual hackathons do not provide the same level of face-to-face time that is crucial to collaborative work, they did allow for more attendees to gather and share their opinions. Going forward, the community leadership has decided to have one in-person hackathon and one virtual hackathon each year, to balance the advantages of both.

Results

Below are a number of short success stories from the BrAPI community. These tools, applications, and infrastructure projects serve as another indicator of community growth and success over the past 5-10 years. These stories clearly illustrate all the different ways the BrAPI Standard can be used productively and in practice. Figure [2](#) contains a summary of the tools described below.






























	Core				Phenotyping				Genotyping				Germplasm			
	Generation/ Collection	Storage	Visualization	Analysis	Generation/ Collection	Storage	Visualization	Analysis	Generation/ Collection	Storage	Visualization	Analysis	Generation/ Collection	Storage	Visualization	Analysis
 Field Book					✓	✓										
 GridScore					✓	✓	✓									
 ClimMob	✓	✓			✓	✓										
 ImageBreed						✓	✓	✓								
 PHIS		✓			✓	✓		✓						✓		
 PIPPA		✓			✓	✓								✓		
 Trait Selector BrAPP							✓									
 DART Sample Submission									✓							
 DARTView											✓	✓				
 DivBrowse										✓	✓	✓				
 Flapjack							✓				✓	✓				
 GIGWA										✓	✓	✓				
 PHG									✓	✓		✓				
 AGENT													✓	✓	✓	
 FLORILÈGE														✓	✓	
 GLIS													✓	✓		
 Helium						✓	✓							✓	✓	
 MGIS		✓				✓							✓	✓		✓
 BIMS	✓	✓	✓			✓	✓							✓	✓	
 BMS	✓	✓	✓			✓	✓	✓		✓				✓	✓	
 Breedbase	✓	✓	✓	✓		✓	✓	✓		✓				✓	✓	✓
 DeltaBreed	✓	✓	✓			✓	✓	✓		✓				✓	✓	
 FAIDARE			✓				✓				✓				✓	
 Germinate	✓	✓	✓			✓	✓			✓				✓	✓	
 G-Crunch				✓				✓				✓				✓
 QBMS				✓				✓				✓				✓
 Mr. Bean			✓	✓			✓	✓			✓	✓			✓	✓
 SCT															✓	✓
 ShinyBrAPPs			✓	✓			✓	✓			✓	✓			✓	✓

Figure 2: A summary of all the tools described below and the general areas each tool is designed to handle

Phenotyping

Phenotyping is fundamental to plant breeding and genetics research, providing the accurate, high-quality data needed for downstream analyses and selection decisions. Effective phenotyping requires a thorough understanding of both biological research questions and operational data gathering to ensure successful outcomes. Collected data, subsequent analyses, and data visualizations all impact

and shape downstream experiments. The BrAPI specification supports phenotypic data throughout the entire breeding pipeline, including collection, analyses, publication, and archiving. The BrAPI community has developed several BrAPI-compatible tools to facilitate data standardization, efficient storage, and curation of phenotypic data and trait metadata. Ongoing development efforts are creating tools to manage images and other high-throughput phenotypic data sources, further enhancing the precision and efficiency of plant breeding research. By supporting the accurate and efficient collection and storage of phenotypic data, BrAPI compatible tools simplify the conversion of phenotypes into insights that are necessary to help digitize and boost modern breeding and genetics research programs.

Field Book

Data from plant breeding and genetics experiments has traditionally been collected using pen and paper, but this approach often results in transcription errors and delayed analysis. [Field Book²](#), a highly-customizable Android app, was developed to help scientists digitize and organize their phenotypic data as measurements are collected. This effectively improves data collection speed, reduces errors, and enables larger and more robust breeding populations and data sets. Field Book has added support for BrAPI to streamline data transfer to and from BrAPI-compatible servers. Removing the need to manually transfer data files simplifies data exchange between these systems and reduces the opportunities for human error and data loss.

GridScore

[GridScore³](#) is a modern mobile application for phenotypic observations that harnesses technological advancements in the area of mobile devices to enrich the data collection process. GridScore focuses on user experience by closely mirroring the look and feel of printed field plans. It also enriches the experience with a wide range of functionalities including data validation, data visualizations, georeferencing, cross-platform support, and data synchronization across multiple devices. GridScore is a multi-platform tool which works on any reasonably modern device with a web browser including laptops, PCs, tablets and phones. Once created, trials can be transferred to collection devices using a Quick Response (QR) code. Its approach towards data collection uses a top-down view onto the trial and offers field navigation mechanisms using barcodes, QR codes, or guided walks which take the data collector through the field in one of 16 pre-defined orders.

BrAPI has further increased the value of GridScore by integrating it into the overarching workflow, from trial creation, through data collection, and to its ultimate data storage for further processing. Specifically, trial designs as well as trait definitions can be imported into GridScore using BrAPI and a finalized trial can be exported via BrAPI to any compatible database.

ClimMob

[ClimMob⁴](#) is a software suite for a different research paradigm in experimental agriculture. In traditional breeding, a few researchers design complicated trials in search of the best solutions for a few target environments. ClimMob enables many participants to carry out reasonably simple experiments across many environments. Taken together, this data across many environments can be very informative. It applies the principles of citizen science and choice experiments to scale the data collection process, mostly in the format of rankings. Although this data may not be as detailed as from a centralized experiment, it can be very useful to inform decisions to a wide range of locations and environments with increased external validity. ClimMob applications include testing crop varieties, evaluating agronomic practices, and investigating climate resilience strategies. The platform supports experiment design, data collection through mobile apps, and data analysis to provide actionable insights.

During a crop trial, all farmer-collected data is stored in ClimMob. When data collection is complete, the raw data is automatically uploaded via BrAPI to a central breeding database for long-term storage and analysis. To facilitate this synchronization, ClimMob uses BrAPI to retrieve curated germplasm information from breeding databases when designing a trial, significantly enhancing data quality. Additionally, a process has been developed to push analyzed data from ClimMob to the breeding databases, providing breeders with insights into the potential adoption of the tested crop varieties.

ImageBreed

[ImageBreed⁵](#) is an image collection pipeline tool to support regular use of UAVs and UGVs. High-throughput phenotyping has been gaining significant traction lately as a way to collect large amounts of data very quickly. Image collection from unmanned aerial and ground vehicles (UAVs and UGVs) are a great way to collect a lot of raw data all at once, then analyze it later.

When the raw images have been processed through the standardization pipelines in ImageBreed, useful phenotypes can be extracted from the images. The BrAPI standard is used to push these phenotypes back to a central breeding database where they can be analyzed with other data. In addition to this, ImageBreed has the ability to use BrAPI to upload the raw images to the central breeding database, or any other BrAPI compatible long term storage service. In the current version of the standard (V2.1), the BrAPI data models for images are rudimentary, but effective. The ImageBreed team has put in some work into enhancing the BrAPI image data standards, collaborating with others in the community.

PHIS

[PHIS⁶](#), the Hybrid Phenotyping Information System, is an ontology-driven information system based on semantic web technologies, based on the [OpenSILEX](#) framework. PHIS is deployed in several field and greenhouse platforms of the French national [PHENOME](#) and European [EMPHASIS](#) infrastructures. It manages and collects data from basic phenotyping and high throughput phenotyping experiments on a day to day basis. PHIS unambiguously identifies all the objects and traits in an experiment, and establishes their types and relationships via ontologies and semantics.

PHIS has been designed to be BrAPI-compliant. PHIS adheres to the standards and protocols specified by BrAPI and implements various services aligning with the BrAPI standards, encompassing the Core, Phenotyping, and Germplasm modules. This enables integration and compatibility with BrAPI-compliant systems and platforms, such as OLGA, a genebank accessions management system, to retrieve accession information. This prerequisite served as the basis for formalizing the data model, while also facilitating compatibility with other standards, such as the Minimal Information About a Plant Phenotyping Experiment ([MIAPPE⁷](#)). By integrating BrAPI requirements into its structure, PHIS not only meets the standards of the phenotyping field, but also strengthens its capacity for interoperability and effective collaboration in the wider context of plant breeding and related fields. The fact that data within a PHIS instance can be queried through BrAPI services enables indexing of PHIS in the [FAIDARE](#) data portal⁸.

Furthermore, as PHIS offers BrAPI-compliant Web Services, it simplifies the integration and data exchange with other European information systems that handle phenotyping data. The adherence to BrAPI standards ensures a common interface and compatibility, facilitating communication and collaboration between PHIS and other systems in the European context. This interoperability not only eases data sharing, but also promotes a more coherent and efficient approach to the management and use of phenotyping data on various platforms and research initiatives within the European scientific community.

PIPPA

[PIPPA](#)⁹ is a data management system used for collecting data from the [WIWAM](#)¹⁰ range of automated high throughput phenotyping platforms. These platforms have been deployed at different research institutes and commercial breeders across Europe. They can be setup in a variety of configurations with different types of equipment including weighing scales, cameras, and environment sensors. The software features a web interface with functionality for setting up new experiments, planning imaging and irrigation treatments, linking metadata to pots (genotype, growth media, manual treatments), importing data, exporting data, and visualizing data. It also supports the integration of image analysis scripts and connections to a compute cluster for job submission.

To share the phenotype data of the experiments linked to publications, an implementation of BrAPI v1.3 was developed which allowed read only access to the data in the BrAPI standardized format. This server was registered on [FAIDARE](#)⁸ which allows the data to be found alongside data from other BrAPI compatible repositories.

As the BrAPI ecosystem has matured, it has created a clear path for the further development of PIPPA. The BrAPI specification demonstrates how to share data in a manner consistent with the FAIR principles,¹¹ which are becoming best practices in plant research data management. The BrAPI technical standard, in combination with the [MIAPPE](#)⁷ scientific standard, have served as guidelines in the current development effort of the PIPPA project. This development is focused on delivering a public BrAPI v2.1 endpoint and making more high throughput datasets publicly available via BrAPI.

Trait Selector BrAPP

The [Trait Selector BrAPP](#) is used to search and select useful traits, using a visual aid to help the user find exactly what they need. Instead of searching through a long list of possible traits, the user is presented with a cartoon image of a species. They can then click on pieces of the image to show traits associated to that part of the plant. For a breeder, they might use it to quickly find specific traits to study. For a genebank user, they might use it to find varieties that have a specific trait they are interested in.

The Trait Selector can be integrated into any website or system, assuming there is a BrAPI compatible data source available to connect to. A breeding database would need to only implement the BrAPI endpoints for Traits, Observations, and Variables, while a genebank would require Traits and Germplasm Attributes. Any BrAPI server with either of these sets of endpoints implemented could use this BrAPP. CassavaBase and MGIS are two successful examples of the Trait Selector BrAPP in use.

Genotyping

Genotyping has become a cornerstone of most breeding processes, but managing the data can be challenging. Understanding different genotyping protocols for various crops is crucial due to the unique genetic structures of each species. Techniques such as SNP genotyping, Genotyping-by-Sequencing (GBS), SSRs, Whole Genome Sequencing (WGS), and array-based genotyping each offer specific advantages depending on the crop and research objectives. BrAPI supports genotypic data by utilizing existing standards such as VCF¹² and the GA4GH Variants schema¹³. The BrAPI community has developed compatible tools for storing, searching, visualizing, and analyzing genotypic data, making it easier to integrate and utilize this information in breeding programs. Mastery of the various genotyping protocols ensures efficient and effective breeding, while BrAPI compliant tools streamline data management and analysis, enhancing the ability to make data-driven decisions in developing superior crop varieties.

DArT Sample Submission

The DArT genotyping lab is heavily used world wide when it comes to plant genotyping. With over 1200 available organisms and species, client base on every continent and already many million samples processed, DArT provides services for several generic and bespoke genotyping technologies and solutions. Processes of sample tracking and fast data delivery are at the core of the ordering system developed at DArT. The ordering system is tightly integrated with DArTdb - DArT's custom LIMS operational system, which drives laboratory, quality, and analytical processes.

Diversity Arrays Technology was a part of BrAPI community since its inception. DArT developers have worked with the BrAPI community contributing to various aspects of the API specification. One key aspect was establishing a standard API for sending sample metadata to the lab for genotyping. This solution eliminates much of the human error involved with sending samples to an external lab and also allows for an automated process of sample batch transfers. Beyond sample submission, the current implementation also allows for an order status verification, automated data discovery, and data downloads. Data are delivered as standard data packages with self-describing metadata.

The current BrAPI implementation at DArT is in production and it is compatible with the newest BrAPI specification. Further details about DArT's ordering system can be found at [DArT Ordering System](#) and also at [DArT Help](#).

DArTView

[DArTView](#) is a desktop application for marker data curation via metadata filtering. DArTView enables genotype variant data visualization and users can easily identify trends or correlations within their data using the tool. Its primary goal is to overcome tedious manual calculation of marker data through common spreadsheet applications like Excel. Users are able to import marker data from csv files, but DArTView has been recently enhanced to be BrAPI compatible. Users can now use any BrAPI compatible server as an input data source. BrAPI provides a consistent data standard across databases and data resources. DArTView's compatibility with BrAPI also ensures easy integration with other tools and pipelines that would use DArTView for marker filtering and exploration.

Initially developed by Diversity Arrays Technology (DArT), the tool is gaining popularity within the breeding community, especially in Africa. Future releases will focus on enhancing the BrAPI compatibility, making it accessible to more breeders and researchers in the region. A web enabled version of DArTView is in development. This new version will allow for further collaboration opportunities with other interested partners who would like to integrate it as part of their pipelines.

DivBrowse

[DivBrowse¹⁴](#) is a web platform for exploratory data analysis of huge genotyping studies. The software can be run standalone or integrated as a plugin into existing data web portals. It provides a powerful interactive visualization of variant call matrices with hundreds of millions of variants and thousands of samples. It enables easy data import and export by using well established, standardized, bioinformatics file formats.

At its core, DivBrowse combines the convenience of a genome browser with features tailored to the diversity analysis of germplasm. It is able to display genomic features such as nucleotide sequence, associated gene models, and short genomic variants. DivBrowse provides visual access to large VCF files obtained through genotyping experiments. In addition, DivBrowse also calculates and displays variant statistics such as minor allele frequencies, proportion of heterozygous calls, and proportion

missing variant calls. Dynamic Principal Component Analyses (PCA) can be performed on a user specified genomic area to provide information on local genomic diversity.

Parts of the BrAPI Genotyping module are implemented in DivBrowse. There is a server-side component which provides genotypic data that the DivBrowse database can consume. There is also a client-side GUI component which can visualize genotypic data via any external BrAPI endpoint. In addition to BrAPI, DivBrowse has an internal API to control the tool from a hosting web portal. DivBrowse also has an interface to BLAST, which can be used to directly access genes or other genomic features. The modular structure of DivBrowse allows developers to configure and easily embed links to other external information systems.

Flapjack

[Flapjack¹⁵](#) is a multi-platform desktop application for data visualization and breeding analysis (eg, pedigree verification, marker-assisted backcrossing and forward breeding) using high-throughput genotype data. Data can be easily imported into Flapjack from any BrAPI compatible data source with genotype data available. [Flapjack Bytes](#) is a smaller, lightweight and fully web-based counterpart to Flapjack, which can be easily embedded into a database website to provide similar visualizations online. Traditionally supporting its own text-based data formats, Flapjack's use of BrAPI has streamlined the end-user experience for data import and work is underway to determine the best methods to exchange analysis results using future versions of the API.

Gigwa

[Gigwa](#) is a Java EE web application providing a means to centralize, share, finely filter, and visualize high-throughput genotyping data¹⁶. Built on top of MongoDB, it is scalable and can support working smoothly with datasets containing billions of genotypes. It is installable as a Docker image or as an all-in-one bundle archive. It is straightforward to deploy on servers or local computers and has thus been adopted by numerous research institutes from around the world. Notably, Gigwa serves as a collaborative management tool and a portal for exposing public data for genebanks and breeding programs at some CGIAR centers¹⁷. The total amount of data hosted and made widely accessible using this system has continued to grow over the last few years.

The Gigwa development team has been involved in the BrAPI community since 2016 and took part in designing the genotype-related section of the BrAPI standard. Gigwa's first BrAPI-compliant features were designed for compatibility with the Flapjack visualization tool¹⁵. Over time, Gigwa has established itself as the first and most reliable implementation of the BrAPI-Genotyping endpoints. Local collaborators and external partners used it as a reference solution to design a number of tools taking advantage of the BrAPI-Genotyping features (e.g., [BeegMac](#), [SnpClust](#), [QBMS](#)).

Additional use-cases required Gigwa to also consume data from other BrAPI servers. This led to the implementation of BrAPI client features within Gigwa. A close collaboration was established with the Integrated Breeding Platform team developing the widely used Breeding Management System (BMS). This collaboration means both applications are now frequently deployed together; Gigwa pulling germplasm or sample metadata from BMS, and BMS displaying Gigwa-hosted genotypes within its own UI.

PHG

The [Practical Haplotype Graph](#) (PHG) is a graph-based computational framework that represents large-scale genetic variation and is optimized for plant breeding and genetics¹⁸. Using a pangenome approach, each PHG stores haplotypes (the sequence of part of an individual chromosome) to

represent the collected genes of a species. This allows for a simplified approach for dealing with large scale variation in plant genomes. The PHG pipeline provides support for a range of genomic analyses and allows for the use of graph data to impute complete genomes from low density sequence or variant data.

Users access the crop databases either with direct calls to the PHG embedded server or indirectly using the rPHG library from an R environment. The PHG server accepts BrAPI queries to return information on sample lists and the variants used to define the graph's haplotypes. In addition, PHG users utilize the BrAPI Variant Sets endpoint query to return links to VCF files containing haplotype data. Work on the PHG is ongoing and it is expected to support additional BrAPI endpoints that allow for fine tuned slicing genotypic data in the near future.

Germplasm Management

Germplasm data management is crucial due to the vast quantity of new accessions, variants, and lines created yearly. Germplasm is the basis of variation on which plant breeders rely to upgrade and optimize their breeding programs. This is essential at any scale including individual breeding programs, national initiatives, and international collaborations. BrAPI supports the transmission of germplasm passport data, pedigree trees, and crossing metadata. The BrAPI community has developed compliant tools for storing, searching, and visualizing this metadata, facilitating efficient management. Additionally, there are plans to establish federated networks of genebank data connected via BrAPI, enhancing global accessibility and collaboration in germplasm management.

AGENT

In the global system for ex situ conservation of plant genetic resources (PGR)¹⁹, material is being conserved in about 1750 collections²⁰ totalling ~5.8 million accessions. Unique and permanent identifiers in the form of DOIs are available for more than 1.7 million accessions via the Global Information System²¹ of the International Treaty on Plant Genetic Resources for Food and Agriculture. Each DOI is linked to some basic descriptive data that facilitates the use of these resources, mainly passport data. Many DOIs are also linked to additional data from different domains or will be in the future. However, a data space beyond the most basic information is needed that includes genotypic and phenotypic data. This space will help to answer questions about the global biological diversity of plant species, the detection of duplicates, the tracking of provenance for the identification of genetic integrity, the selection of the most suitable material for different purposes, and to support further applications in the field of data mining or AI. In this context, the aim of the [AGENT project](#), funded by the European Commission, is to develop a concept for the digital exploitation and activation of this PGR via European ex situ genebanks according to the FAIR principles¹¹ and to test it in practice using two important crops, barley and wheat. Thirteen European genebanks and five bioinformatics centers are working together and have agreed on standards and protocols for data flow and data formats²² for the collection, integration, and archiving of genotypic and phenotypic data.

The BrAPI specification is one of the agreed standards, that are detailed in the AGENT guidelines for dataflow²³. The implemented BrAPI interface enables the analysis of current and historic genotypic and phenotypic information. This will drive the discovery of genes, traits, and knowledge for future missions, complement existing information for wheat and barley, and use the new data standards and infrastructure to promote better access and use of PGR for other crops in European genebanks. The AGENT database backend aggregates curated passport data, phenotypic data, and genotypic data on wheat and barley accessions of 18 project partners. This data is accessible via [BrAPI endpoints](#) and explorable in a [web portal](#). Genotyping data uses the DivBrowse¹⁴ storage engine and its BrAPI interface. Soon, the BrAPI implementation will be expanded to enable the integration of analysis pipelines in the AGENT portal, such as the FIGS+ pipeline developed by ICARDA²⁴. There is also a plan

to integrate the data collected by the AGENT project into the European Search Catalogue for Plant Genetic Resources (EURISCO)²⁵.

Florilège

[Florilège](#) is a web portal designed primarily for the general public to access public plant genetic resources held by Biological Resource Centers across France. Through this portal, users can browse accessions from over 50 plant genera, spread across 19 genebanks. It allows users to view available seeds and plant material, including options for ordering material. Florilège provides a centralized access to the various French collections of plant genetic resources available to the public.

Florilège retrieves accession information from several BrAPI compliant systems. Key among these are OLGA, a genebank accessions management system, and GnpIS, an INRAE data repository for plant genetic resources, phenomics, and genetics^{26,27}. Using BrAPI to gather data from these systems reduced development efforts and enabled standardized data retrieval. As a result, BrAPI has become the de facto standard within the French plant genetic resources community for exchanging information. During development, the Florilège team also proposed several enhancements to the BrAPI specifications themselves, such as additional support for Collection objects or improved reference linking, to better accommodate their specific use case.

GLIS

The [Global Information System \(GLIS\)](#) on Plant Genetic Resources for Food and Agriculture (PGRFA) of the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) is a web-based global entry point for PGRFA data²¹. It allows users and third-party systems to access information and knowledge on scientific, technical, and environmental matters to strengthen PGRFA conservation, management, and utilization activities. The system and its portal also enable recipients of PGRFA to make available all non-confidential information on germplasm according to the provisions of the Treaty and facilitates access to the results of their research and development.

Thanks to the adoption of Digital Object Identifiers (DOIs) for Multi-Crop Passport Descriptors (MCPD) of PGRFA accessions, the GLIS Portal provides access to 1.7 million PGRFA in collections conserved worldwide. Of these, over 1.5 million are accessible for research, training and plant breeding in the food and agriculture domain.

The Scientific Advisory Committee of the ITPGRFA have repeatedly welcomed efforts on interoperability among germplasm information systems. In this context, the GLIS Portal adopted the BrAPI v1 in 2022. Integrating BrAPI among the GLIS content negotiators facilitates queries and the exchange of content for data management in plant breeding. The Portal also offers other protocols (XML, DarwinCore, JSON and JSON-LD) to increase data and metadata connectivity. In the near future, depending on the availability of resources, upgrading to BrAPI v2 is planned.

Helium

[Helium](#)²⁸ is a plant pedigree visualization platform designed to account for the specific problems that are unique to plant pedigrees. A pedigree is a representation of how genetically discrete individuals are related to one another and is therefore a representation of the genetic relationship between individual plant lines, their parents and progeny. Plant pedigrees are often used to check for potential genotyping or phenotyping errors, since these errors, by the very nature of Mendelian inheritance, are constrained by the pedigree structure in which they exist²⁹. The accurate representation of pedigrees, and the ability to pull pedigree data from different data sources is important in plant

breeding and genetics. Therefore, ways to visualize and interact this complex data in meaningful ways is critical.

From its [original desktop interface](#), Helium has developed into a web-based visualization platform implementing BrAPI calls to allow users to import data from other BrAPI compliant databases. The ability to pull data from BrAPI compliant data sources has significantly expanded Helium's capability and utility within the community. Helium is used in projects ranging in size from tens to tens of thousands of lines and across a wide variety of crops and species. While originally designed for plant data³⁰ it has also found utility in other non-plant projects³¹ highlighting its broad utility. BrAPI also allows Helium to provide direct dataset links to collaborators, allowing the original data to be held with the data provider and utilizing Helium for its visualization functionality. Our current Helium deployment includes example BrAPI calls to a barley dataset at the James Hutton Institute to allow users to test the system and features it offers.

MGIS

The [Musa Germplasm Information System \(MGIS\)](#) serves as a comprehensive community portal dedicated to banana diversity, a crop critical to global food security³². MGIS offers detailed information on banana germplasm, focusing on the collections held by the CGIAR International Banana Genebank (ITC)³³. It is built on the Drupal/Tripal technology, like BIMS³⁴ and Florilège.

Since its inception, MGIS developers have actively participated in the BrAPI community. The MGIS team pushed for the integration of the Multi-Crop Passport Data (MCPD) standard into the Germplasm module of the API. MCPD support was added in BrAPI v1.3, and MGIS now provides passport data information on ITC banana genebank accessions (with GLIS DOI), synchronized with [Genesys](#). MGIS also enriches the passport data by incorporating additional information from other germplasm collections worldwide. All the germplasm data is available through the BrAPI Germplasm module implementation. For genotyping data, MGIS integrates with Gigwa¹⁶, which provides a tailored implementation of the BrAPI genotyping module. Furthermore, MGIS supports a set of BrAPI phenotyping endpoints, facilitating the exposure of morphological descriptors and trait information supported by ontologies like the Crop Ontology³⁵. MGIS has integrated the Trait Selector BrAPP, and there are use cases implemented to interlink genebank and breeding data between MGIS and the breeding database MusaBase.

Breeding and Genetics Data Management

While specialty data management is important for some use cases, often breeders want a central repository or access point of critical data. General breeding and genetics data management systems and web portals support some level of phenotypic, genotypic, and germplasm data, as well as trial, equipment, and people management. By enabling BrAPI support, these larger systems can connect with smaller tools and specialty systems to provide more functionality under the same user interface. There are several breeding data management systems developed in the BrAPI community, each with their own strengths.

BIMS

[BIMS](#) (Breeding Information Management System)³⁴ is a free, secure, and online breeding management system which allows breeders to store, manage, archive, and analyze their private breeding program data. BIMS enables individual breeders to have complete control of their own breeding data along with access to tools such as data import/export, data analysis, and data archiving for their germplasm, phenotype, genotype, and image data. BIMS is currently implemented in five community databases, the Genome Database for Rosaceae³⁶, CottonGEN³⁷, the Citrus Genome

Database, the Pulse Crop Database, and the Genome Database for Vaccinium. BIMS in these five community databases enables individual breeders to import publicly available data so that they can utilize public data in their breeding program. BIMS is also implemented in the public database breedwithbims.org that any crop breeder can use.

Right now, BIMS primarily utilizes BrAPI to connect with the Field Book Android App², enabling seamless data transfer between BIMS and the app. Data transfer through BrAPI between BIMS and other resources such as BreedBase³⁸, GIGWA¹⁶, and Breeder Genomics Hub is on the way. Hopefully, the BIMS development team can easily reuse some of the solved use cases and workflows created by others in the BrAPI community.

BMS

The [Breeding Management System \(BMS\)](#), developed by the [Integrated Breeding Platform \(IBP\)](#), is a suite of tools designed to enhance the efficiency and effectiveness of plant breeding. BMS covers all stages of the breeding process, with the emphasis on germplasm management and [ontology](#)-harmonized phenotyping. It also features analytics and decision-support tools. With its focus on interoperability, BMS integrates smoothly with BrAPI, facilitating easy connections with a broad array of complementary tools and databases. Notably, the BMS is often deployed together with [Gigwa](#) to fulfill the genotyping data management needs of BMS users.

The [brapi-sync](#) tool, a significant component of BMS's BrAPI capabilities, was developed by the IBP and released as a BrAPP for community use. Brapi-sync is designed to enhance collaboration among partner institutes within a network such as Innovation and Plant Breeding in West Africa ([IAVAO](#)). The tool enables the sharing of germplasm and trial metadata across BrAPI-enabled systems. It helps overcome traditional barriers to collaboration, ensuring data that was once isolated within specific programs or platforms can now be easily shared, integrated, and synchronized.

Additionally, brapi-sync improves data management by maintaining links to the original source of each entity it transmits. This retains the original context of the data and establishes a traceability mechanism for accurate data source attribution and verification. Such practices are crucial for maintaining data integrity and fostering trust among collaborative partners, ensuring access to accurate, reliable, and current information.

Breedbase

[Breedbase](#) is a comprehensive breeding data management system^{38,39} that implements a digital ecosystem for all breeding data, including trial data, phenotypic data, and genotypic data. Data acquisition is supported through data collection apps such as Fieldbook², Coordinate, and InterCross, as well as through drone imagery, Near Infra-Red Spectroscopy (NIRS), and other technologies. Search functions, such as the Search Wizard interface, provide powerful query capabilities. Various breeding-centric analysis tools are available, including mixed models, heritability, stability, PCA, and various clustering algorithms. The original impetus for creating Breedbase was the advent of new breeding paradigms based on genomic information such as genomic prediction algorithms⁴⁰ and the accompanying data management challenges. Thus, complete genomic prediction workflow is integrated in the system.

The BrAPI interface is crucial for Breedbase. Breedbase uses BrAPI to connect with the data collection apps, other projects such as CLIMMOB⁴, and native BrAPPs built into the Breedbase webpage. Users also appreciate the ability to connect to Breedbase instances using packages such as [QBMS](#)⁴¹ for data import into R for custom analyses. The Breedbase team has been part of the BrAPI community since its inception, and has continuously adopted and contributed to the BrAPI standard.

DeltaBreed

[DeltaBreed](#) is an open-source breeding data management system designed and developed by Breeding Insight to support USDA-ARS specialty crop and animal breeders. DeltaBreed differs from other related systems in that it is customizable to small breeding teams and generalized enough to support the workflows of diverse niche species. DeltaBreed is a unified system that connects a variety of BrAPI applications (see list below). BrAPI integration allows the complexity underlying interoperability to be hidden, shielding users from multifactorial differences between various applications. DeltaBreed, adhering to the BrAPI model, establishes data standards and validations for users and provides a singular framework for data management and user training.

DeltaBreed users need not be aware of BrAPI or the specifics of underlying applications but will notice that BrAPI interoperability reduces the need for human-mediated file transfers and data manipulation. Field Book users, for example, can connect to their DeltaBreed program, authenticate, and pull studies and traits directly from DeltaBreed to Field Book on their data collection device. The subsequent step of pushing observations from Field Book to DeltaBreed is straightforward via BrAPI, but is pending implementation until observation transaction handling is improved, intentional and inadvertent repeated measures are differentiated, and a data staging area is implemented for quality control.

Breeding Insight integrated several BrAPI applications to support 2021 phenotypic data collection by USDA-ARS blueberry breeders. DeltaBreed was used to create traits in Breedbase, and Field Book was used to pull studies and traits from Breedbase. The workflow also permitted users to push Field Book observations back to Breedbase via BrAPI. This effort served as a successful proof of concept for multi-application BrAPI integration, but highlighted limitations to the process of accepting BrAPI observations from Field Book. The Breeding Insight team is actively working with the rest of the BrAPI community to correct these limitations in future versions of the specification.

DeltaBreed is integrated with many other BrAPI community projects and tools. There is a BrAPI enabled connection, either in development or production, with all of the following tools: [BrAPI Java Test Server](#), [BreedBase](#), [Field Book](#), [Gigwa](#), [QBMS](#), [Mr Bean](#), [Helium](#) and the [Pedigree Viewer](#) BrAPP.

FAIDARE

[FAIDARE](#)⁸ is a data discovery portal providing a biologist friendly search system over a global federation of 40 plant research databases at the time of writing. It allows users to identify data resources using a full text search approach combined with domain specific filters. Each search result contains a link back to the original database for visualization, analysis, and download. The indexed data types are very broad and include genomic features, selected bibliography, QTL, markers, genetic variation studies, phenomic studies, and plant genetic resources. This inclusiveness is achieved thanks to a two stage indexation data model. The first index, more generic, provides basic search functionalities and relies on five fields: name, link back URL, data type, species, and exhaustive description. To provide more advanced filtering, the second stage indexation mechanism takes advantage of BrAPI endpoints to get more detailed metadata on germplasm, genotyping studies and phenotyping studies.

The indexation mechanism relies on a [public software package](#) that allows data resource managers to request the indexation of their database. This BrAPI client is able to extract data from any BrAPI 1.3 and 1.2 endpoint. The development of BrAPI 2.x indexation will be initiated in 2025. Since not all databases are willing to implement BrAPI endpoints, it is possible to generate metadata as static BrAPI compliant JSON files, using the BrAPI standard as a file exchange format.

The FAIDARE architecture has been designed by elaborating on the BrAPI data model mixed with the GnplS Software Architecture²⁶. It uses an Elasticsearch NoSQL engine that searches and serves enriched versions of the BrAPI JSON data model. FAIDARE also includes a BrAPI endpoint using all indexed metadata. It has been adopted by several communities including the ELIXIR and EMPHASIS European infrastructures, and the WheatIS of the Wheat-Initiative. Several databases are added each year to the FAIDARE global federation, allowing to increase both the portal and the BrAPI adoption.

Germinate

[Germinate](#)^{42,43} is an open-source plant genetic resources database that combines and integrates various kinds of plant breeding data including genotypic data, phenotypic trials data, passport data, images, geographic information and climate data into a single repository. Germinate is tightly linked to the BrAPI specification and supports a majority of BrAPI endpoints for querying, filtering, and submission.

Germinate integrates and connects with other BrAPI-enabled tools such as GridScore for phenotypic data collection, Flapjack for genotypic data visualization, and Helium for pedigree visualization. Additionally, due to the nature of BrAPI, Germinate can act as a data repository for any BrAPI-compatible tool. Thanks to the interoperability provided by BrAPI, the need for manual data handling becomes a rarity with the direct benefit of faster data processing, fewer to no human errors, data security, and data integrity.

Analytics

Modern breeding programs can utilize data management systems to maintain both phenotypic and genotypic data. Numerous systems are available for adoption. To fully leverage the benefits of digitalization in this ecosystem, breeders need to utilize data from different sources to make efficient data-driven decisions. With increased computational power at their disposal, scientists can construct more advanced analysis pipelines by combining various data sources.

The tools developed by the BrAPI community can pull in data from multiple BrAPI compatible data sources and provide enhanced analytical functionality. In many cases, there is no longer a need to import and export large data files to a local computational environment just to run standard analytical models. These tools are able to extract the data they need from a data source without much human intervention or human error.

G-Crunch

G-Crunch is an upcoming user-facing analysis tool that integrates genomic and phenotypic data to fulfill the need for simple, user driven analytics requests. It includes a generic user interface and the ability to swap out data sources and analysis tools. The G-Crunch team hopes to streamline repeatable, debuggable, simple analytic requests and results.

G-Crunch, as a tool, couldn't feasibly exist without BrAPI. The support of BrAPI interfaces allows G-Crunch to use one unified request method, and adapt to the user's (BrAPI-compliant) existing network of tools. This lowers the barrier to entry for adoption, and makes analysis pipelines easily repeatable.

QBMS

The [QBMS](#)⁴¹ R package eliminates technical barriers scientists experience when using the BrAPI specification in their analysis scripts and pipelines. This barrier arises from the complexity of managing API backend processes, such as authentication, tokens, TCP/IP protocol, JSON format,

pagination, stateless calls, asynchronous communication, database IDs, and more. To bridge this gap, the QBMS package abstracts the technical complexities, providing breeders with stateful functions familiar to them when navigating their GUI systems. It enables them to query and extract data into a standard data frame structure, consistent with their use of the R language, one of the most common statistical tools in the breeding community.

Since its release on the official CRAN repository in October 2021, the QBMS R package has garnered over 9400 downloads. Several tools, such as MrBean, rely on the QBMS package as their source data adapter. Moreover, the community has started building extended solutions on top of it. QBMS can serve as a cornerstone in the breeding modernization revolution by providing access to actionable data and by enabling the creation of dashboards to reduce the time between harvest and decision-making for the next breeding cycle.

Mr.Bean

[Mr.Bean⁴⁴](#) is a graphical user interface designed to assist breeders, statisticians, and individuals involved in plant breeding programs with the analysis of field trials. By utilizing innovative methodologies such as SpATS for modeling spatial trends, and autocorrelation models to address spatial variability, Mr.Bean proves highly practical and powerful in facilitating faster and more effective decision-making. Modeling Genotype-by-environment interaction poses its challenges, but Mr.Bean offers the capability to explore various variance-covariance matrices, including Factor Analytic, compound symmetry, and heterogeneous variances. This aids in the assessment of genotype performance across diverse environments.

Mr.Bean boasts flexibility in importing different file types, yet for users managing their data within data management systems (DMS), the process of downloading from their DMS and importing it into Mr.Bean can be cumbersome. To address this issue, QBMS was integrated into the back-end. This feature prompts users to input the URL of a BrAPI compatible server, enter their credentials (if necessary), and select the specific trial they wish to analyze. Subsequently, users can seamlessly access their dataset through BrAPI and utilize it across the entire Mr.Bean interface.

SCT

The [Sugarcane Crossing Tool](#) (SCT) is a lightweight RShiny dashboard application designed to receive, process, and visualize data from a linked BreedBase³⁸ instance. This application is being developed collaboratively with members of the [Sugarcane Integrated Breeding System](#), who have advocated for an application that assists them in designing crosses based on queried information from a list of available accessions. By leveraging existing community resources, the team has been able to develop a simple, BrAPI-enabled, application without possessing extensive programming knowledge or experience. The SCT is presented as an inspiration for similarly positioned scientists to consider developing custom applications for specific tasks.

The crossing tool utilizes a modified version of the [BrAPI-R](#) library to access a compliant database, and it employs standard R/JavaScript packages to aggregate and visualize data. Modules within the application allow breeders to query the database (through BrAPI) for information relevant to their decision-making process. This includes the number and sex of flowering accessions, deep pedigree and relatedness information, summarized trial data, and the prior frequency and success of potential cross combinations. Future versions of this tool will provide additional decision support (e.g. ranked potential crosses) to enhance the accuracy and efficiency of crossing.

ShinyBrAPPs

Data management systems are generic and robust centralized applications, with a large community of users, long term development cycles and release plans. BrAPI compliance offers these systems the opportunity to add functionalities in a modular way through the development of external plugin applications that can quickly fulfill specific needs of a group of users. [R-Shiny](#) is a R-package that opens the possibility to develop rich and productive interactive web applications to R users and developers. As such it allows user communities to quickly prototype and produce applications that are finely tailored to their needs, thus improving adoption and daily use of data management systems. The Breeding Management System (BMS) of the IBP and Gigwa are BrAPI compliant and are being widely used by breeding programs, including national breeding programs in Africa. CIRAD and the IBP teams have been working together as part of the [IAVAO](#) breeders community to develop the Shiny-BrAPPs, a set of R-Shiny applications using BrAPI as a core technology for data exchange. These applications are connected to BMS and/or Gigwa and provide tools for specific use cases. So far, four applications have been developed covering the fields of trial data quality control, single trial statistical analysis, breeding decision support, and raw genotyping data visual inspection.

The “BMS trial data explorer” retrieves data from a single multi-location trial and displays data counts and summary boxplot for all variables measured in different studies. It also provides an interactive distribution plot to easily select observations that require curation and a report of candidate issues that needs to be addressed by the breeder. The “STABrAPP” tool is an application for single trial mixed model analysis. It basically provides a GUI to the [StatGen-STA](#) R package. The “DSBrAPP” tool is a decision support tool helping breeders to select germplasm according to their various characteristics and save this germplasm list into BMS. These first three apps are grouped into a single repository ([ShinyBrAPPs](#)) with modular code shared across applications and make use of the [brapir-v1](#) and [brapir-v2](#) R packages. Finally, the “[snpclust](#)” tool enables a user to check and manually correct the clustering of fluorescence based SNP genotyping data.

General Infrastructure

Adopting BrAPI compatibility into an existing system can be difficult sometimes. The BrAPI Community has developed several tools to make adoption easier. This includes things like pre built code libraries, connectors to other technology standards, and mappers to alternate data types or data files. The goal is to lower the barrier to entry for the BrAPI community, making it easier for other groups to get started and connect their existing data to the standard.

BrAPIMapper

[BrAPIMapper](#) is a full BrAPI implementation designed to be a convenient wrapper for any breeding related data source. BrAPIMapper is provided as a Docker application that can connect to a variety of external data sources including MySQL or PostgreSQL databases, generic REST services, flat files (XML, JSON, CSV/TSV/GFF3/VCF, YAML), or any combination of these. It provides an administration user interface to map BrAPI data models to external data sources. The interface allows administrators to select the BrAPI specification versions to use and which endpoints to enable. Data mapping configuration import and export features simplify upgrades to future BrAPI versions; administrators only have to map missing fields or make minor adjustments. BrAPIMapper supports the primary BrAPI features including paging, deferred search results, user lists, and authentication. Access restrictions to specific endpoints can be managed through the administration interface as well. This tool aims to accelerate BrAPI services deployment while ensuring specification compliance.

BrAPI2ISA

Since the release of BrAPI 1.3, efforts have been made to incorporate support for the [MIAPPE](#) (Minimal Information About a Plant Phenotyping Experiment)² standard into the specification,

achieving full compatibility in BrAPI 2.0. Consequently, BrAPI now includes all attributes necessary for MIAPPE compliance, adhering to standardized descriptions in accordance with MIAPPE guidelines. In some communities and projects, phenotyping data and metadata are archived and published as structured ISA-Tab files, validated using the [MIAPPE ISA configuration](#)⁴⁵. Although ISA-Tab is easy to read for non-technical experts due to its file-based approach, it lacks programmatic accessibility, particularly for web applications.

[MIRA](#) enables the automatic deployment of a BrAPI server on a MIAPPE-compliant dataset in ISA-Tab format, facilitating programmatic access to these datasets. It is deployable from a Docker image with the dataset mounted. The tool leverages the mapping between MIAPPE, ISA-Tab, and BrAPI, eliminating the need for parsing or manual mapping of datasets compliant with (meta-)data standards. By providing programmatic access through BrAPI, MIRA facilitates the integration of phenotyping datasets into web applications.

The [BrAPI2ISA](#) service functions as a converter between a BrAPI-compatible server and the ISA-Tab format. The tool simplifies, automates, and facilitates the archiving of data, thereby enhancing data preservation and accessibility. The BrAPI2ISA tool is compatible with BrAPI 1.3 and welcomes community contributions to support the latest versions of BrAPI.

GraphQL Data-warehouse

Using the [Zendro](#) set of automatic software code generators, a fully functional, efficient, and cloud-capable BrAPI data-warehouse has been created for the current version of the BrAPI data models. Unlike most BrAPI compliant data sources, this data-warehouse supports a GraphQL API rather than a RESTful API. This API provides secure access to data read and write functions for all BrAPI data models. It provides create, read, update, and delete (CRUD) functions that are standardized and accept the same parameters for all data models.

The GraphQL server is particularly rich in features. Records are paginated using the highly efficient cursor based pagination model as proposed in the GraphQL standard. Logical filters allow for exhaustive search queries, whose structure is highly intuitive and based around logical triplets. A large collection of operators is available and triplets can be combined to logical search trees using “and” or “or” operators. Searches can be extended over relationships between data models, thus enabling a user to query the warehouse for exactly the required data. Access security is implemented with the OAuth2 user authentication standard⁴⁶. Authorization is based on user roles and can be configured differently for each single data model read or write function. The generated graphical interface allows for the integration of interactive scientific plots and analysis tools written in JavaScript or WebAssembly.

The Zendro data-warehouse is capable of forming an efficient cloud of data servers. This is achieved simply by linking other Zendro based warehouses that expose the same GraphQL API to the same data models, or a subset of data models. Any network of such Zendro GraphQL servers can be set up using this configuration approach. The code generated then exposes full access to all data records stored on any node of the network, while maintaining full security control at each node. Importantly, the warehouses are programmed in such a way that any number of data servers can be joined without loss of efficiency.

Discussion

BrAPI for Breeders and Scientists

The BrAPI technical specification document is meant to be read and used by software developers. However, the purpose of the specification, and the community around it, is to make things faster, easier, and cheaper for the breeders and scientists working on breeding, genetics, phenomics and other agricultural projects. BrAPI offers a convenient path to automation, interoperability, and data integration for software tools in those domains. All of the software described above could be made interoperable with manual effort, moving and editing data files by hand from tool to tool. However, when the basic structure and flow of data becomes automated, breeders and scientists can spend less time on data management and more time focusing on the science. For many, the ultimate goal is the development of a digital ecosystem: a collection of software tools and applications that can all work together seamlessly. In this ideal digital ecosystem, data is collected digitally from the beginning, reducing as much human error as possible. The data is checked by quality control and stored automatically, then it can be sent to any internal tool or external lab for further analysis with just the click of a button. This idea might sound too good to be true, but as more tools start sharing a universal data standard, automating data flow becomes easier, and the community gets closer to total interoperability.

Looking Ahead

The BrAPI specification will continue a controlled and necessary growth. It will enable more use cases and new types of data that might include newer scientific techniques and technologies. There will be careful evaluation of the relevance of using REST web service approaches, and in particular BrAPI, for things like drone imaging data, spectroscopy, LIDAR, metabolomics, transcriptomics, high-throughput phenotyping, pan genomes, and machine learning analysis. All of these technologies can open new avenues for research and development of new crop varieties. However, they will also generate more data, more types of data, and require data sharing between different software applications and data repositories. The BrAPI project leadership and community is committed to building the standards to support these new use cases as they arrive and become accepted by the scientific community. In fact, small groups within the BrAPI community have already start building generic data models and proposed communication standards for many of the technologies listed above. These community efforts will eventually become part of the BrAPI standard in a future version of the specification document.

Expanding the BrAPI specification is important for the community, however it is just as important not to reinvent or compete with existing functional standards. Additions to the BrAPI specification are reviewed thoroughly by the community to make sure BrAPI is compliant with existing standards and data structures. For example, the community has requested compliance with the GFF3 standard for genomic data and the GeoTIFF standard for aerial image data. Pieces of these existing popular data structures might be integrated into the overall BrAPI standard documentation. In some cases, BrAPI will only reference other standards instead of including them in the specification. For example, there have been community discussions around developing connections with the NOAA CDO standard for weather data, or the Galaxy Analytics API for analytics pipeline controls and information. These standards are perfectly adequate on their own, recreating them in the BrAPI standard would be redundant and outside the main scope of the project.

Conclusion

The BrAPI project only exists because of the community of software engineers, biologists, and other scientists who support and use it. While there were many tools and use cases presented here, it is not an exhaustive list of all BrAPI compliant systems. As long as the standard continues to be supported, there is potential for exponential growth of the community. As more groups make their tools BrAPI compliant, these tools can be shared with the community. As more BrAPI compliant tools are shared with the community, more groups can see the value in implementing BrAPI in their own tools. This feedback loop will allow the community to strengthen and grow.

If this manuscript is your first introduction to the BrAPI project, the authors invite you to join the community. More information is always available at brapi.org.

Methods

The BrAPI Project day-to-day operations are run by the BrAPI Project Coordinator, overseen by the grant PI and Co-PI. The BrAPI Project Coordinator is responsible for the general maintenance of the project infrastructure, as well as coordinating updates to the standard. They organize community events and encourage collaboration between community groups. Long term planning and organization is handled by the BrAPI Advisory board. This is a board of 6 community members who are elected by the community to represent their interest in the project.

The standard documentation is stored and maintained in a GitHub repository. The core documentation is written using the OpenAPI 3 documentation standard, and can be easily transformed into other documentation standards as needed. Copies of the core documentation is published on the API documentation sites Apiary and SwaggerHub for maximum accessibility by the community. All these online locations are public, and the specification has a standard MIT open source license.

New versions of the BrAPI standard are developed periodically based on community demand. Problems and enhancements are collected by the community over time, tracked in GitHub issues, then implemented together to create a new stable version. This ensures the standard stays up-to-date and relevant to the community, but maintains a certain level of stability over time. Minor version updates are designed to be backward compatible to further enhance the stability of the standard.

As discussed above, hackathon events are the primary way the BrAPI community stays together. One in-person and one virtual event per year maintain project momentum and social comradery. The hackathons provide a dedicated time to discuss issues and enhancements with the specification, particular use cases, and generally how the community is run and organized.

Data Availability Statement

No data was generated from this project.

Code Availability Statement

The all of software and documentation generated by the BrAPI project is free, public, and open source. Everything is available under the MIT open source license, and can be accessed through brapi.org. Most of the other software projects referenced and discussed here are also open source and the text contain links to their repositories or project pages. However, the authors take no responsibility for their availability or licensing.

Competing Interests Statement

The authors declare no competing interests.

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