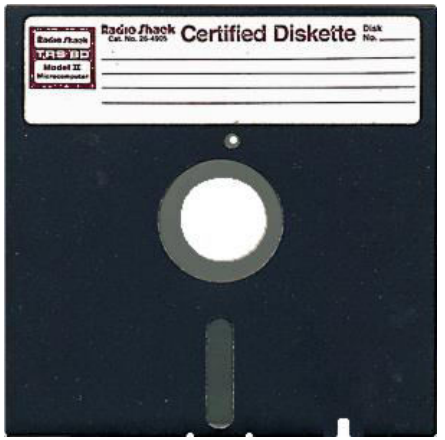
Introduction to the Sweetpotato (SP) Database Infrastructure

Purpose & Goals

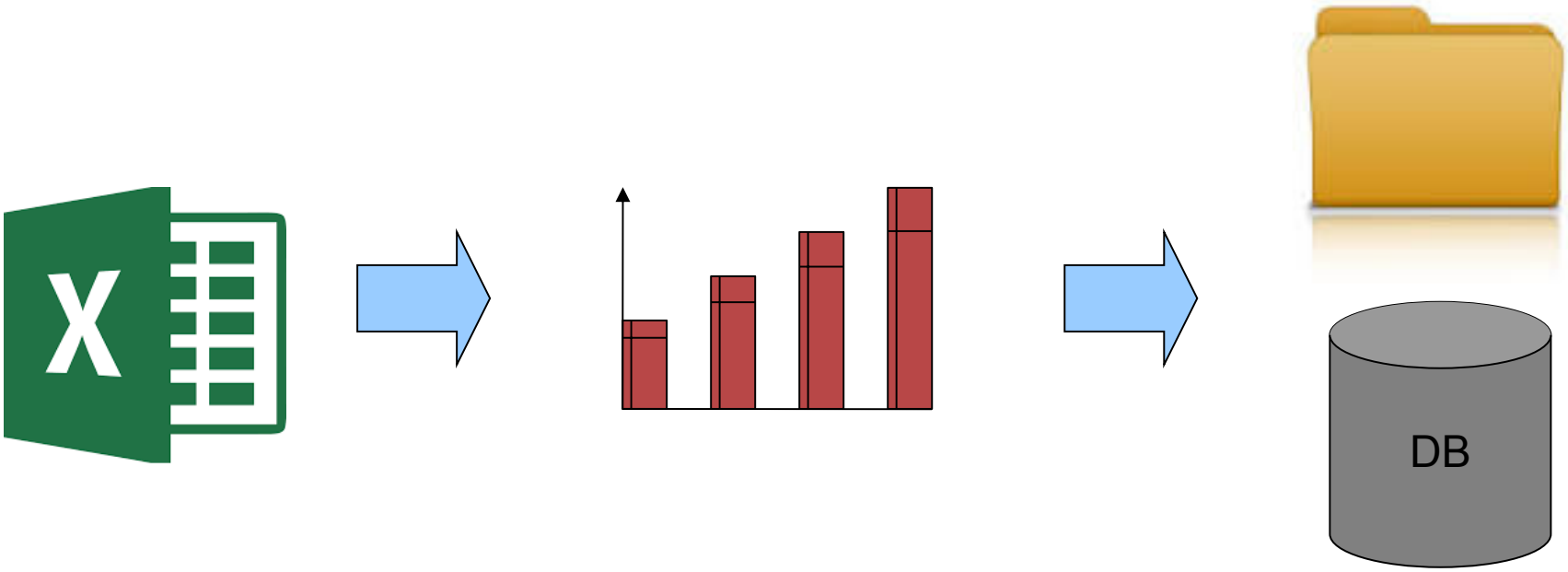
- Efficient storage of all SP breeding data
- Trial data, phenotypic and genotypic information, metadata
- Incorporate analysis tools
- Easy querying: Slice data by year, location, program, etc.
- Enable new, genome-based breeding methods

Rony Swennen’s banana breeding notebooks on their way to Belgium

1980s: The Personal Computer Revolution



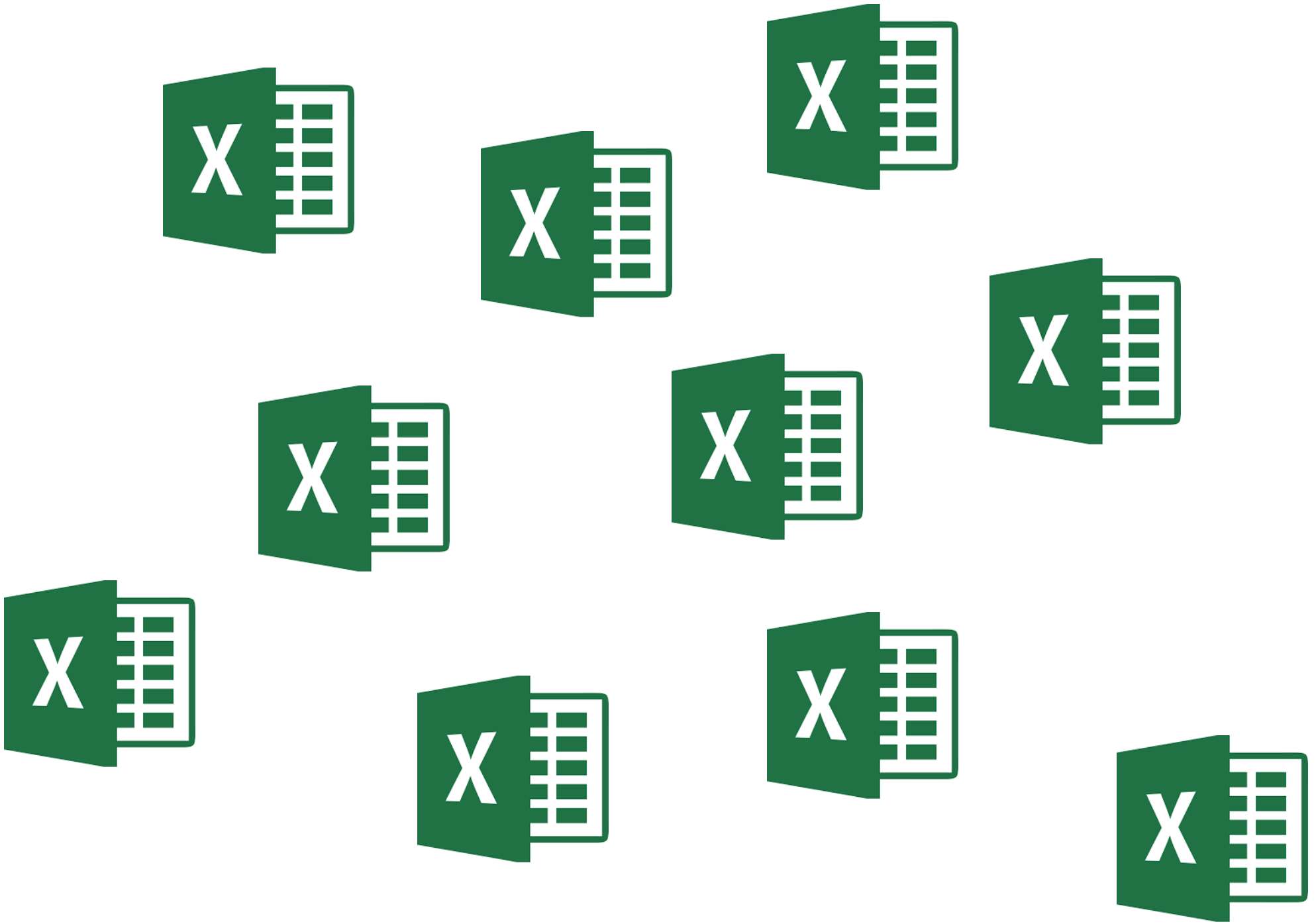
Excel-based data management

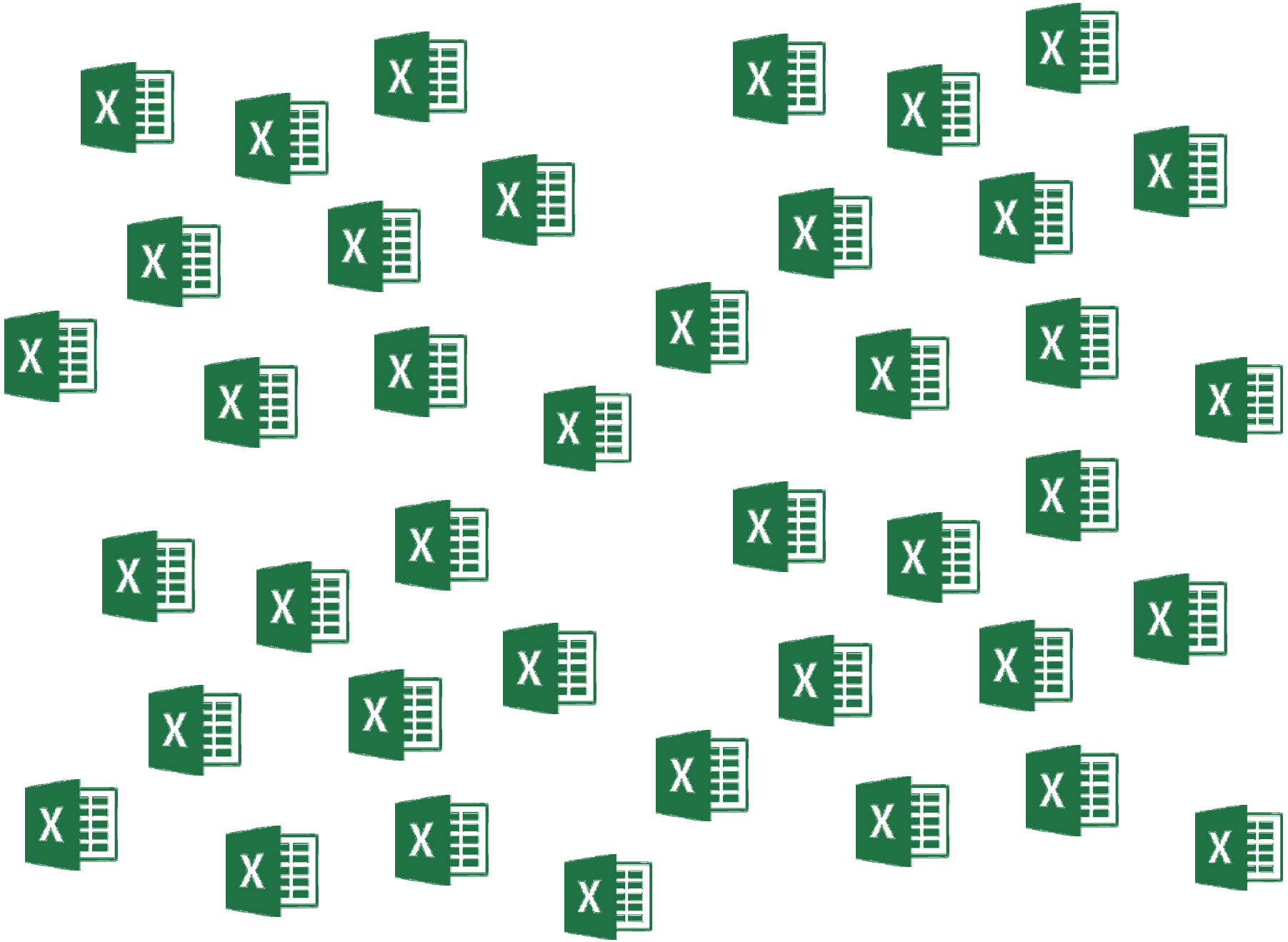


Experiment planning & Data Capture

Data Analysis

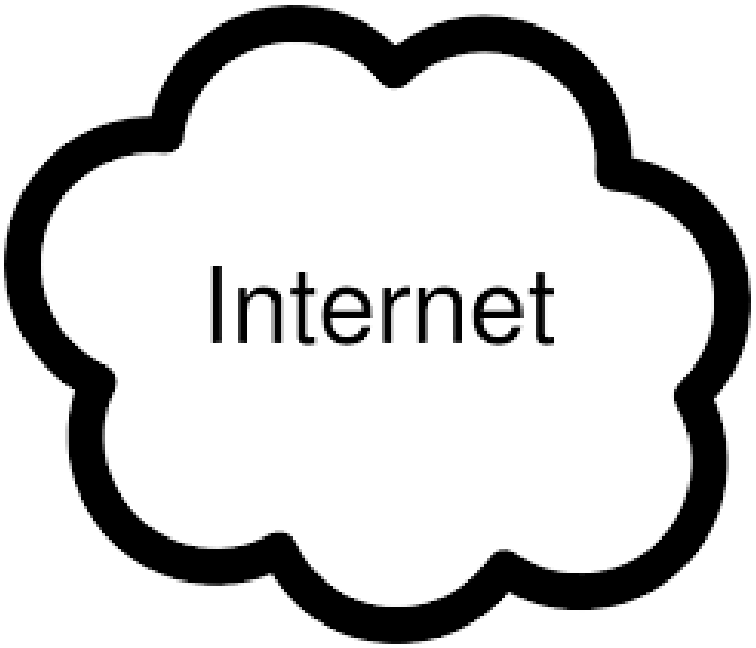
Storage





Data Management with Excel

- Plusses
  - Easy to use
  - User has complete control
- Minuses
  - Sharing Data
  - Combining Data
    - Data Analysis difficult across sheets
  - Data Integrity
  - Becomes difficult to manage for large datasets
  - Difficult to manage genotyping information


Internet

Data management using the “cloud”

- Most data is managed using the web
  - Youtube for videos
  - Google for documents
  - Flickr, iCloud etc. for photos
  - Twitter for status updates
  - etc.
- What about breeding data?

Data Infrastructure

Main Datastore

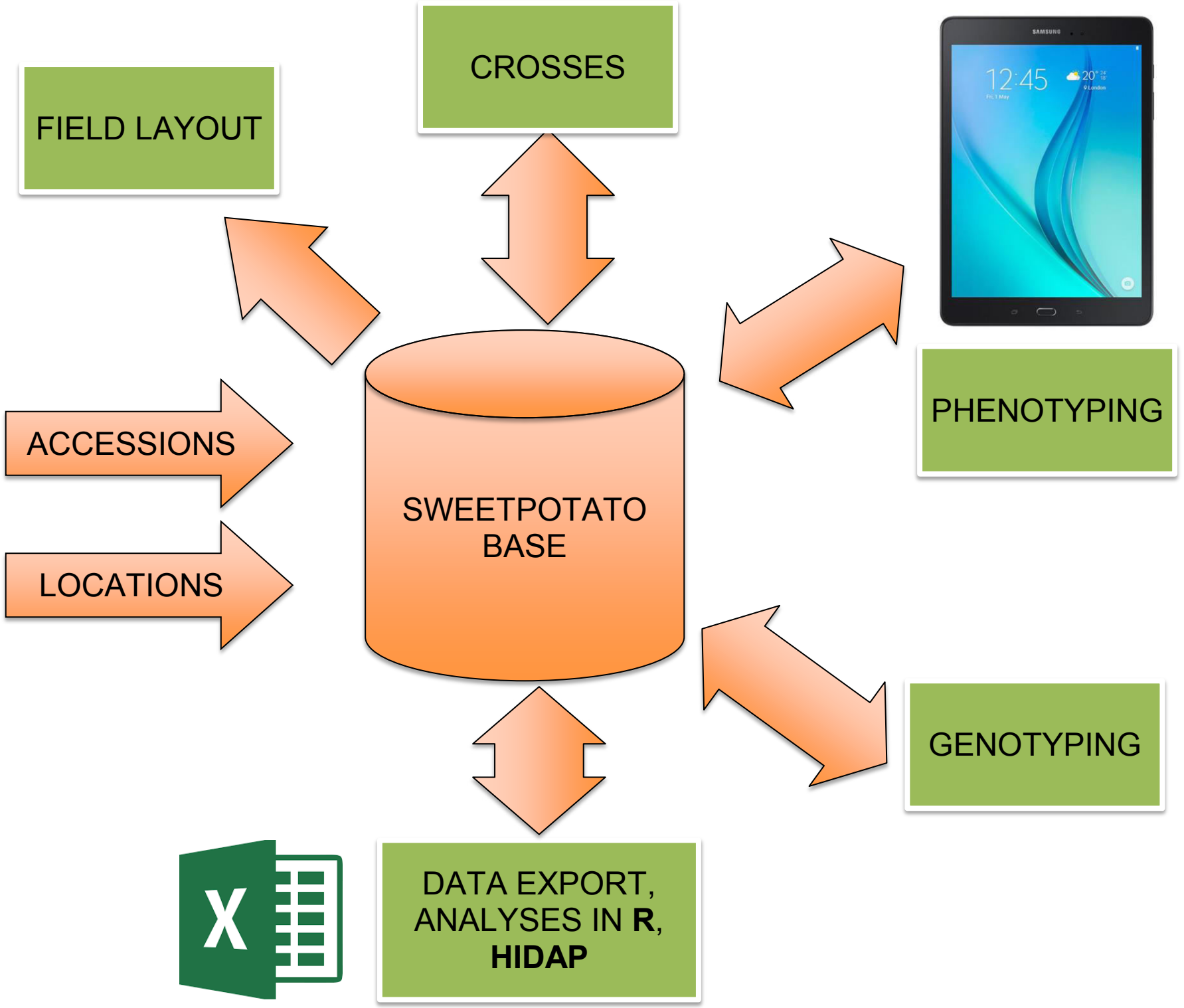
- https://sweetpotatobase.org/

Analysis (integrated with sweetpotatobase)

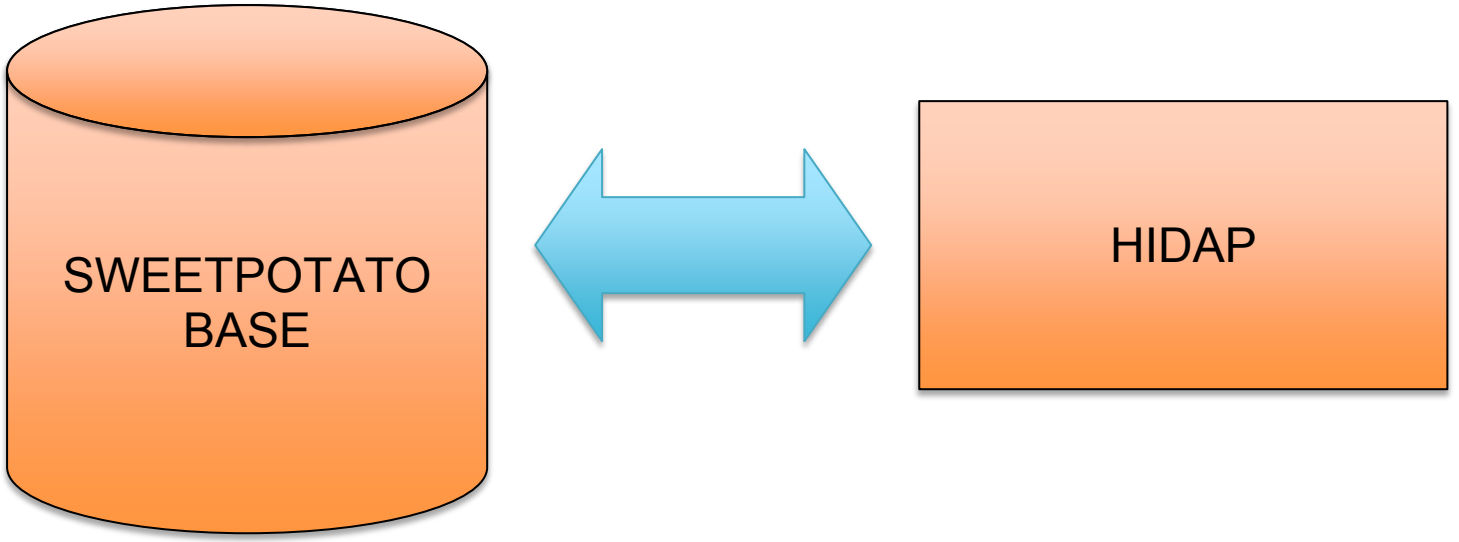
- http://hidap.sgn.cornell.edu/

Data Collection

- Android FieldBook App
- AccuDataLogger


FIELD LAYOUT
CROSSES
PHENOTYPING
ACCESSIONS
LOCATIONS
SWEETPOTATO BASE
GENOTYPING
DATA EXPORT, ANALYSES IN **R**, **HIDAP**

BrAPI



- The Breeding API
  - Application Programming Interface
- Standardized way to exchange breeding data between applications over the internet
- http://brapi.org/

Database Requirements

Standardization of

- Trait dictionary and measurement procedures
  - Ontologies (Reinhard)
- Naming of plant accessions

Genotyping data

- Can be extremely voluminous data
  - (GBS, etc)
- Must be integrated with phenotypic data
- For Cassavabase, already 1.5 billion data points
- Hard to manage without a database

Data Security on the Web

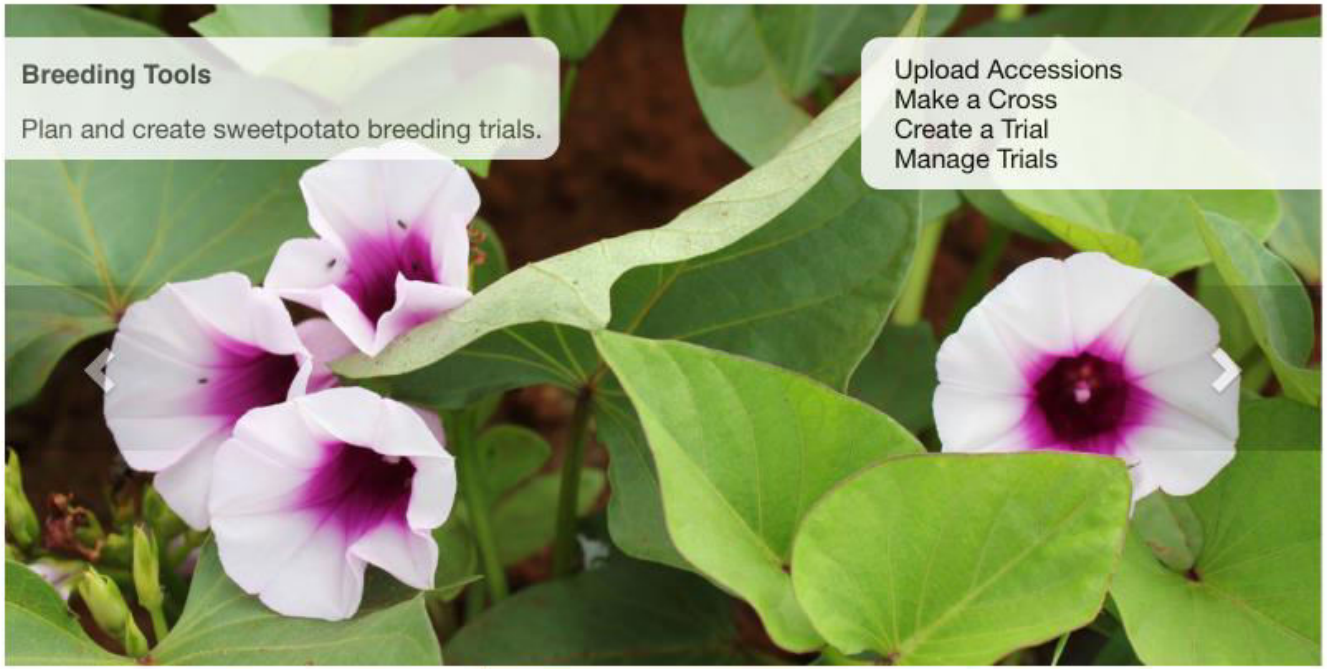
- Data protected by logins
- Different levels of user access privileges
- Regular on-site and off-site backups

Open Data Policy

- Data on Sweetpotatobase are open
- Need a user account to download
- Downloads are tracked by account

sweetpotatobase.org

SweetPotatoBase Search Manage Analyze About Login



Search | Breeding Tools | Phenotypes | Genotypes | GT4SP Project | Slideshare

You have already accepted the website usage policy. Thank you.

Site News

Phenotype Demo

A powerpoint covering how phenotyping and round

Featured Publication

Featured Publication

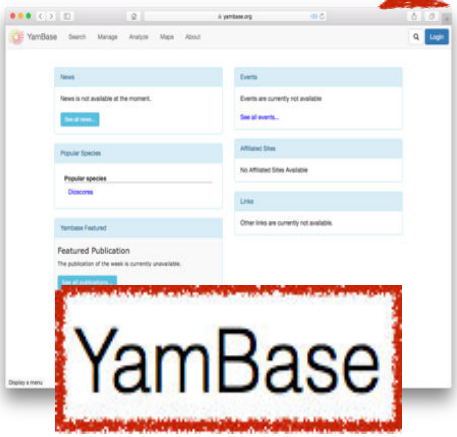
https://solgenomics.net

https://github.com/solgenomics

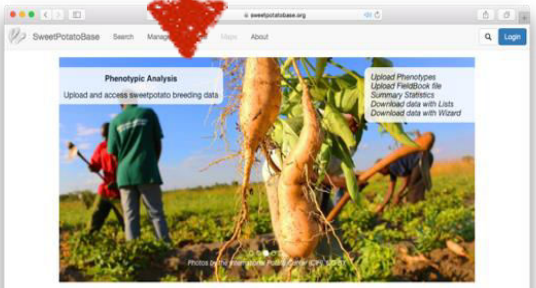
https://cassavabase.org

Citrus Greening

https://citrusgreening.org



https://yambase.org



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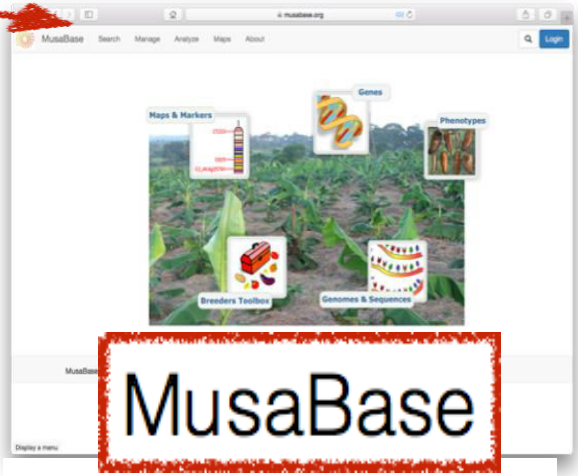

https://musabase.org

“Cloud” approach

- Plusses
  - Easy to use through a web browser
  - No software installation necessary
    - Software is continuously updated
  - All data automatically integrated
    - Query over several years, locations, etc. possible
  - Integrates phenotypic with genotypic data
- Minuses
  - Internet needs to work

Asante!