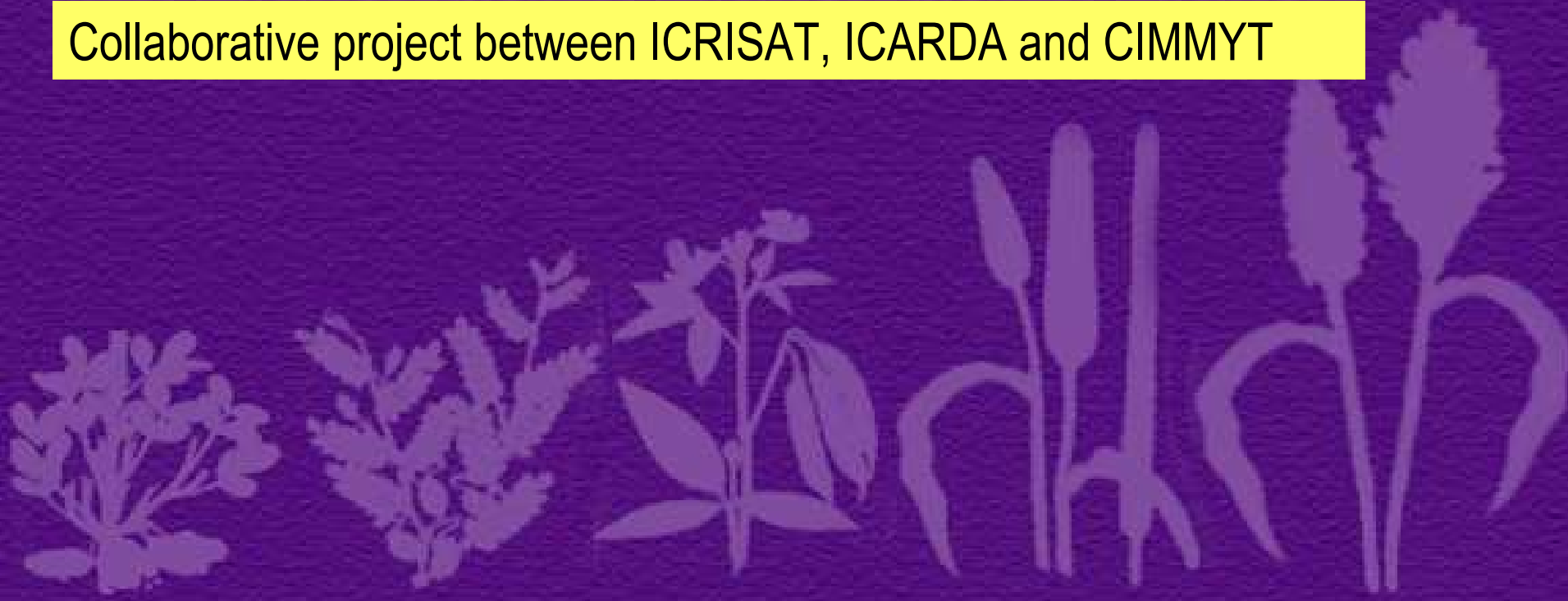




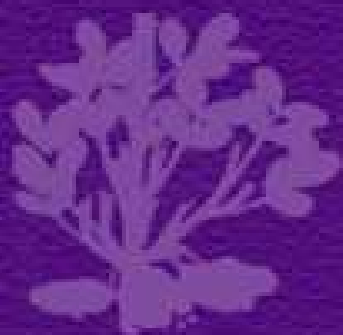
# Software for genotyping workflow

Collaborative project between ICRISAT, ICARDA and CIMMYT

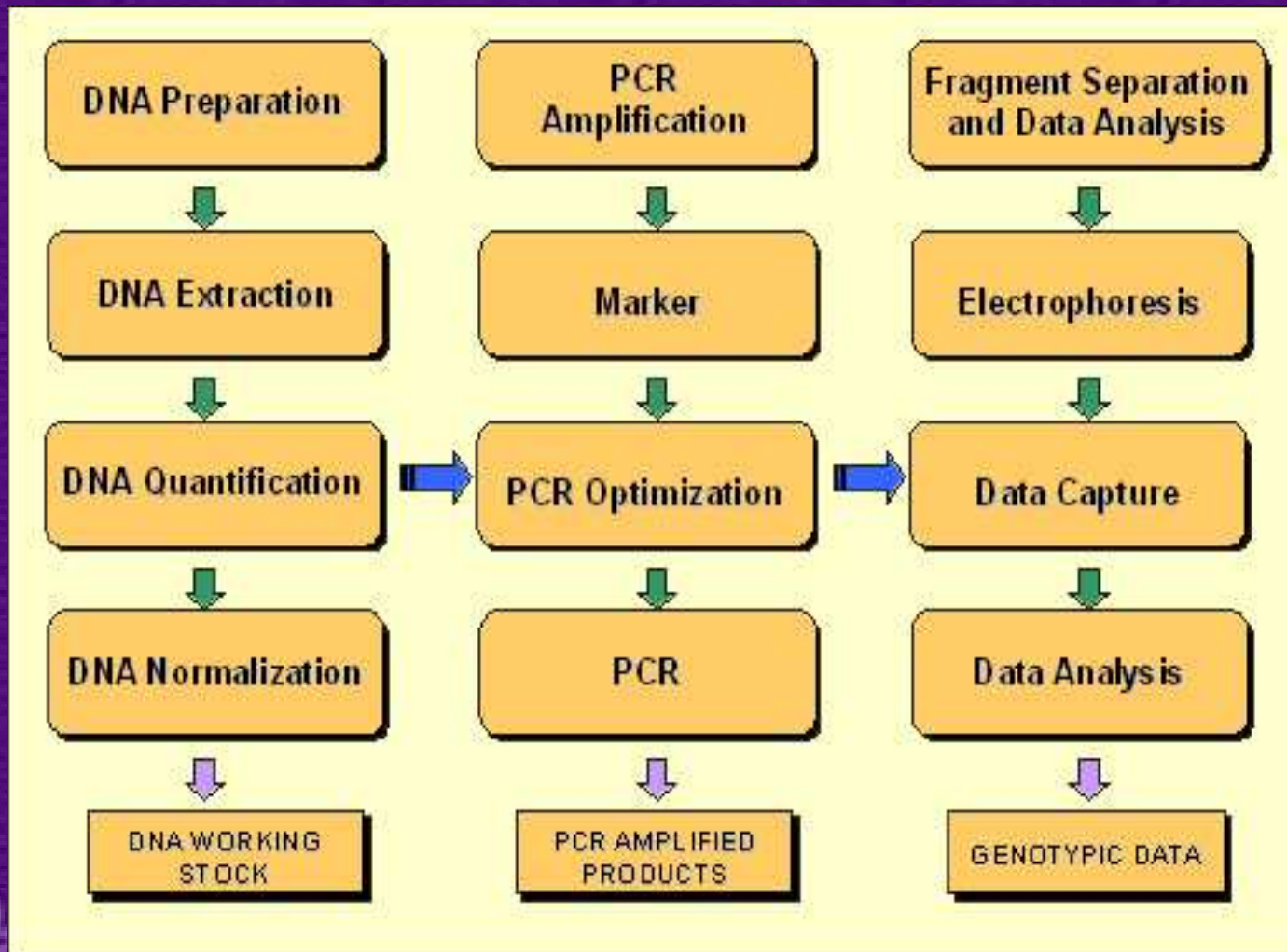




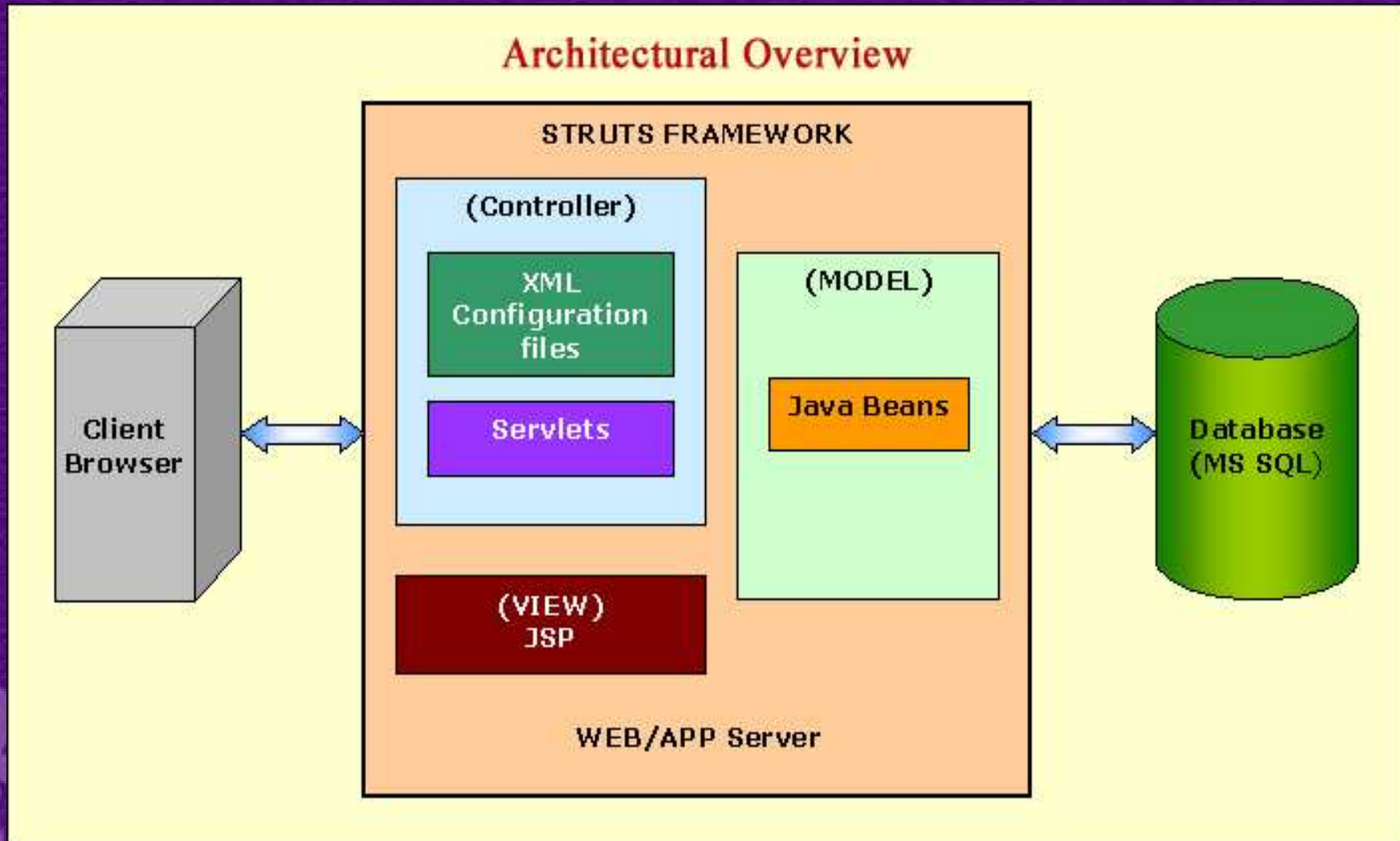
- A data capture software that feeds into the data source layer of the GCP platform
- Development : java, 3 tier architecture
- Has evolved from a 2-tier OS dependent application.
- User driven development : functionality and GUI
- Application has evolved: modular development, considers issues in genotyping data.



# The genotyping workflow



# System Architecture



# The database

## Experiment - Startup

Experiment_Master	
(PK)	Experiment_Name
	Description
	Location
	Year_Of_Experiment
	No_Of_Genotypes
	User_Id
	Crop_Name
	Project_Name
	Study_Name
	Date_of_Creation
	Date_of_Correction

Genotype_Traitdetails	
(FK)	LIMS_Id
	Trait_Name
	Trait_Value

Genotype_Master	
(PK)	LIMS_Id
	Genotype_Id
(FK)	Experiment_Name
	User_Id
	Date_of_Creation
	Date_of_Correction

## Sample Tracking

DNA_Extraction_Well	
(FK)	DNA_Plate_Id
(FK)	LIMS_Id
	Col_Id
	Row_Id

DNA_Extraction_Tracking	
(PK)	DNA_Plate_Id
	DNA_Extraction_Protocol
	Plate_Type
	User_Id
	Date_of_Creation
	Date_of_Correction

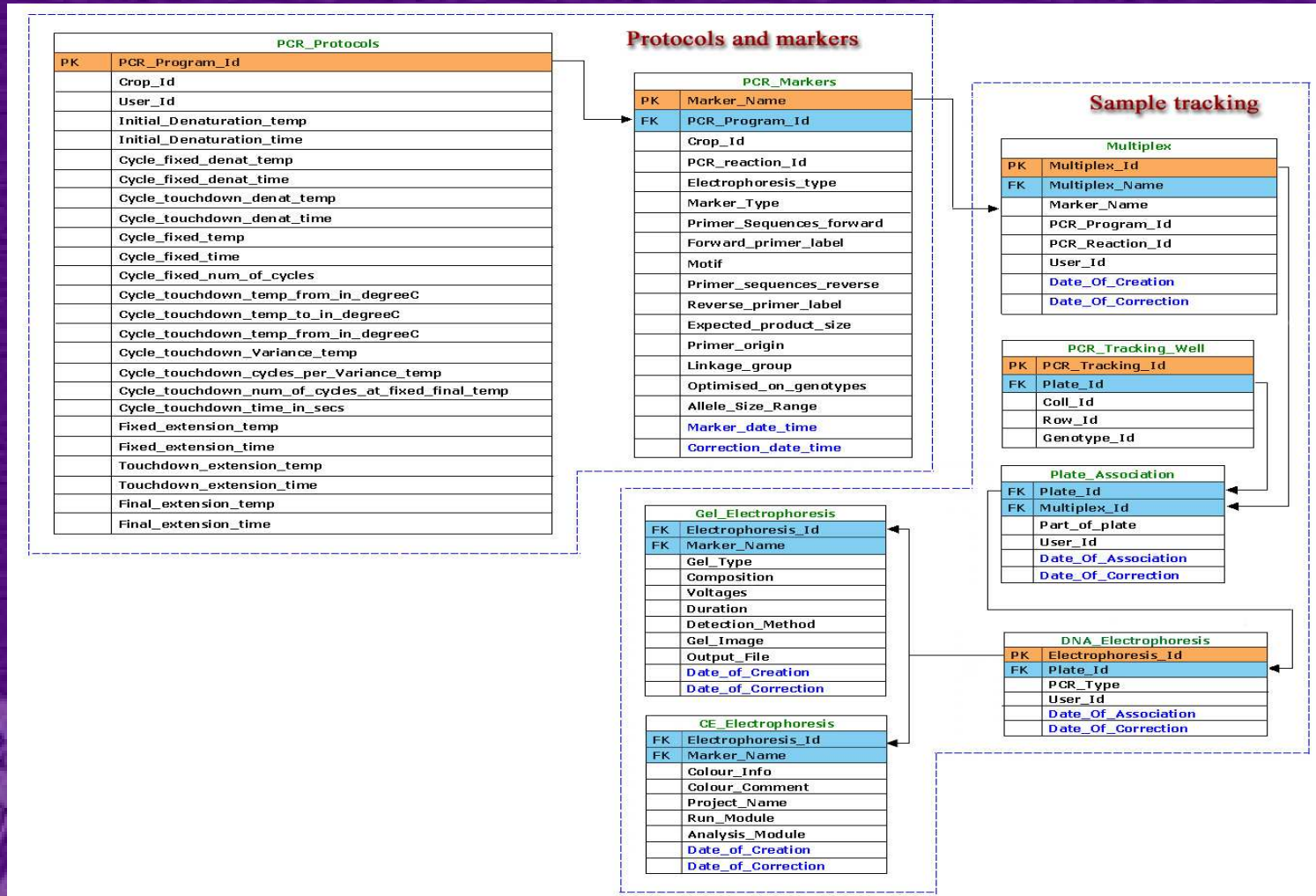
DNA_Dilution	
(FK)	DNA_Plate_Id
(FK)	DNA_Quantification_Set
	Dilution_Concentration
	Dilution_Reagent
	Total_Volume
	Remarks
	User_Id
	Date_Of_Creation
	Date_Of_Correction

DNA_Quantification_Trackingdetails	
(FK)	DNA_Plate_Id
(FK)	DNA_Quantification_Set
	Col_Id
	Row_Id
	DNA_Concentration
	Tecanbackground
	Tecansamples

DNA_Quantification_Tracking	
(FK)	DNA_Plate_Id
(PK)	DNA_Quantification_Set
	Protocols_Selected
	DNA_Quantification_Protocol
	Concentration_Type
	Dilution_Factor_Value
	Gel_Image
	User_Id
	Date_of_Creation
	Date_of_Correction



# The database





# Functional highlights



- Generates extraction plates, PCR plates, input files that can be read by the software on the Tecan (robotics) machine , creates plate records for the ABI 3100/3700 data collection software.
- Stock calculation, marker sets/multiplex sets.

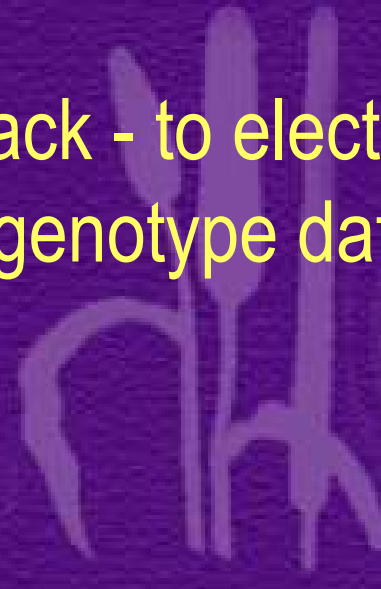




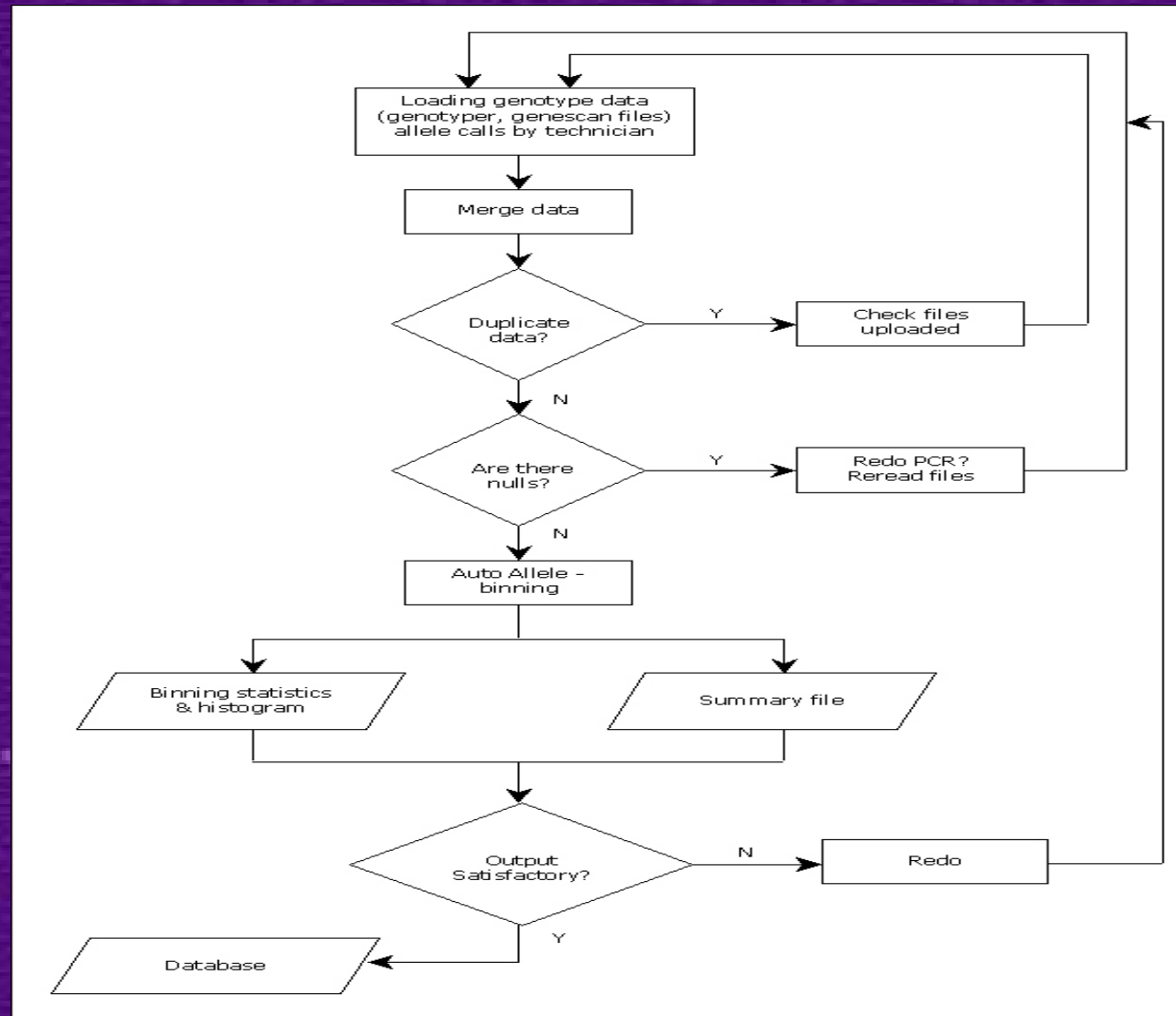
# Functional highlights



- Ensuring data quality.
- Automated allele binning, uses a slight variation of the method of Idury and Cordon, 1997. Coded in Java and embedded within LIMS.
- Provides functions to trace back - to electrophoresis files or sample source for any genotype data.



# Data loading and auto-binning





- Application for high throughput genotyping of SSR data.
- Being used at ICRISAT.
- Application installed and tested at CIMMYT.
- Being tested at ILRI, ICRISAT-Nairobi and IITA.





The genotyping LIMS project page:

<http://www.icrisat.org/gt-bt/lims/lims.html>

The older version of the LIMS is available at:

<http://www.icrisat-intranet/lims/user.html>

Demonstration of the  
[Genotyping LIMS in Java](#)

