



# ShiNyP: Platform for SNP Analysis and Visualization

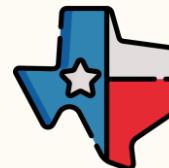
## Teddy (Yen-Hsiang Huang)



MS Student in Agronomy at NCHU, Taiwan



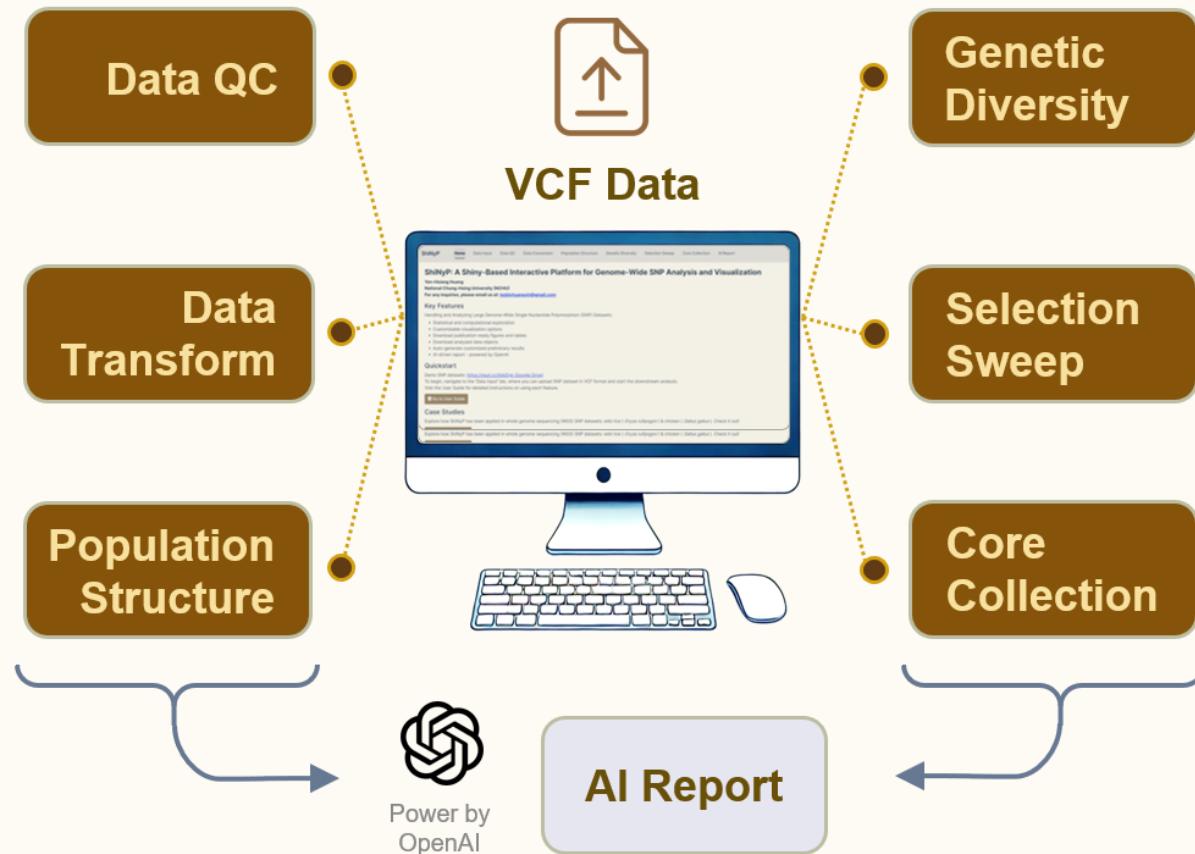
Visiting Student at TAMU, Texas



teddyenn2@gmail.com



# ShiNyP: Platform for SNP Analysis and Visualization



#Real-time  
#Interactive  
#Customizable

One VCF → 70+ outputs

# Shiny: A web application framework for R

## *ShiNyP* was built on Shiny framework



## SNP: Single Nucleotide Polymorphisms

### *ShiNyP* only accept SNP data as input





## Resources



[https://github.com/TeddYenn/ShiNyP\\_PAG32](https://github.com/TeddYenn/ShiNyP_PAG32)



Huang et al. *ShiNyP*: An Interactive *Shiny*-Based Platform for Genome-Wide SNP Analysis and Visualization

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# Population Structure?

2

*"ShiNyP"*

3

~Demo~

4

Shiny Framework



Resources



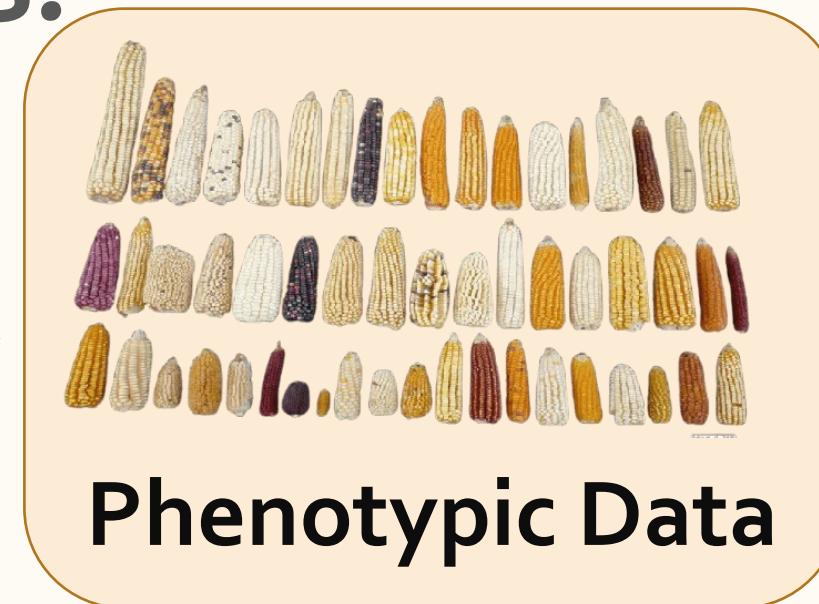
[https://github.com/TeddYenn/ShiNyP\\_PAG32](https://github.com/TeddYenn/ShiNyP_PAG32)



# GWAS?



## Diversity Collection



## Phenotypic Data



Sample 1 CTA~~A~~GTACA  
Sample 2 CTATGTAGA  
Sample 3 CTATGTACA  
Sample 4 CTA~~A~~GTAGA

## Genotypic Data (SNP)

Sample 1 CTAAGTACA  
Sample 2 CTATGTTAGA  
Sample 3 CTATGTCACA  
Sample 4 CTAAGTAGA

## Genotypic Data (SNP)

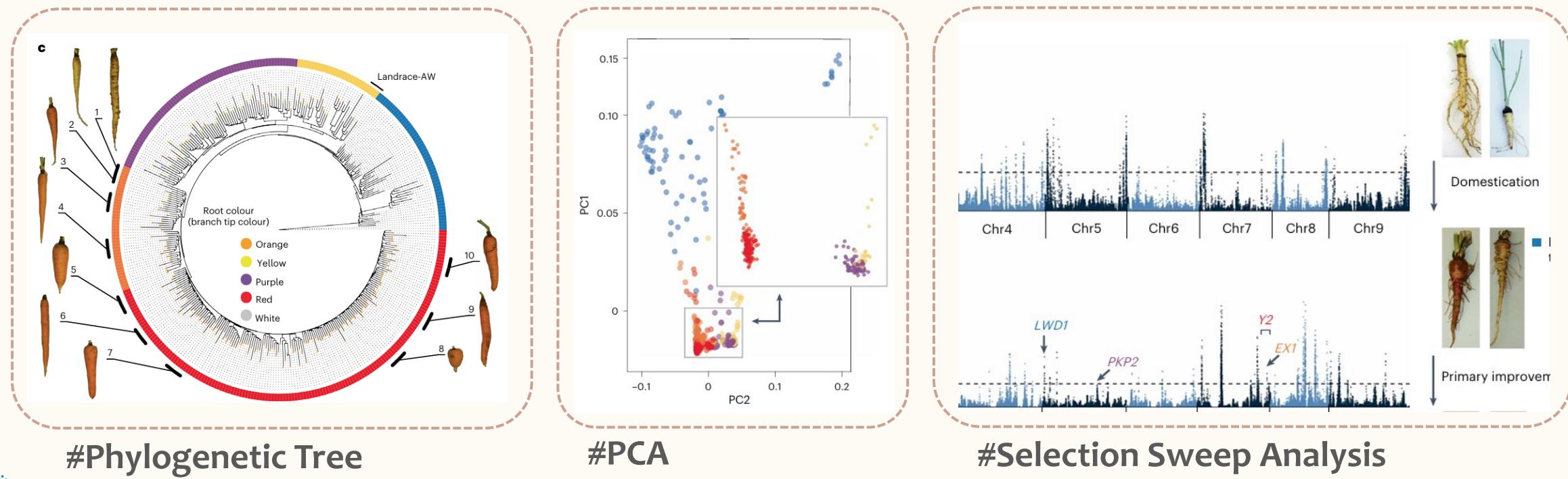


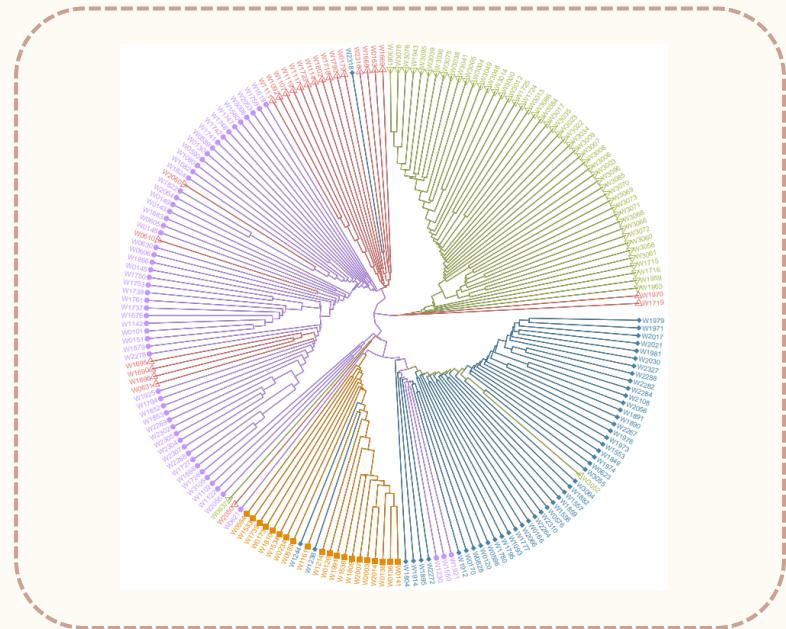
Explore Genetic Variance

Structure,  
Phylogeny,  
Diversity,  
Distance,  
Differentiation,  
Key Features...

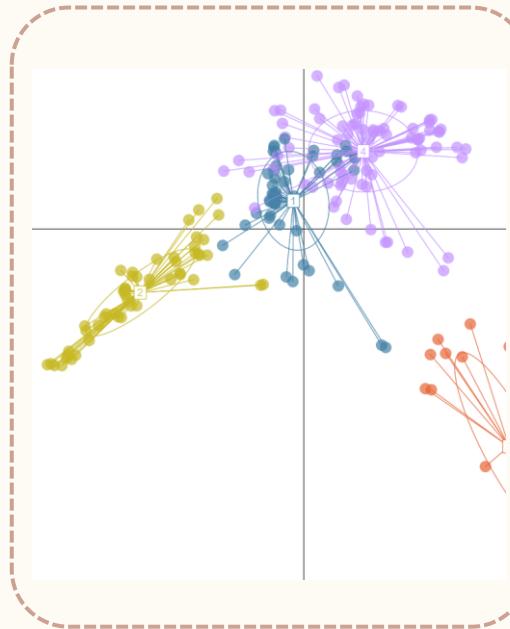
# Exploring SNP Data...

Comprehensively understand your “Diversity Collection”, not just the GWAS results.

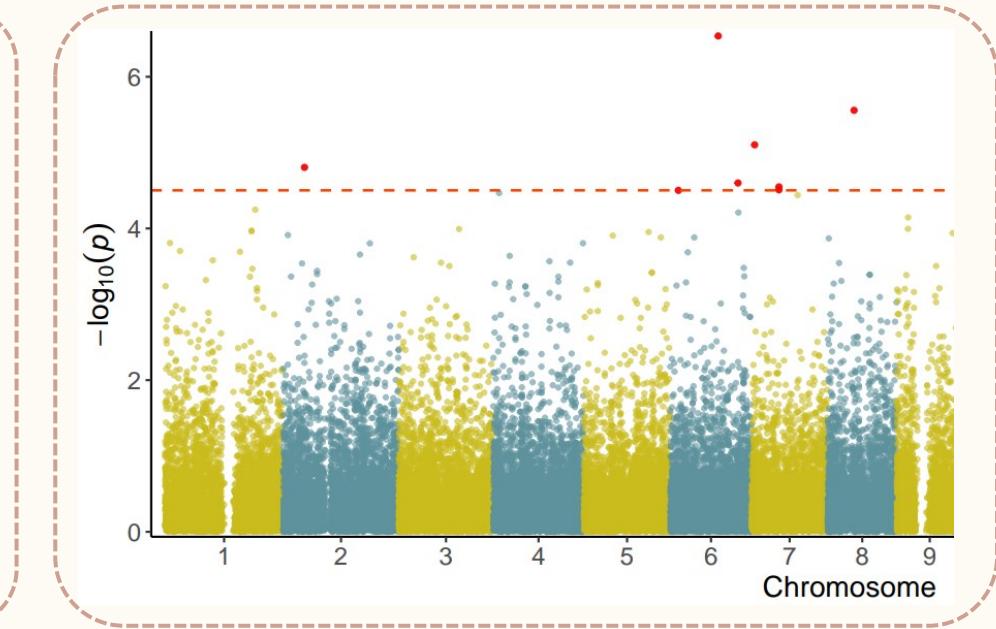




## #Phylogenetic Tree



## #PCA



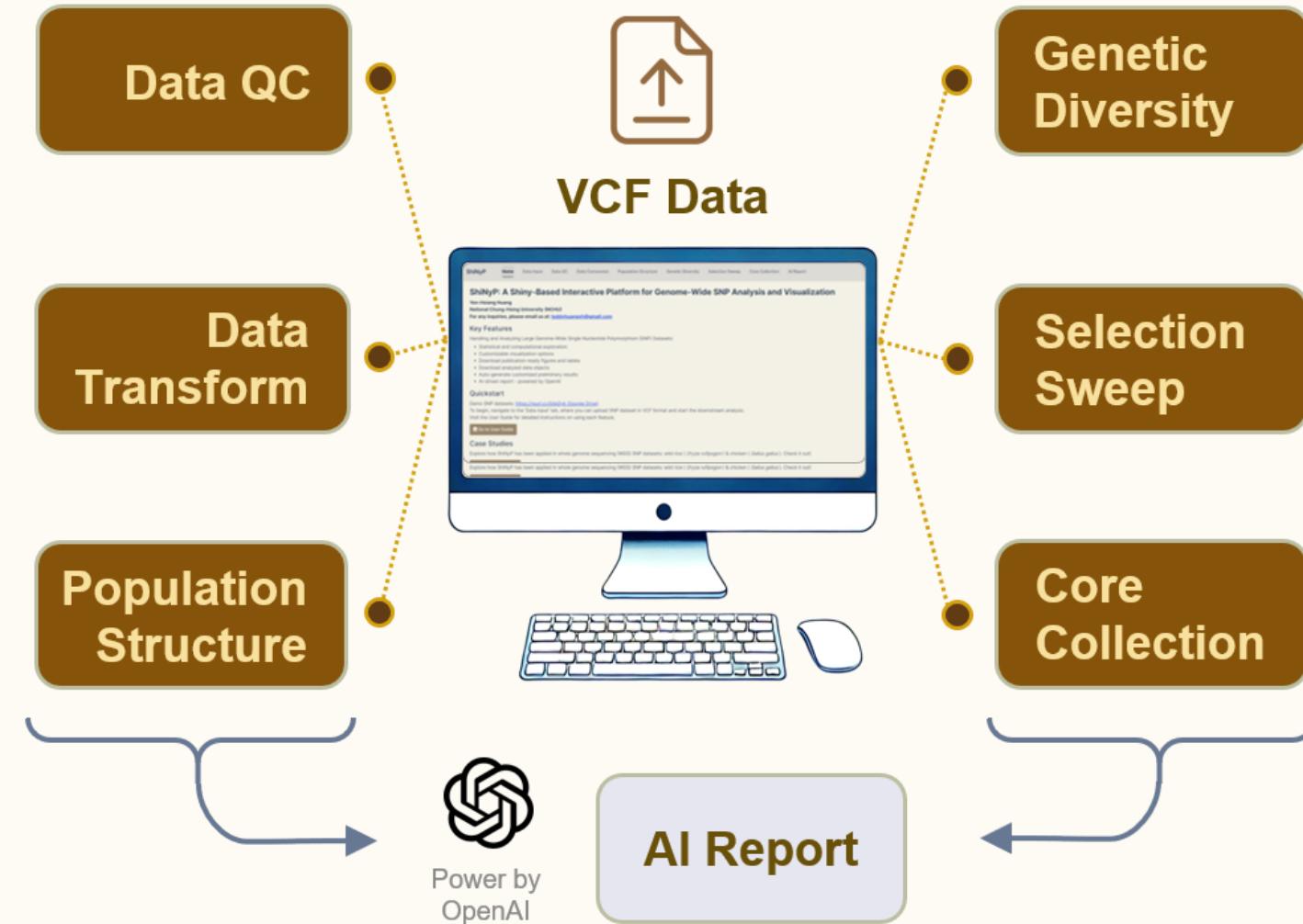
# #Selection Sweep Analysis



# ShiNyP do that!!



# ShiNyP: Platform for SNP Analysis and Visualization



**Input:** Genome-wide biallelic SNP in Variant Call Format (VCF).

**Analysis:** Data QC, population genetics analysis.

**Output:** Publication-ready figures, tables, objects, and AI-driven report.

## Step 1: Pre-install Required Package

```
install.packages("BiocManager")
BiocManager::install(version = "3.19")
BiocManager::install(c("qvalue", "SNPRelate", "ggplot2"), force = TRUE)
```

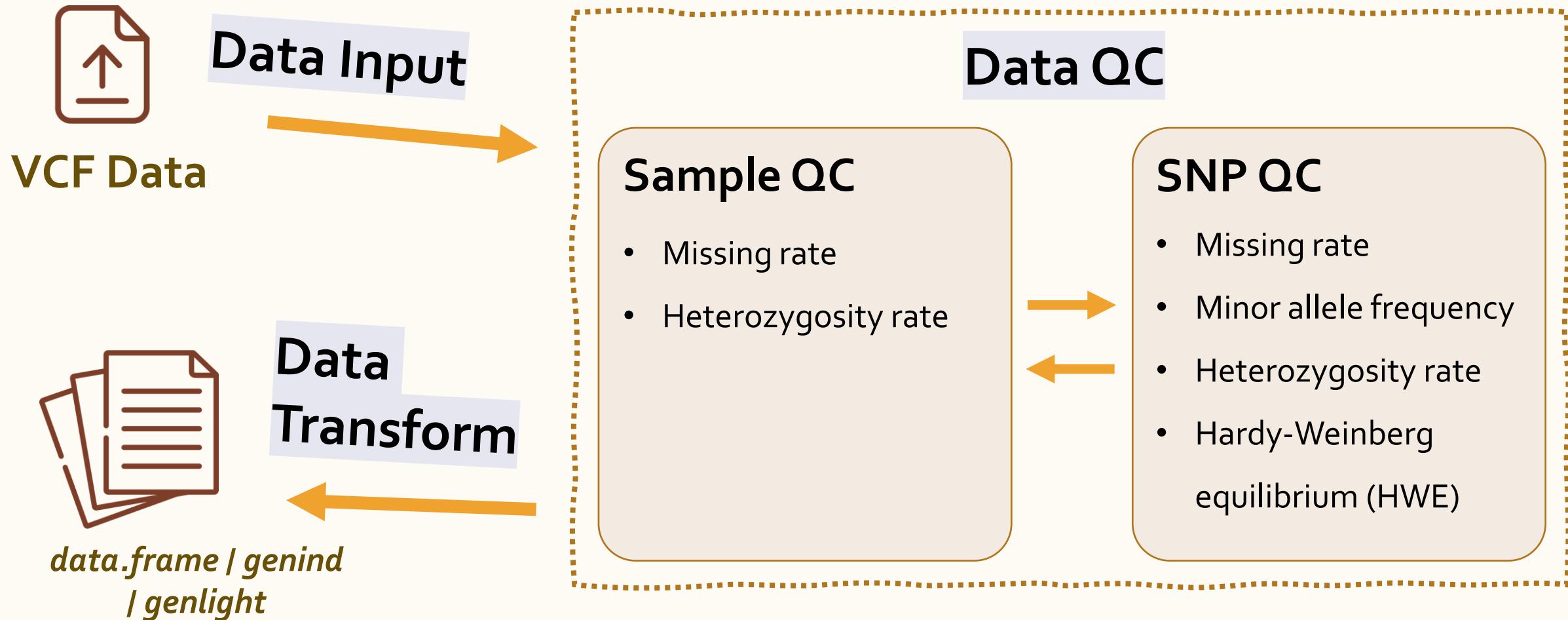
## Step 2: Install the *ShiNyP* Package from GitHub

```
install.packages("remotes")
remotes::install_github("TeddYenn/ShiNyP_Test", force = TRUE)
```

## Step 3: Start the ShiNyP Platform

```
library(ShiNyP)
ShiNyP::run_ShinyP()
```





http://127.0.0.1:6627 | Open in Browser |  www.BANDICAM.com | 

**ShiNyP**  Home Data Input Data QC Data Transform Population Structure Genetic Diversity Selection Sweep Core Collection AI Report

## ShiNyP: An Interactive Shiny-Based Platform for Genome-Wide SNP Analysis and Visualization

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### Key Features

Real-time Processing, Analysis, and Visualization of SNP Datasets:

- Comprehensive statistical and computational exploration
- Customizable visualization options
- Publication-ready figures and tables
- Reproducible analyzed data objects
- AI-driven report generation

### Quickstart

To begin, navigate to the 'Data Input' page, where you can upload SNP dataset in VCF and start the downstream analysis.  
Visit the User Guide for detailed instructions on using each feature: <https://teddyenn.github.io/ShiNyP-guide>

### Publication

Huang et al. (upcoming 2024) ShiNyP: An Interactive Shiny-Based Platform for Genome-Wide SNP Analysis and Visualization  
Huang et al. *ShiNyP: An Interactive Shiny-Based Platform for Genome-Wide SNP Analysis and Visualization*



`data.frame / genind  
/ genlight`



## Analysis

- **PCA** (Principal Component Analysis)
- **DAPC** (Discriminant Analysis of Principal Components)
- **UPGMA Tree** (Unweighted Pair Group Method with Arithmetic mean)
- **NJ Tree** (Neighbor-Joining)
- **Kinship Analysis**

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**ShiNyP** Home Data Input Data QC **Data Transform** Population Structure Genetic Diversity Selection Sweep Core Collection AI Report

The data has been transformed to data.frame, genind, and genlight formats.  
Enjoy the downstream analysis! (•\_•)

**data.frame to genind**

Status: transformed  
File name: genind\_group\_446\_12833SNPs  
Number of samples: 446  
Number of SNPs: 12833  
Type: genind  
Size: 50.51 MB  
Group Info.: Added

 Download genind File

**genind to genlight**

Status: transformed  
File name: genlight\_446\_12833SNPs  
Number of samples: 446  
Number of SNPs: 12833  
Type: genlight  
Size: 4.21 MB

Dataset for Transformation:  
Input VCF Data (in data.frame) ▾

Number of samples: 446  
Number of SNPs: 12833  
Type: data.frame

1. Transform data.frame to genind  
Group Info. (optional)  
Browse... DAPC\_Group\_Info.csv  
Upload complete  
Transform to genind

2. Transform genind to genlight  
Transform to genlight



data.frame / genind



## Analysis

- **Diversity Parameter**
- **Circos Plot**
- **Genetic Distance**
- **AMOVA** (Analysis of MOlecular VAriance)

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**ShiNyP** Home Data Input Data QC Data Transform Population Structure **Genetic Diversity** Selection Sweep Core Collection AI Report

[Diversity Parameter](#) [Circos Plot](#) [Genetic Distance](#) [AMOVA](#)

 Diversity Parameter

Dataset for analysis:

data.frame file

Number of samples: 446  
Number of SNPs: 12833  
Type: data.frame

Site Info.\* (required)

Browse... Site\_Info\_446\_12833SN **Upload complete**

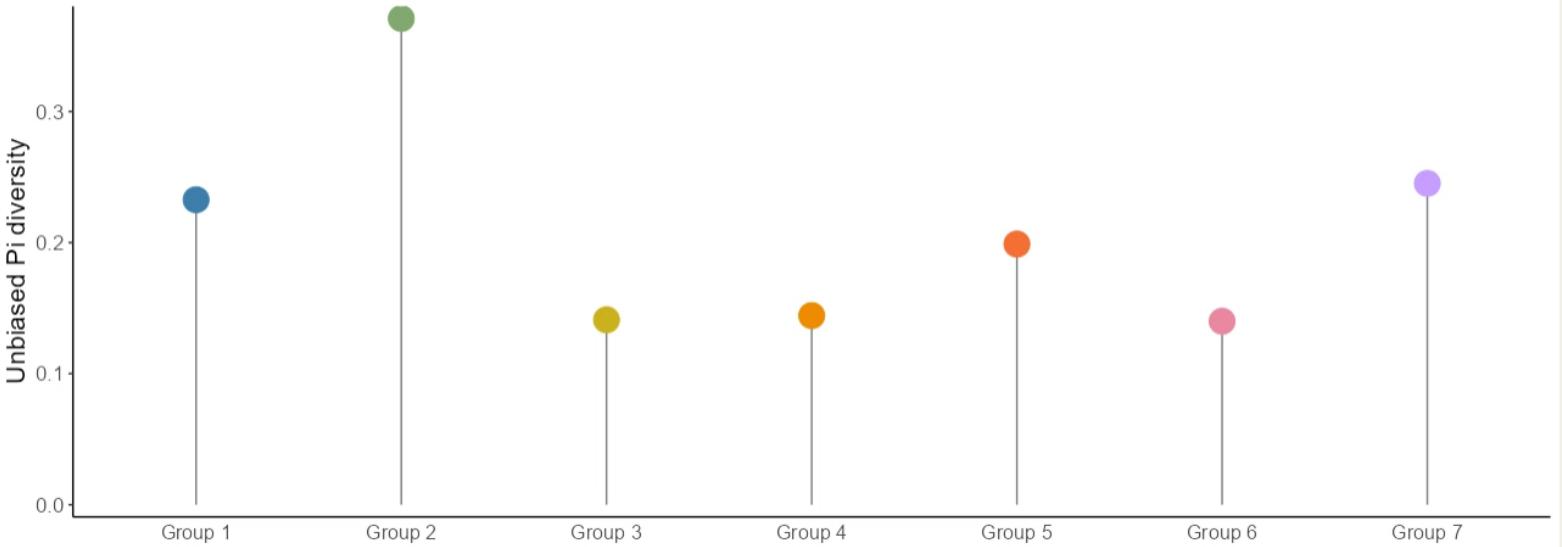
Group Info. (optional)

Browse... DAPC\_Group\_Info.csv **Upload complete**

**Run Diversity Analysis** **Reset**

The analysis of genetic diversity is complete.  
Please review the results.

**Plot of Genetic Diversity Statistics by Group**



Group	Unbiased Pi diversity
Group 1	~0.22
Group 2	~0.35
Group 3	~0.14
Group 4	~0.14
Group 5	~0.20
Group 6	~0.14
Group 7	~0.24

By each group:

Huang et al. ShiNyP: An Interactive Shiny-Based Platform for Genome-Wide SNP Analysis and Visualization



data.frame / genind



## Analysis

- **pcadapt** (Luu et al., 2017)
- **OutFLANK** (Whitlock & Lotterhos, 2015)
- **IBS** (Identity By State)

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**ShiNyP** Home Data Input Data QC Data Transform Population Structure Genetic Diversity **Selection Sweep** Core Collection AI Report

pcadapt OutFLANK IBS Manhattan Plot Plus

**PCA-based genome scan for selection (pcadapt)**

Dataset for pcdadapt:

data.frame file

Number of samples: 446  
Number of SNPs: 12833  
Type: data.frame

Site Info.\* (required)

Browse... Site\_Info\_446\_12833SN **Upload complete**

The number of PC axes retained

Manhattan Plot

The pcdadapt analysis is complete.

P-value adjustment method: Benjamini & Hochberg (FDR)

Level of significance (alpha): 0.005

[Download pcdadapt p-value \(per site\)](#)

Number of significant SNPs: 563

-----

Chr 1: 83 significant SNPs  
Chr 2: 89 significant SNPs  
Chr 3: 130 significant SNPs  
Chr 4: 22 significant SNPs  
Chr 5: 57 significant SNPs  
Chr 6: 12 significant SNPs  
Chr 7: 32 significant SNPs  
Chr 8: 40 significant SNPs  
Chr 9: 37 significant SNPs  
Chr 10: 37 significant SNPs  
Chr 11: 15 significant SNPs  
Chr 12: 9 significant SNPs

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*data.frame*



## Analysis

- Core Sample Set
- Core SNP Set

[Data QC](#)[Data Transform](#)[Population Structure](#)[Genetic Diversity](#)[Selection Sweep](#)[Core Collection](#)

http://127.0.0.1:6627 | Open in Browser |  Publish

**ShiNyP** Home Data Input Data QC Data Transform Population Structure Genetic Diversity Selection Sweep **Core Collection** AI Report

Core Sample Set Core SNP Set 

**Core Sample Set**

Dataset for core sample set:

data.frame file

Number of samples: 446  
Number of SNPs: 12833  
Type: data.frame

Coverage (%)

90 100

Coverage differences between iterations

0.001

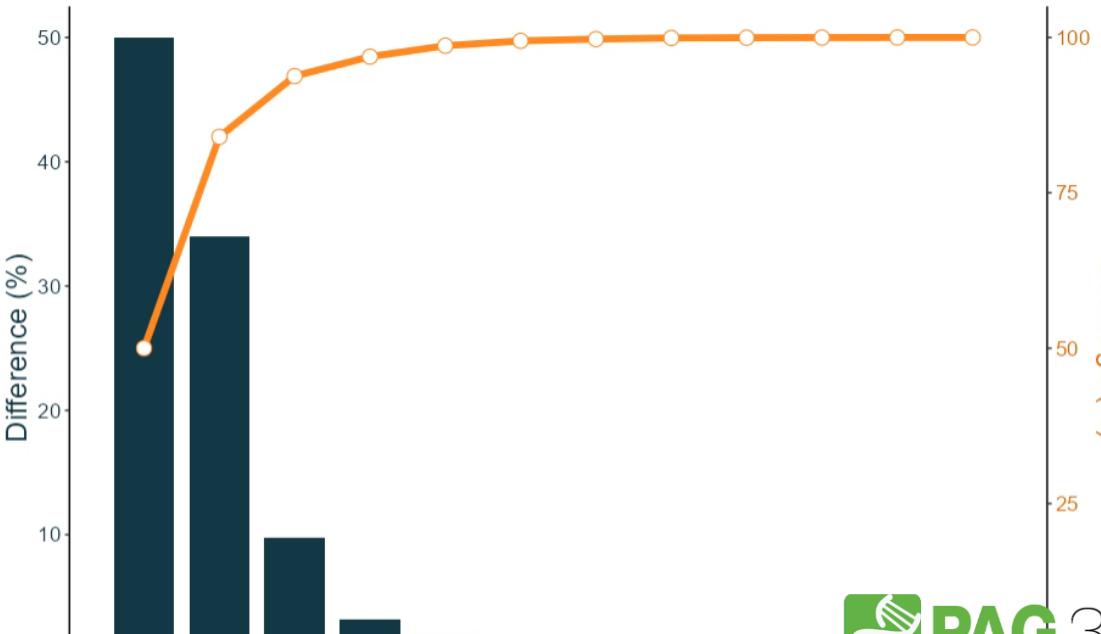
The core sample set is completed.

**Core Sample Set**

Number of core samples: 12 (2.69%)  
Total coverage: 100%  
Core sample IDs: W2025; W3078; W1083; W01

 Download Core Samples Set in data.frame  
 Download Core Sample Info.

**Coverage Plot of Core Sample Set**



Difference (%)

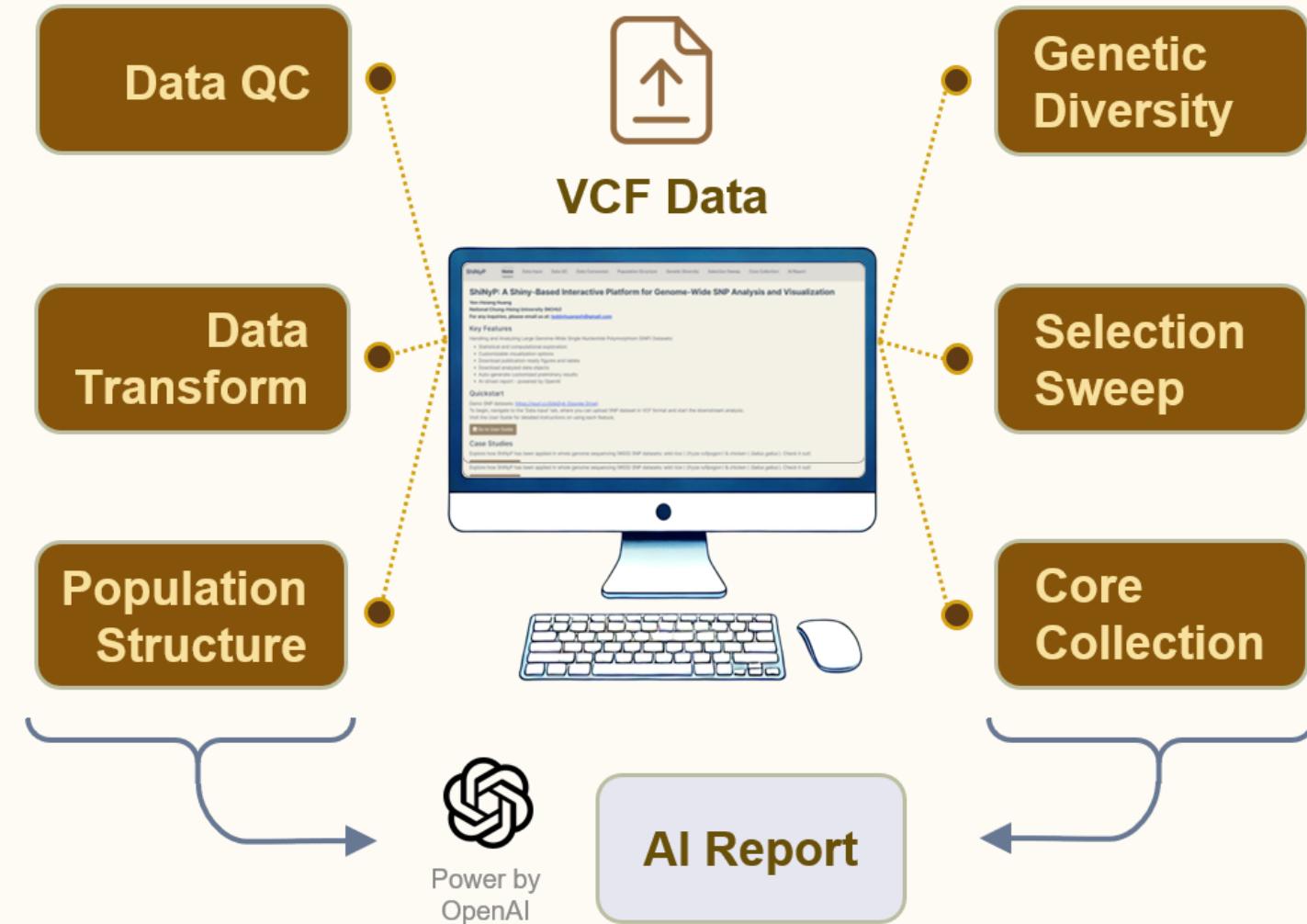
Coverage (%)

50 100  
40 75  
30 50  
20 25

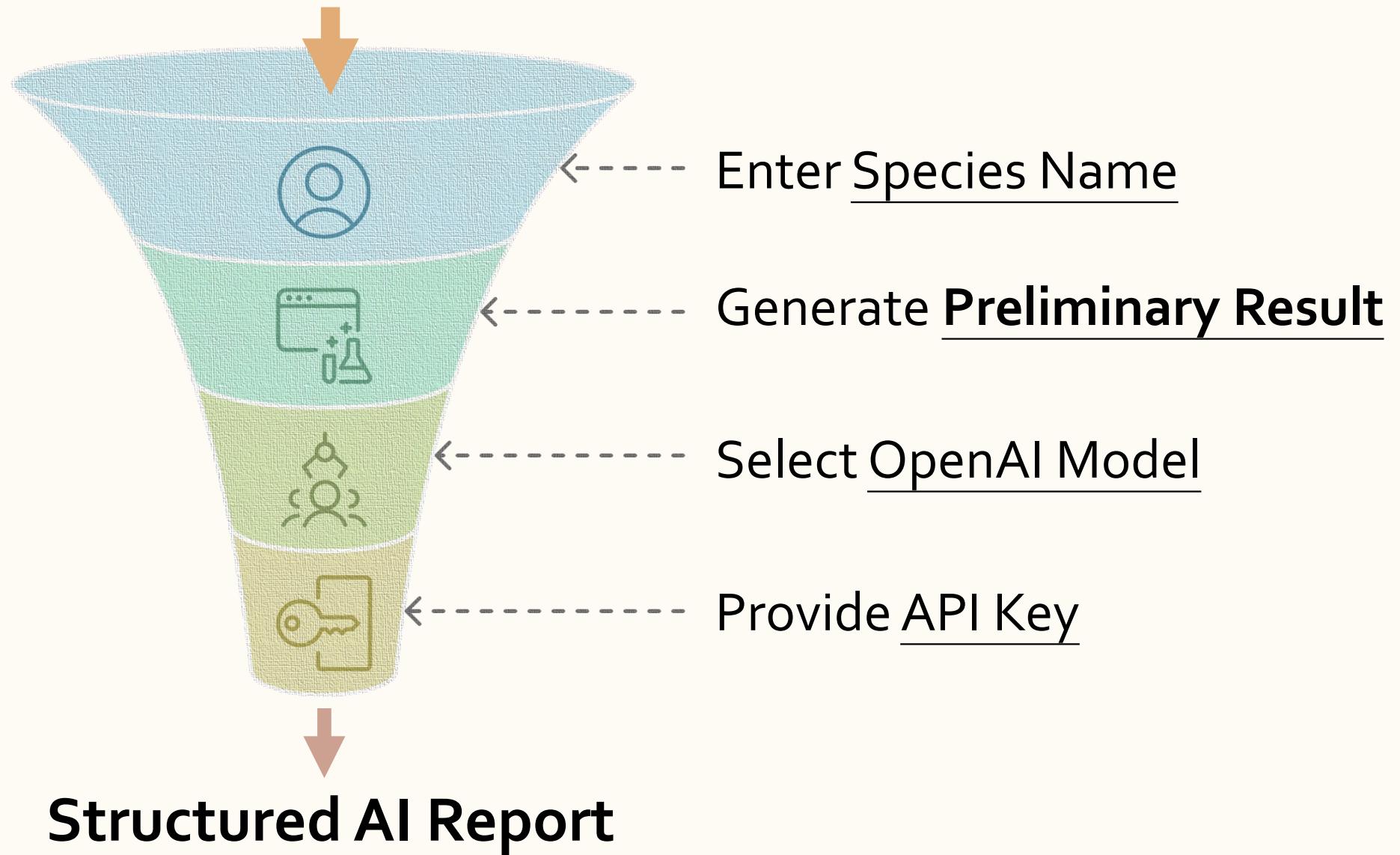
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# ShiNyP: Platform for SNP Analysis and Visualization



# SNP Data Analysis



[PCA](#) [DAPC](#) [UPGMA Tree](#) [NJ Tree](#) [Kinship](#) [Scatter Plot Plus](#) [Tree Plot Plus](#)

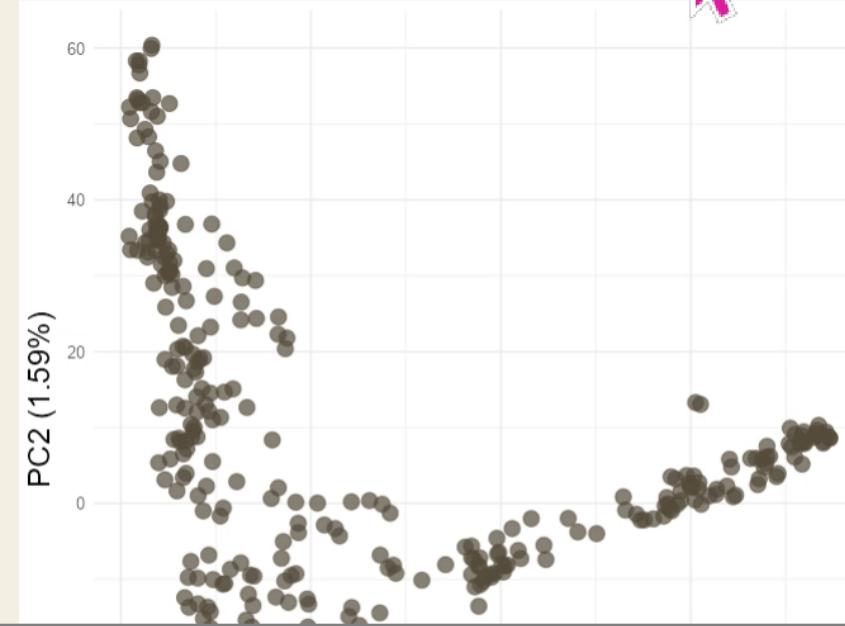
## Principal Component Analysis (PCA)

Dataset for PCA:

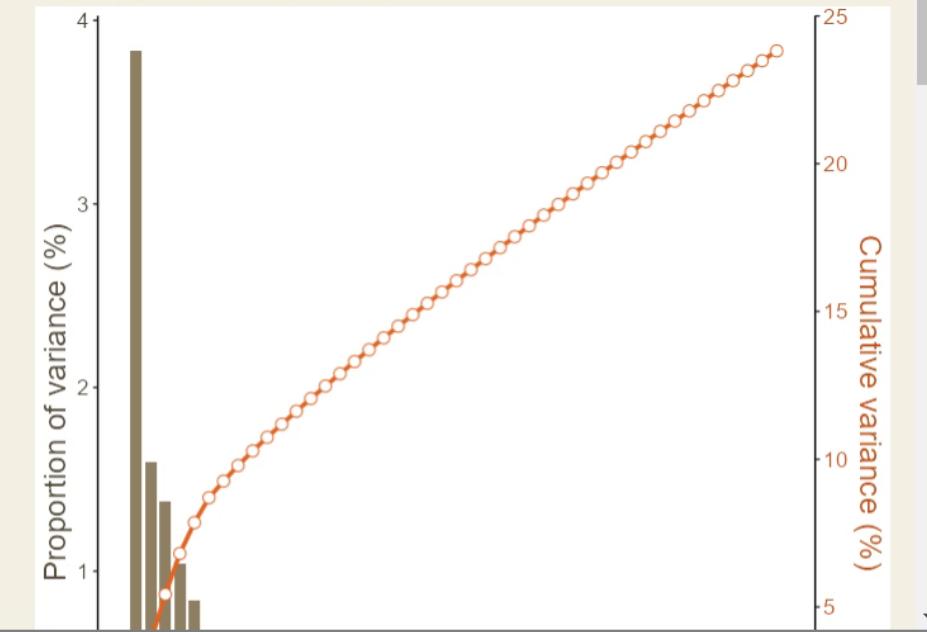
Number of samples: 446  
Number of SNPs: 12833  
Type: data.frame

The PCA is complete.  
Please select the PCs for the X and Y axes of the 2D PCA plot.  
Try adjusting the number of PCs and observe the explained variance plot.

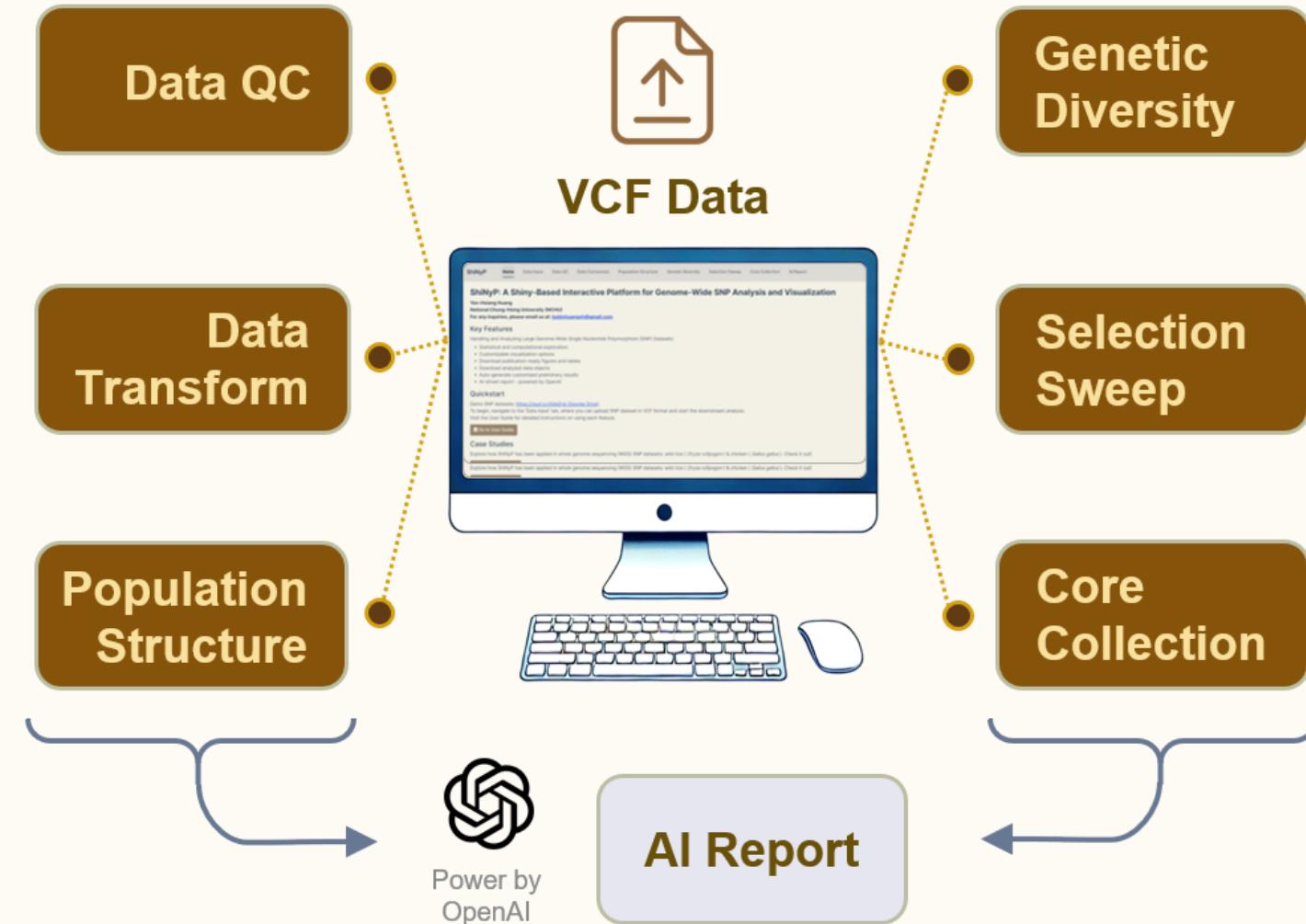
### PCA Scatter Plot

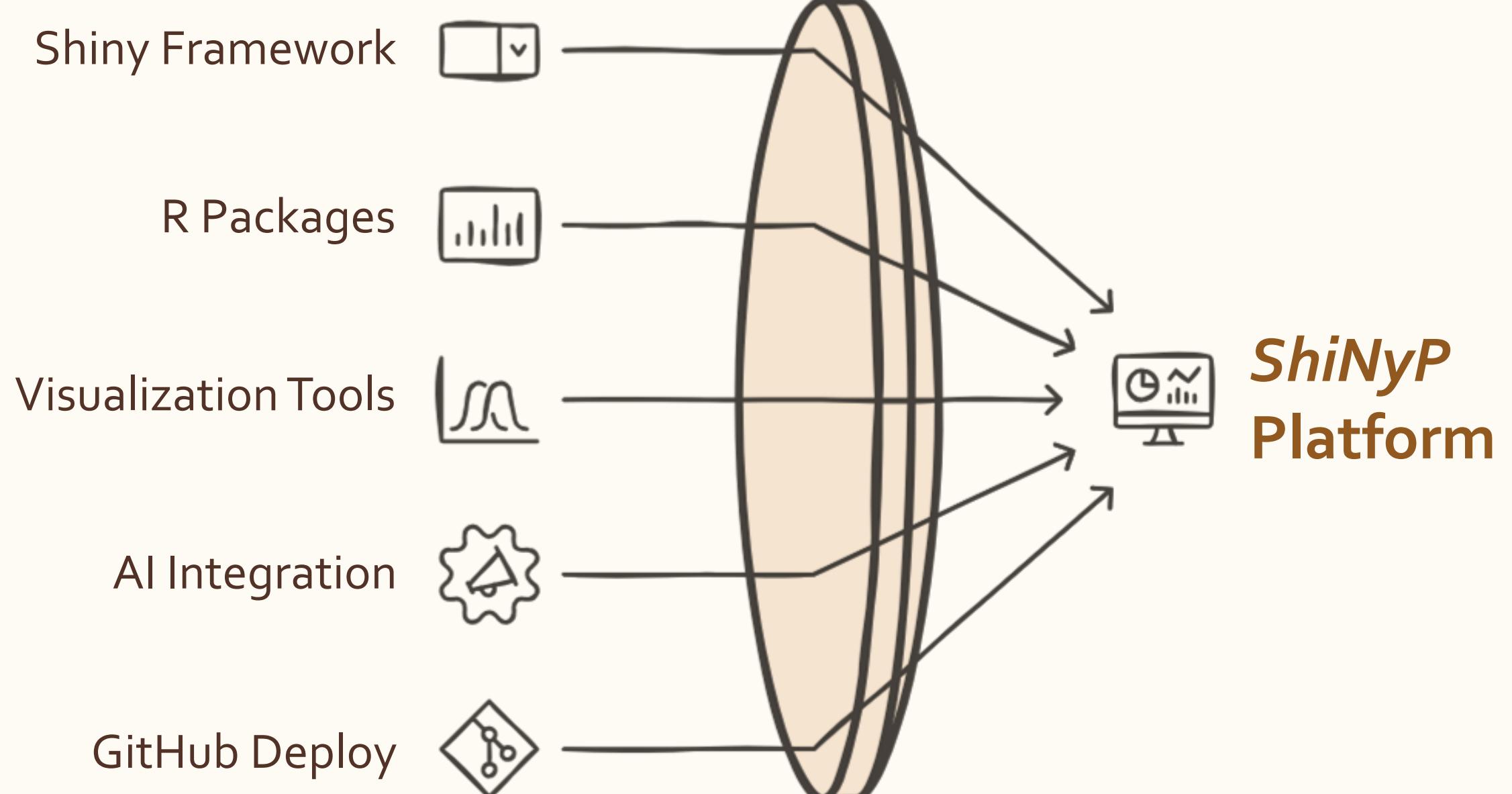


### PC Explained Variance Plot



# ShiNyP: Platform for SNP Analysis and Visualization







# Shiny-Based Framework



"statgenGWAS", "pcadapt" ...

## Data Processing & Analysis



"circlize", "ggthemes", ...

## Visualization & Outputs

Deploy



GitHub

Access



or



```
##### UI #####
ui = fluidPage(
  sliderInput(inputId = "n", "Sample size", min = 0, max = 1000, value = 100, step = 10),
  plotOutput(outputId = "hist")
)

#####
# SERVER #####
server = function(input, output, session) {
  output$hist = renderPlot({
    hist(rnorm(input$n), main = "Normalized Histogram of Random Numbers", )
  })
}

#####
# RUN #####
shinyApp(ui = ui, server = server)
```





# Shiny-Based Applications

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**StructuRly**: SNP data analysis (Criscuolo et al., 2021)

**PSReliP**: SNP data analysis (Solovieva et al., 2023)

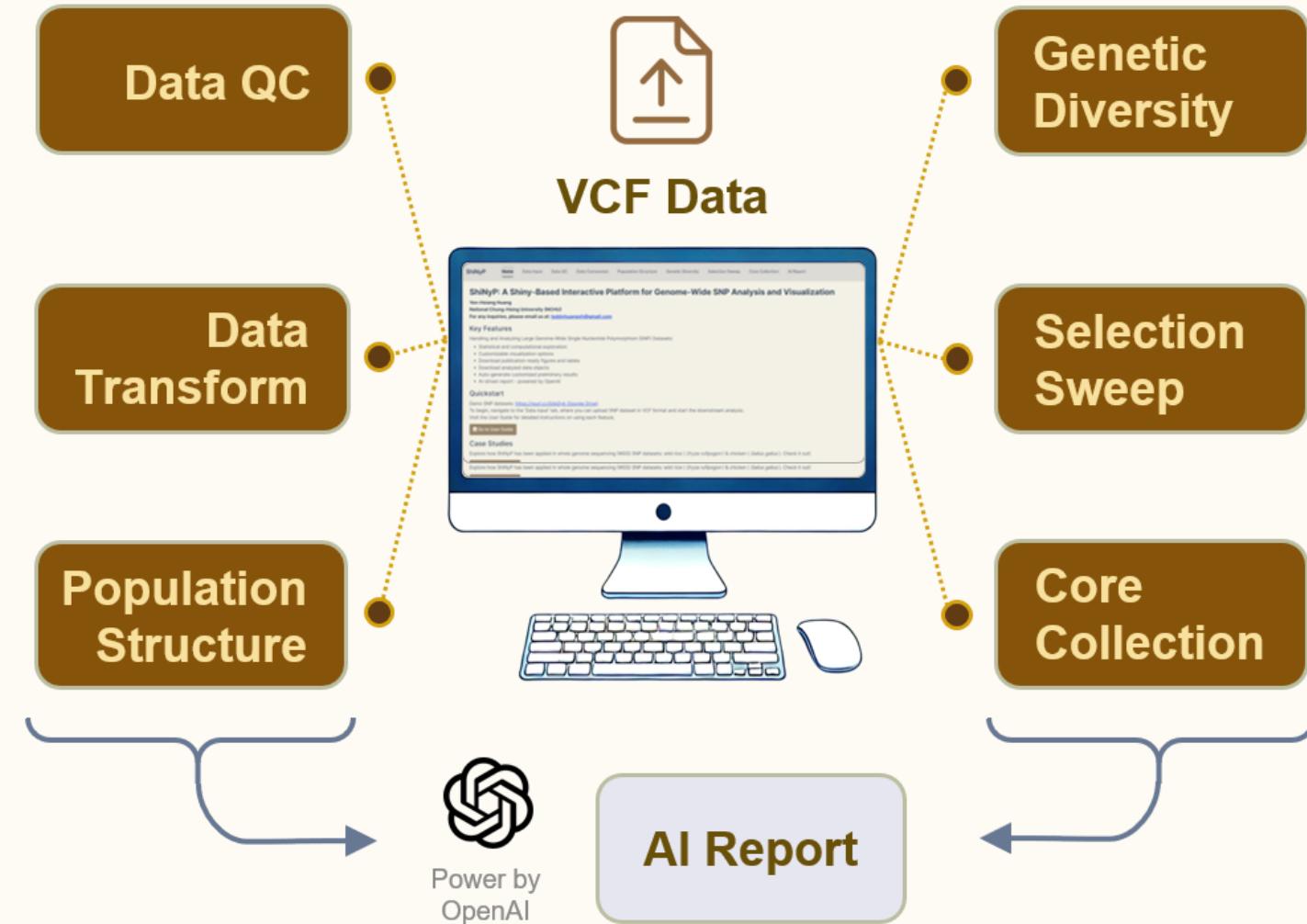
**BIGapp**: SNP data analysis (Sandercock et al. @PAG32 Jan. 12, 2:30 PM )

**iDEP**: RNA data analysis (Ge et al., 2018)

**ROGUE**: RNA data analysis (Farrel et al., 2023)



# ShiNyP: Platform for SNP Analysis and Visualization





# Real-time Processing, Analysis, and Visualization of SNP Datasets.



```
remotes::install_github("TeddYenn/ShiNyP_Test")  
ShiNyP::run_ShinyP()
```

Run *ShiNyP* on your laptop/desktop!



# User Manual:

<https://teddyenn.github.io/ShiNyP-guide/>



# Thank You!



# QA Time



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