



ShiNyP: Platform for SNP Analysis and Visualization

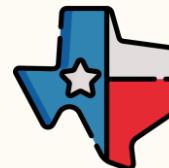
Teddy (Yen-Hsiang Huang)



MS Student in Agronomy at NCHU, Taiwan



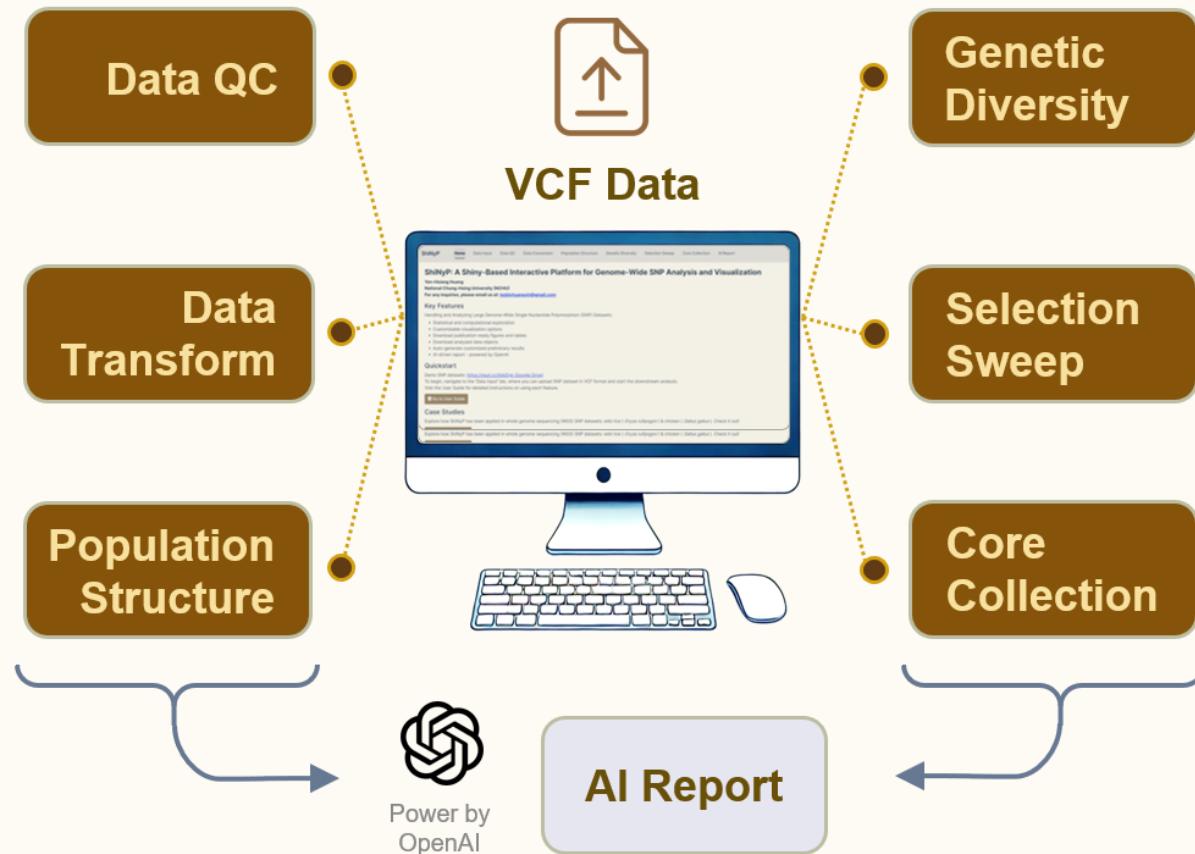
Visiting Student at TAMU, Texas



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

GitHub repo:
[TeddYenn/ShiNyP_PAG32](https://github.com/TeddYenn/ShiNyP_PAG32)



1

Population Structure?

2

"ShiNyP"

3

~Demo~

4

Shiny Framework



Resources



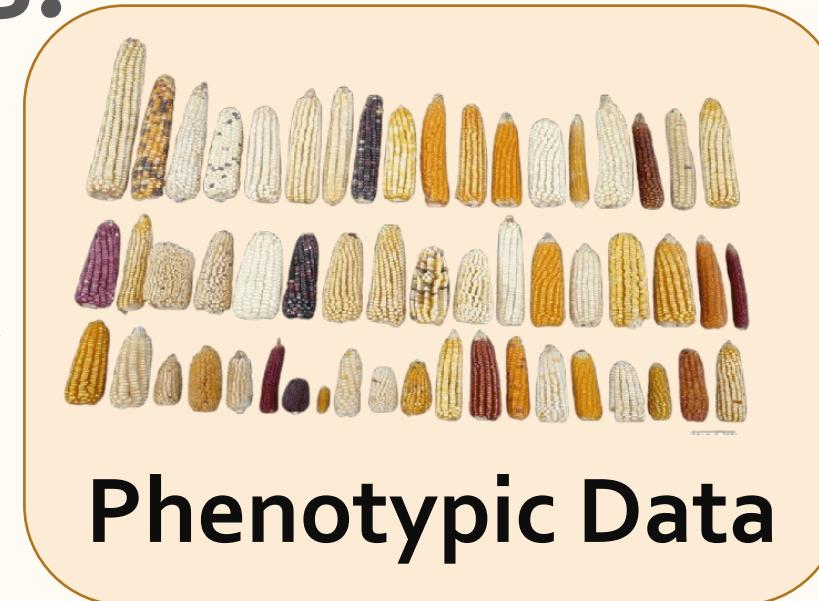
https://github.com/TeddYenn/ShiNyP_PAG32



GWAS?



Diversity Collection



Phenotypic Data



Sample 1 CTAAGTACA
Sample 2 CTATGTAGA
Sample 3 CTATGTACA
Sample 4 CTAAGTAGA

Genotypic Data (SNP)

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

Genotypic Data (SNP)

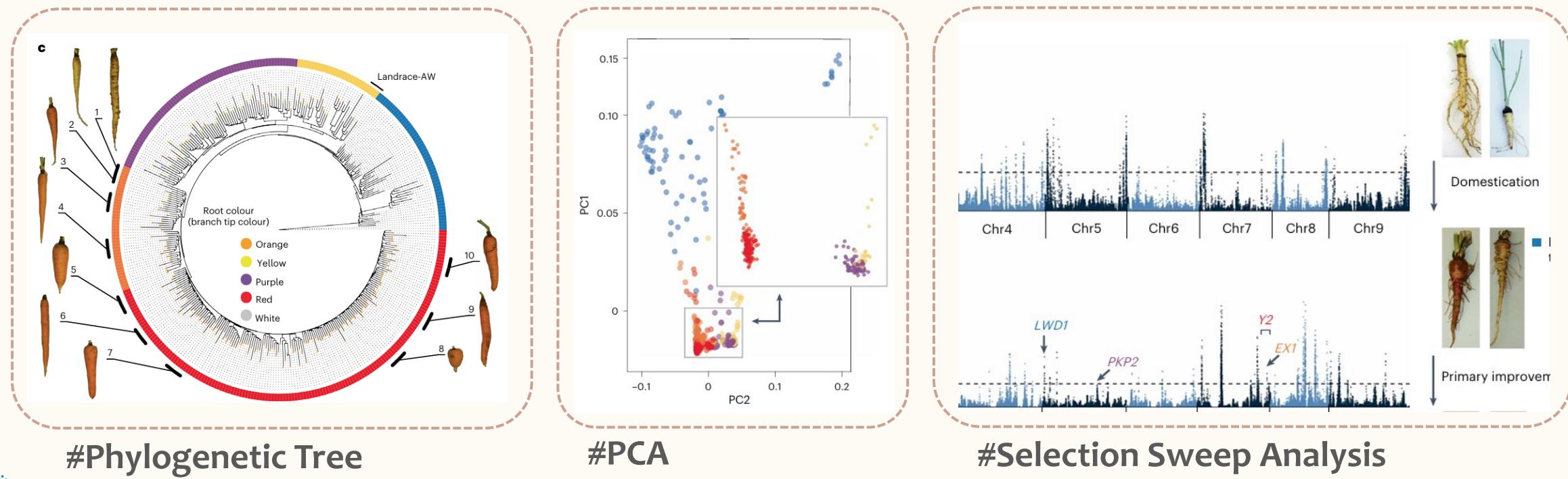


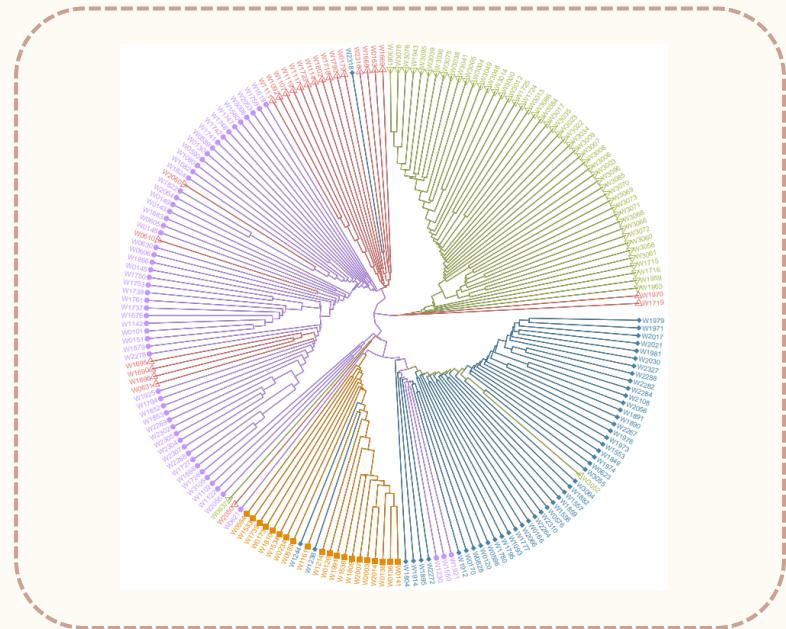
Explore Genetic Variance

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

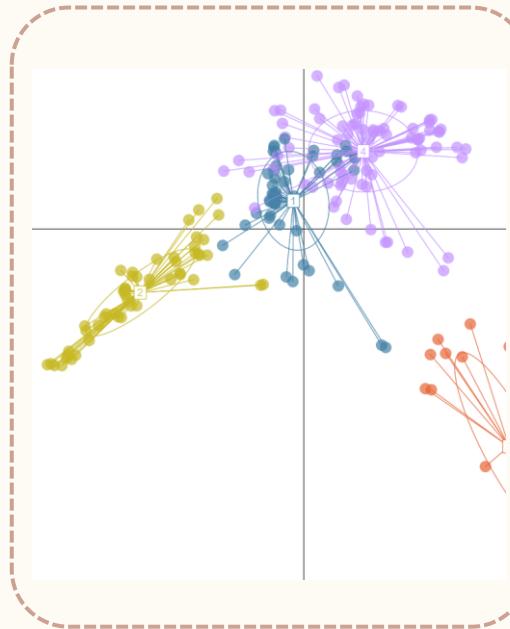
Exploring SNP Data...

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

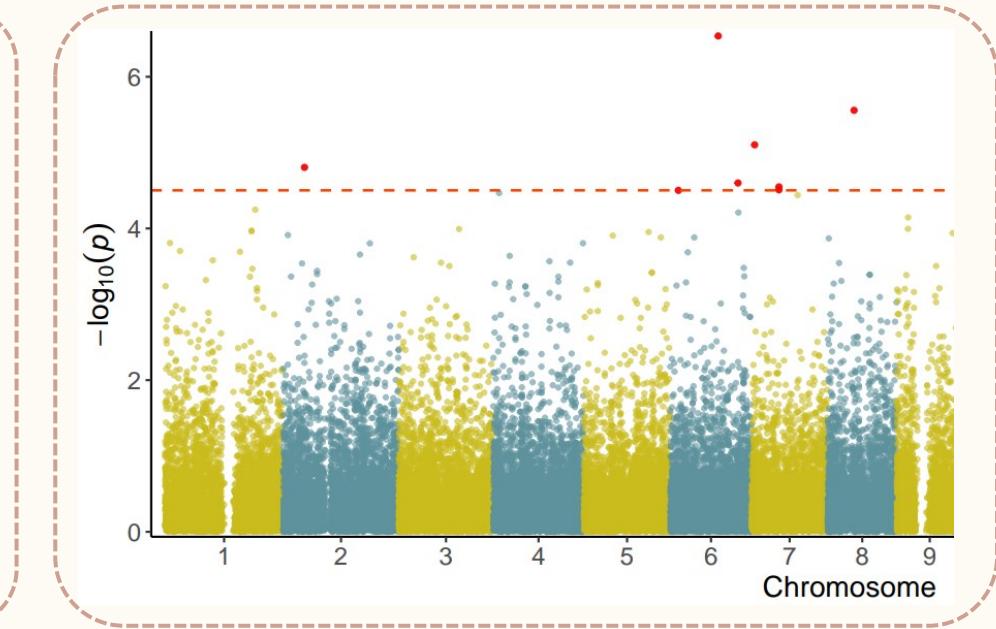




#Phylogenetic Tree



#PCA



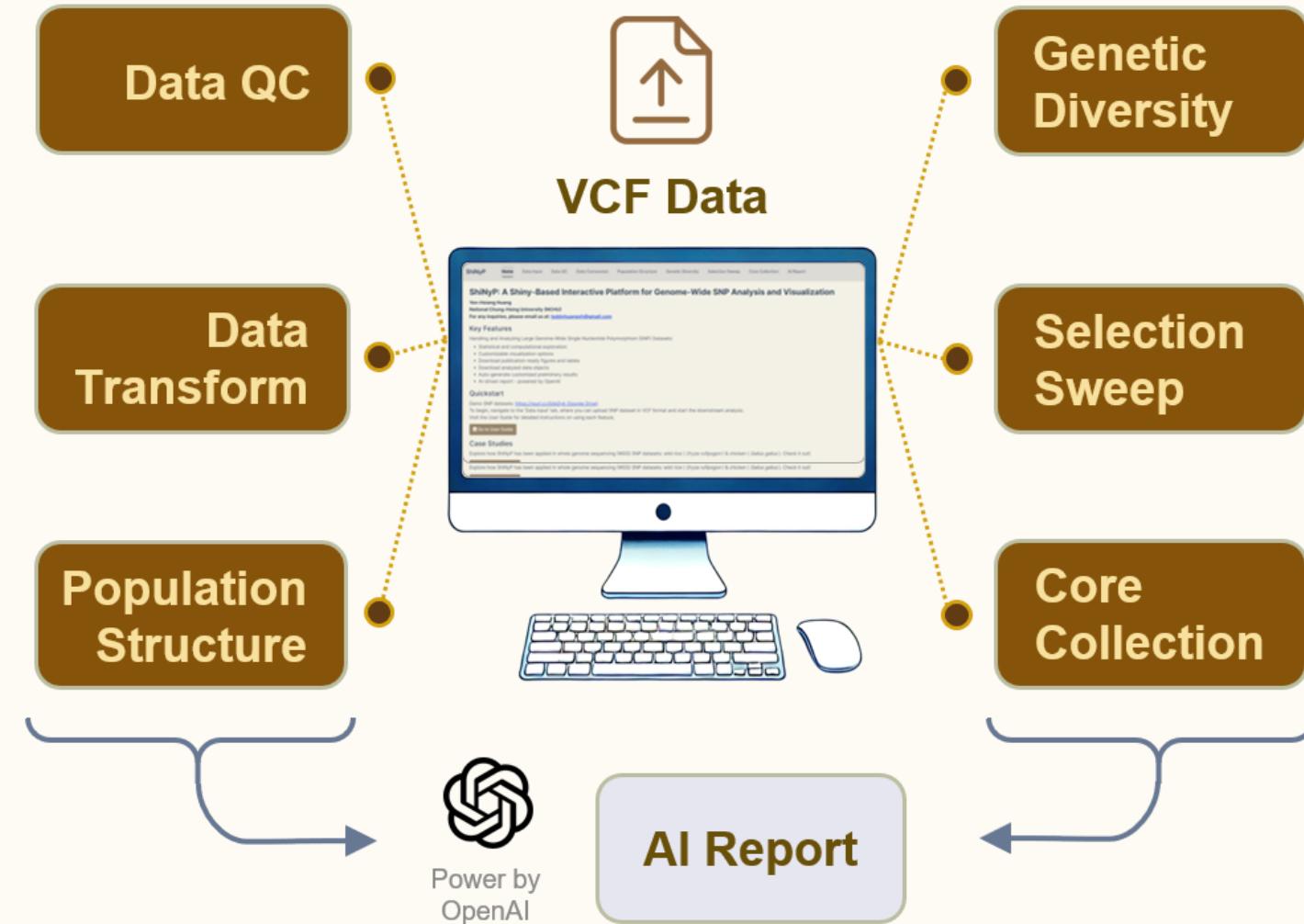
#Selection Sweep Analysis



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)
```

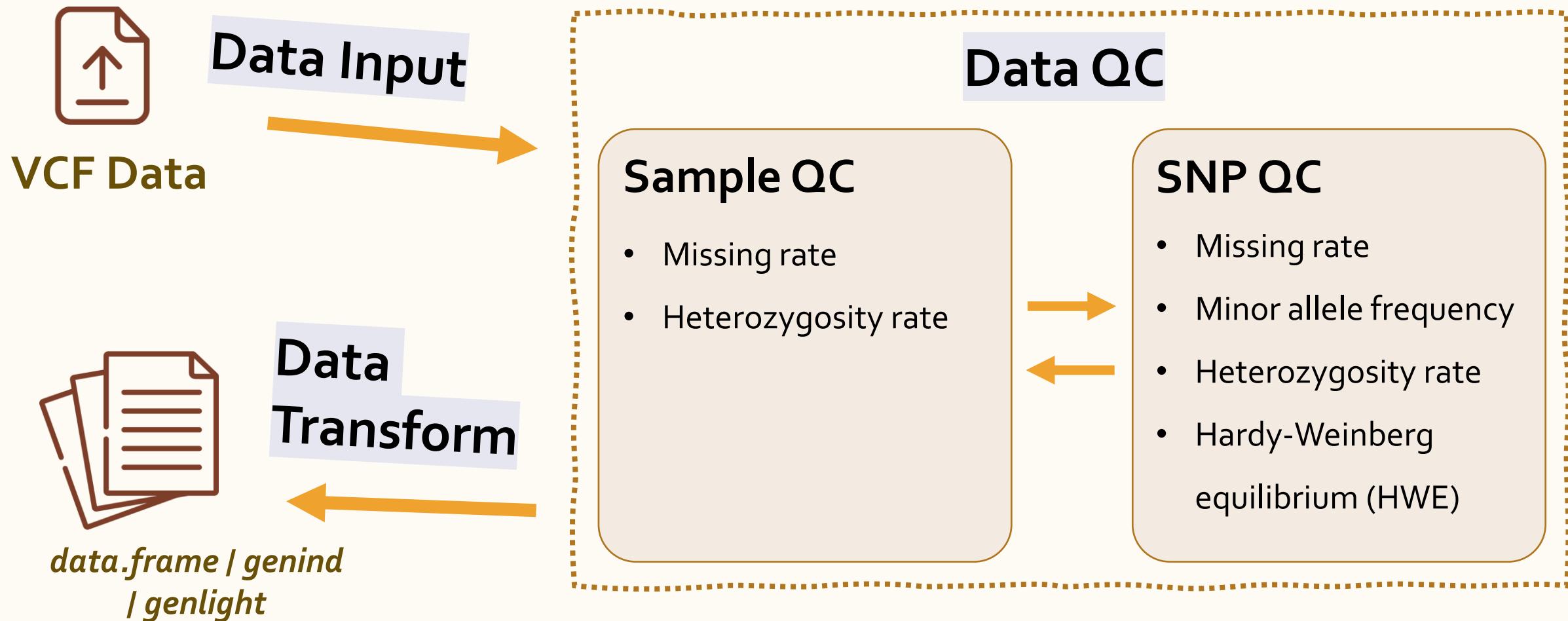
Step 2: Install the *ShiNyP* Package from GitHub

```
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

Yen-Hsiang Huang
National Chung-Hsing University (NCHU), Taiwan
For any inquiries, please email us at: teddyhuangyh@gmail.com

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

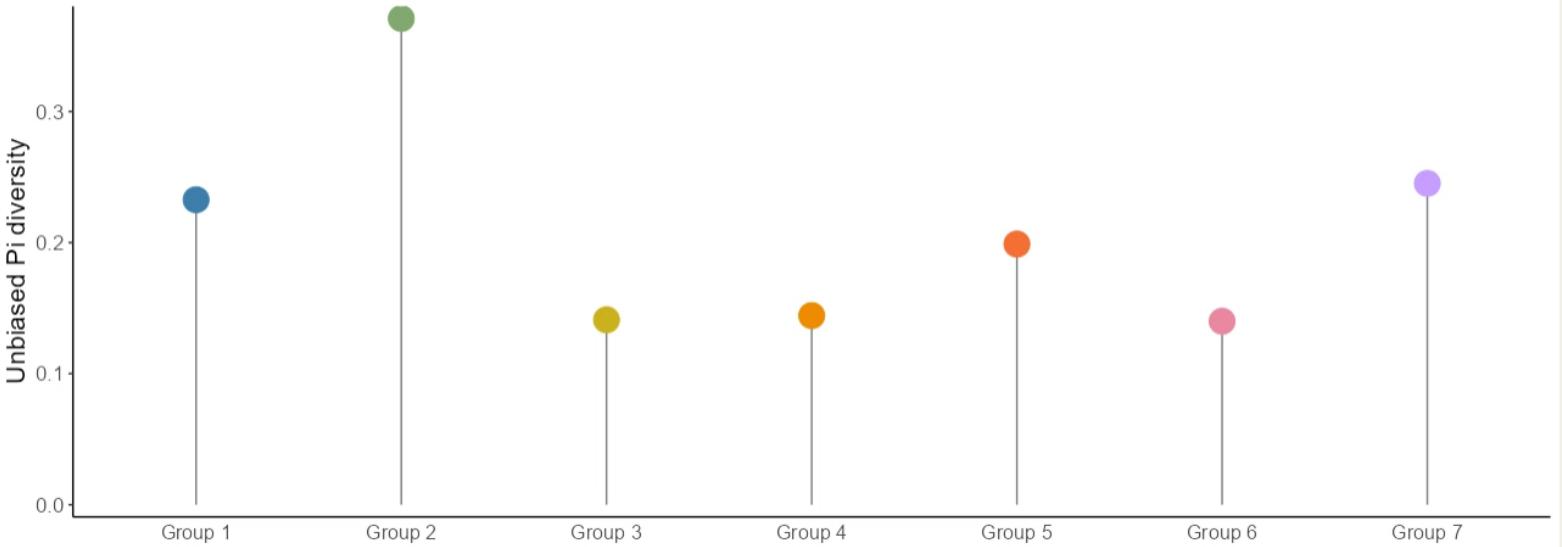
[www.BANDICAM.com](#)

Diversity Parameter Circos Plot Genetic Distance AMOVA

 Diversity Parameter

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

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

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

PAG 32



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](#)

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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

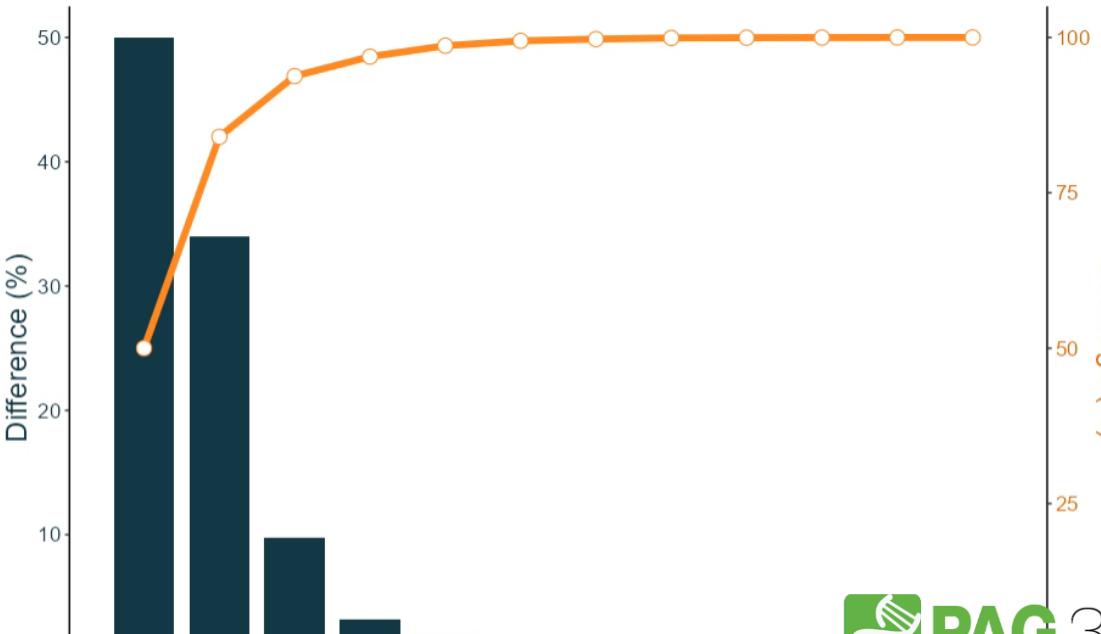
The core sample set is completed.

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 (%)

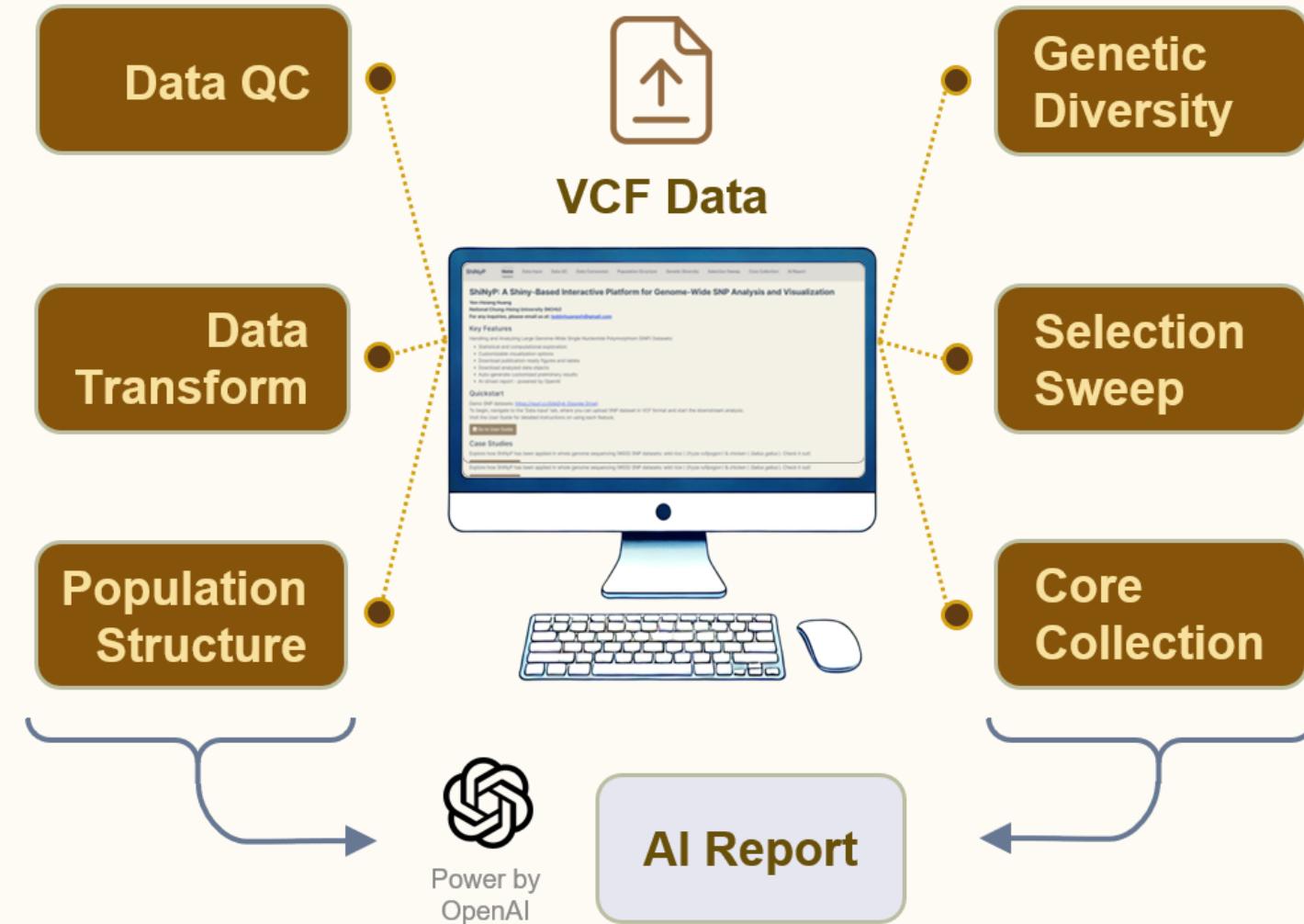
Coverage (%)

50 100
40 75
30 50
20 25

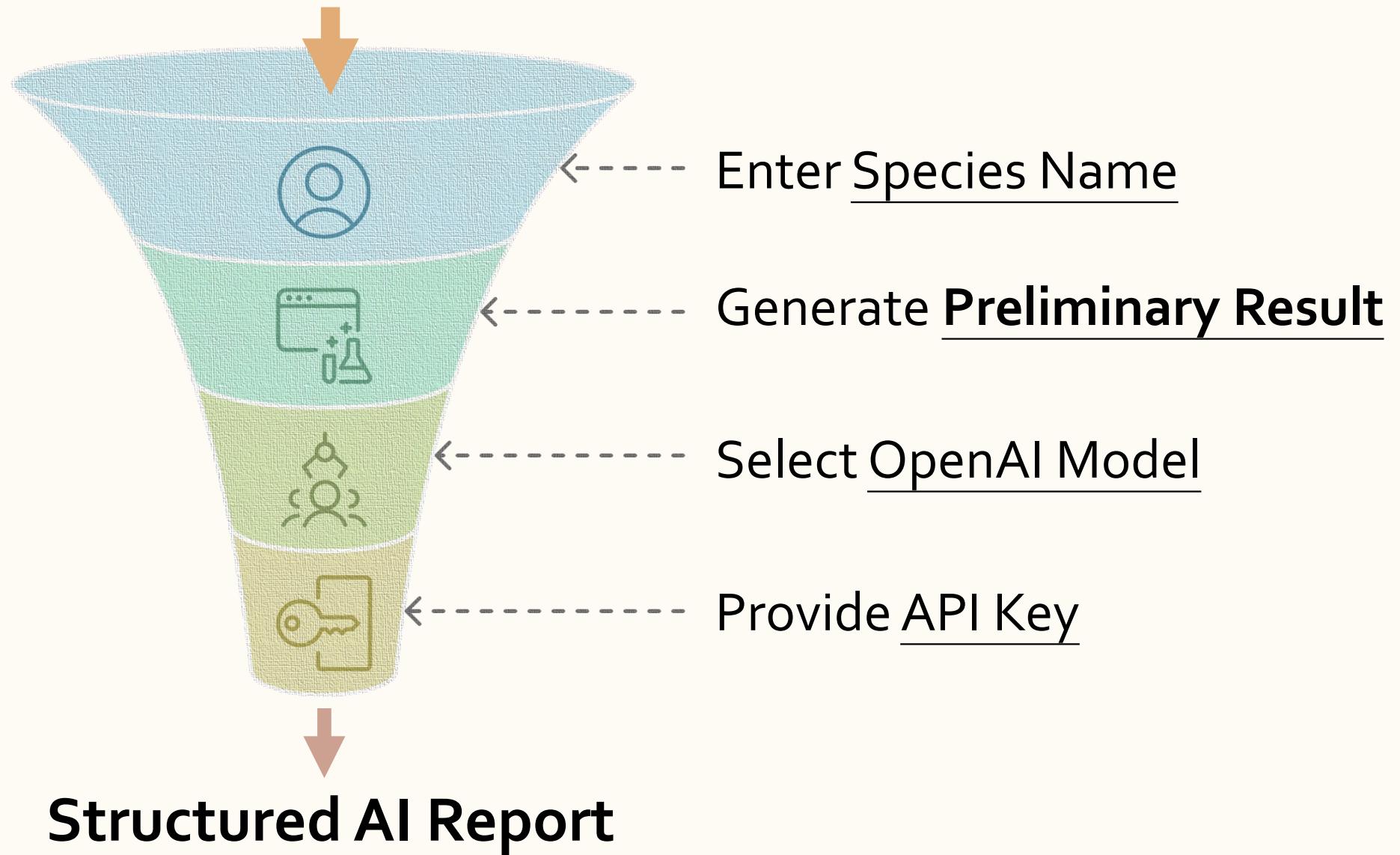
Huang et al. ShiNyP: An Interactive Shiny-Based Platform for Genome-Wide SNP Analysis and Visualization

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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](#)

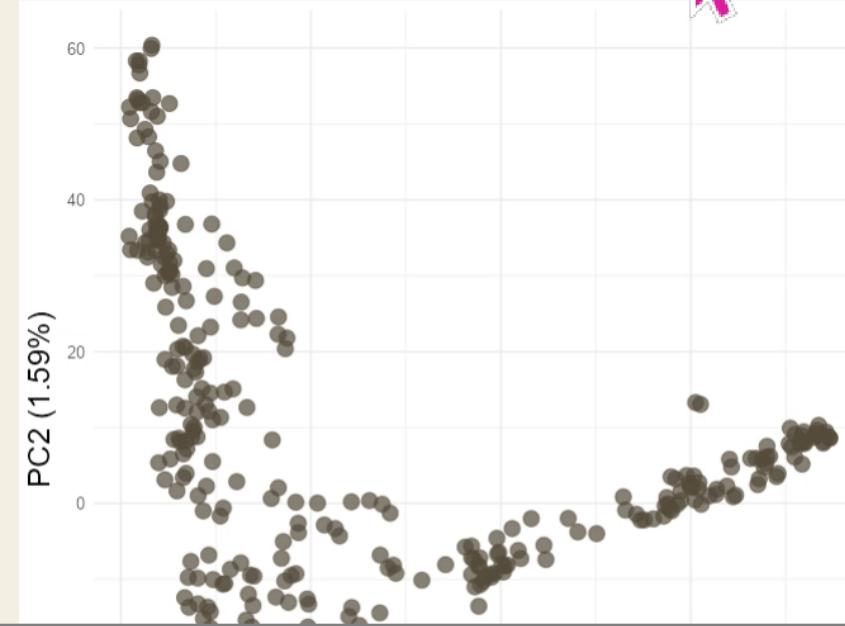
Principal Component Analysis (PCA)

Dataset for PCA:

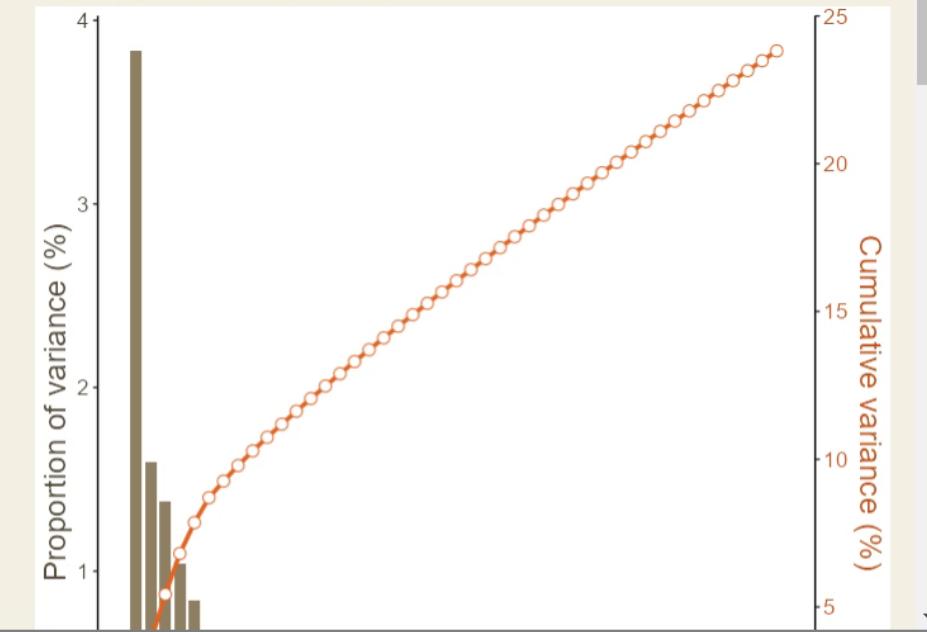
Number of samples: 446
Number of SNPs: 12833
Type: data.frame

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.

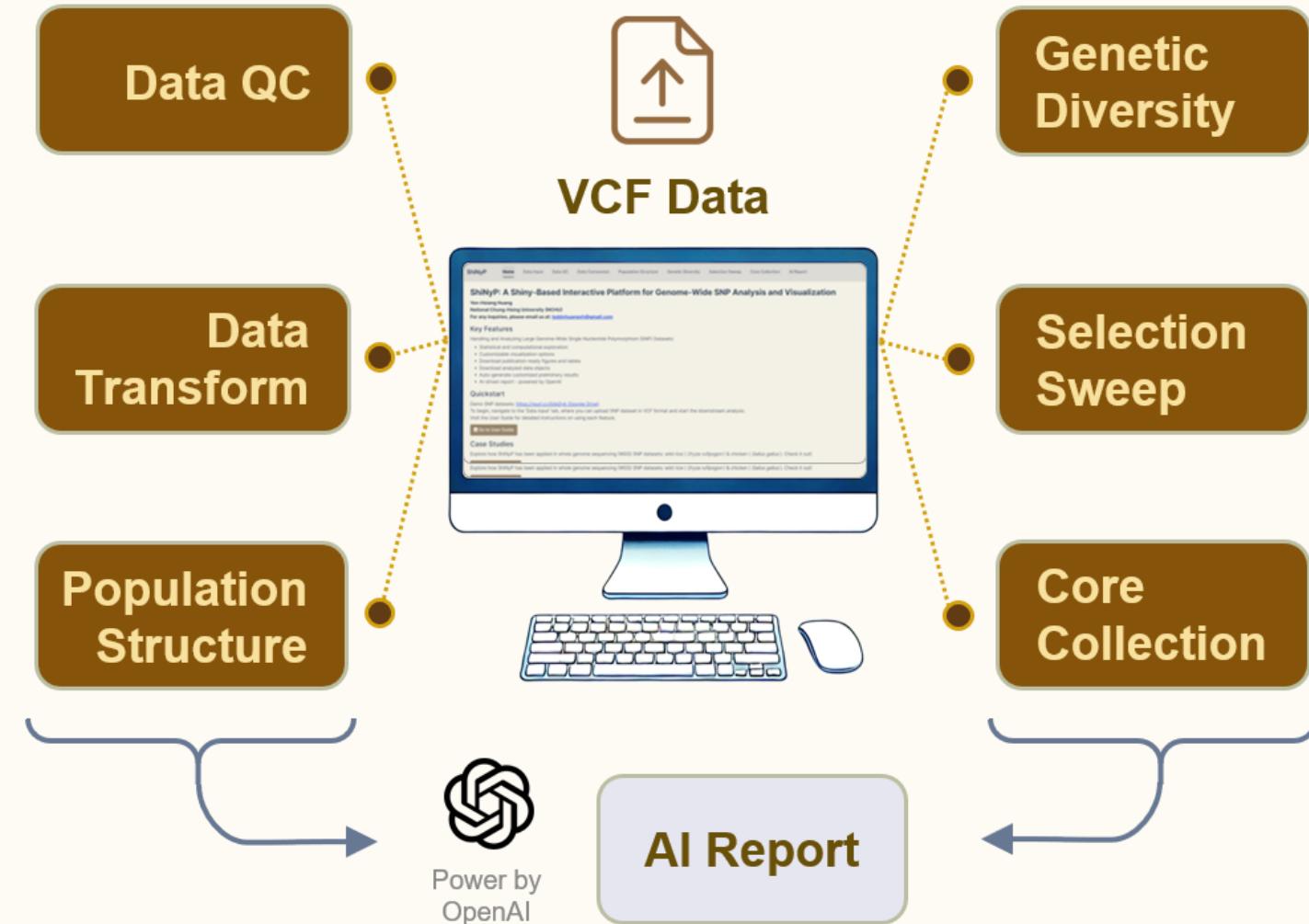
PCA Scatter Plot



PC Explained Variance Plot



ShiNyP: Platform for SNP Analysis and Visualization





Shiny Framework



R Packages



Visualization Tools



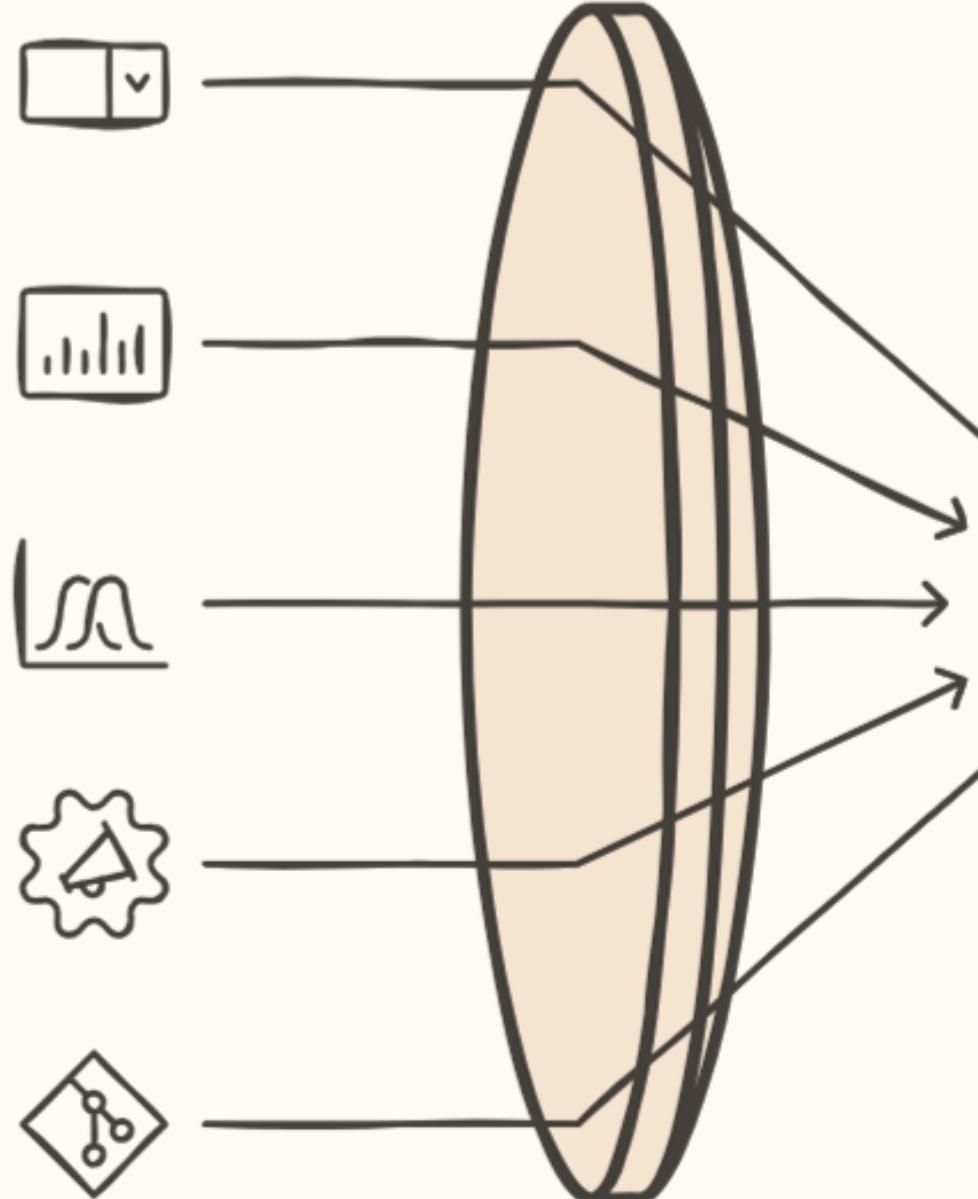
AI Integration



GitHub Deploy



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ShiNyP Platform



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

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)

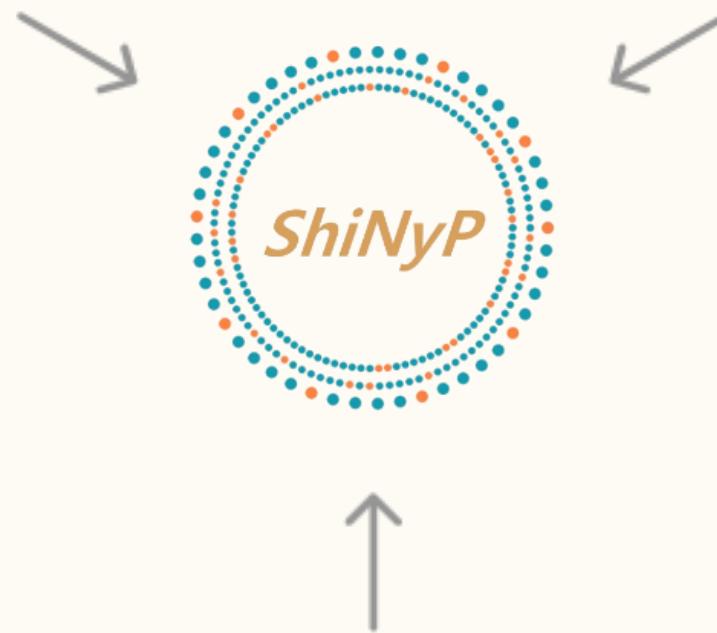
iDEP: RNA data analysis (Ge et al., 2018)

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



Intuitive
Interface

Shiny
Framework





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!



Thank You!

Thank my advisors & colleagues:

Dr. Chung-Feng Kao

Mr. Sudip

Dr. Endang Septiningsih

Ms. Roly

Dr. Michael Thomson

Ms. Merve

Ms. Lumi Chen

Ms. Khushboo

Mr. Protik





Resources



Feedback Form

