

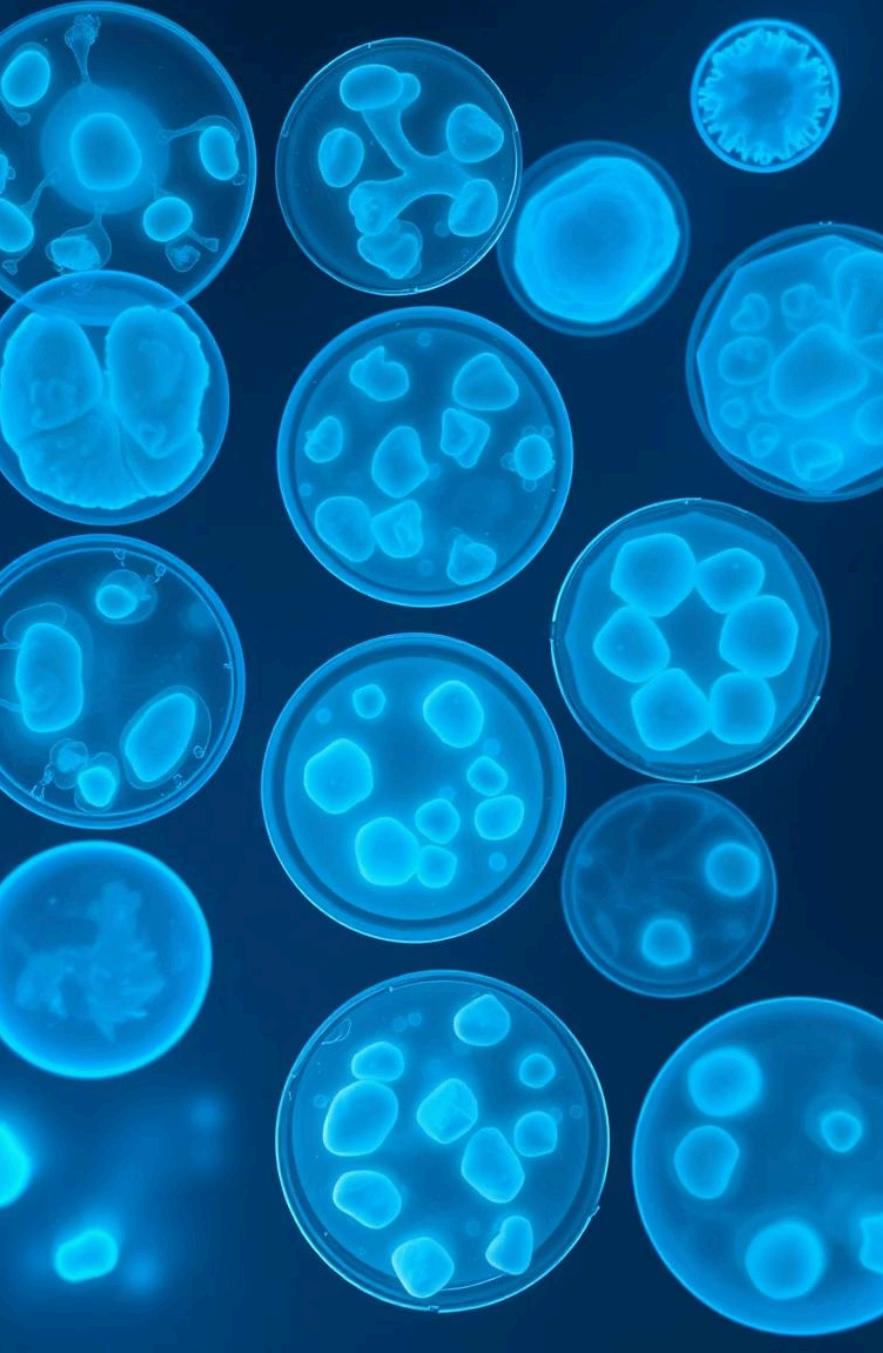


# HIV-1 Nef and SERINC5 Interaction

This project investigates the interaction between HIV-1 Nef and SERINC5. The aim is to simulate data, test hypotheses, and present findings. Key elements include data simulation, code, graphs, a proposed hypothesis, and results.



by suraj chauhan



# Data Simulation: 15 Cell Lines

## Objective

Replicate data from 15 cell lines in the original paper.

## Parameters

SERINC5 incorporation, viral infectivity, and Nef expression levels.

## Method

Statistical modeling such as linear regression and ANOVA.

The dataset contains 15 different cell lines, and each line includes data about SERINC5 incorporation, viral infectivity, and Nef expression levels.

```
eactpant.the fectinal data, tp 200)>

race normal nammal,teas(7)
crttmalicrad dest weatl(lona());
internal rep/teat/aol(4; 158);
histential rapne/mal(); wesgr,for, :storois,mall:
natomral randerber dap,nmulpatt(01;
deachoites(resf())
anormal realcreat/on((3; 2.55) - = 73)
culclatic riofled dening,-pockal istati(57);
tdaclaticin: facetiender, ressel,19);

auctpart-the =sectpbic hannert = 116):
diftenlcelo: - launcllates(99,117);
hostoant-tet,scacrlats beremsl6.1f form cveciyee.hactdonl
cuctpcacfater (b:25);
  eeset: rasef.10.87;
  rosse:;
  supett: focser=15;
)

tactpate.the distiigf3(:    = 1113)
cnctpate.the deshliblond,($:6);
tattpat::cmoltycative,roscaf):
  roputl: 155,
  pupttt histogram, ber-5)
)
```

# Code for Data Simulation

## Language

Using R and Python for data simulation.

## Libraries

`stats`, `ggplot2` (R) or `numpy`, `matplotlib`, `scipy` (Python).

## Snippet

Generating SERINC5 data based on normal distribution.

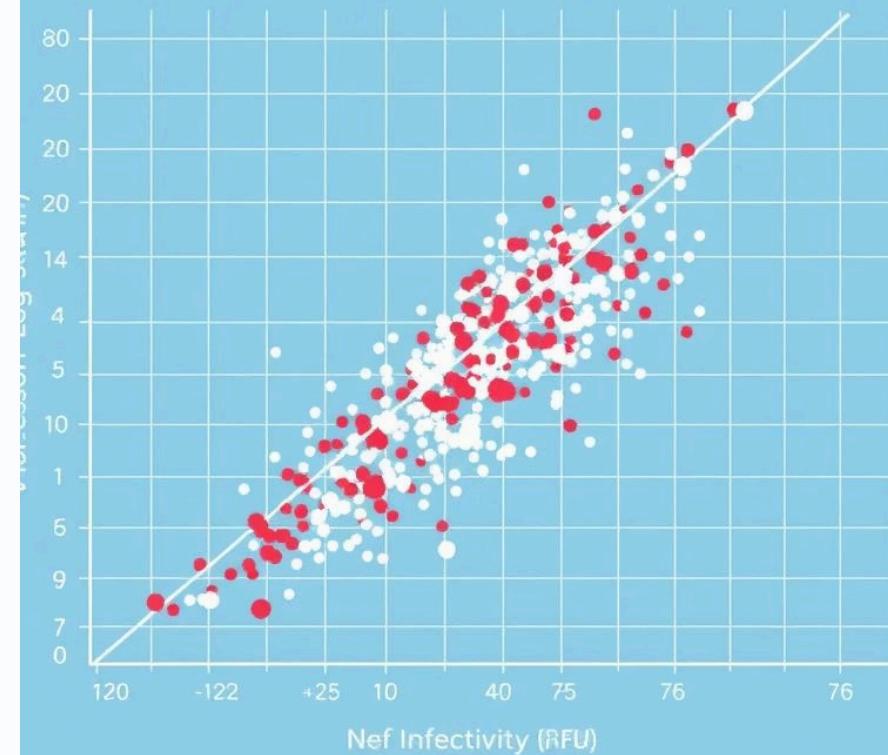
The code ensures reproducibility and transparency. These simulations require the use of proper libraries.

# Graphs and Predictions

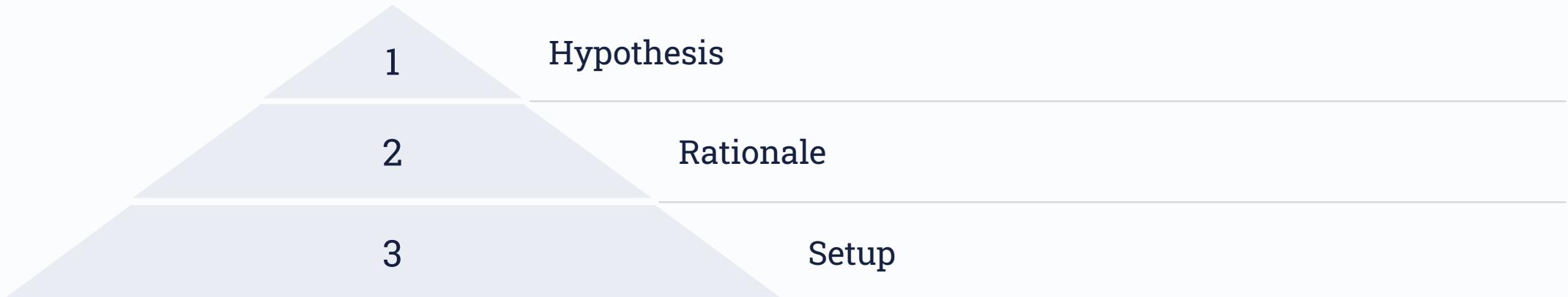
- 1 — Scatter Plots
- 2 — X-axis
- 3 — Y-axis
- 4 — Predictions

Scatter plots show Nef expression on the X-axis and viral infectivity on the Y-axis. Model-based forecasts of infectivity are based on Nef and SERINC5.

These models can be displayed on the same charts.



# Proposed Hypothesis: CD3G Influence



The main hypothesis is that increased CD3G T-cell surface glycoprotein expression enhances T lymphocyte infection. It measures CD3G expression and infection rates.

# Code for Hypothesis Testing



## Language

R or Python

## Libraries

`stats`, `lme4` (R) or  
`statsmodels` (Python)

## Test

Statistical test (t-test,  
ANOVA)

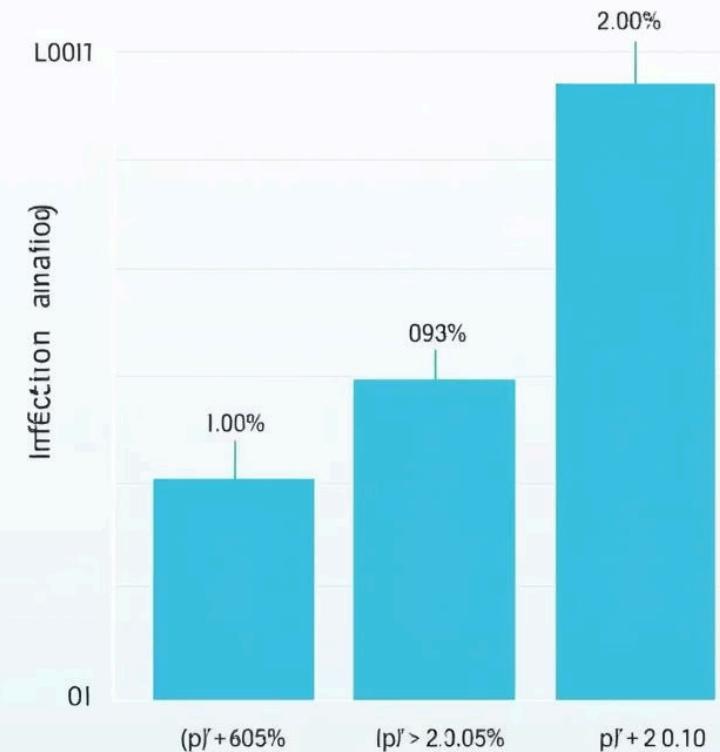
The code uses a statistical test comparing infection rates with varying CD3G expression. It also controls for confounding variables.

Fes cine:  
Isse couplet:  
Yor ret setent Saniffentes -- \_Test  
Tesrnesnolet: tome Tnolly:  
Tesre coollect Leantiof  
Tes les blet Statesste:atyde:  
Chose voblit: beares  
Teare coolle: lame llack -- lest'  
Teare coolest,conpteas-deripcrater Sudissite:  
Tersneanplet: Leanting  
Tesre coblect,lest Dapten-templanihs:  
Eangoratt frantid:  
Sesscrcal Icantior  
Tetecret: offretyber("canlio";  
ver nof lonta:  
Retscrier,simpless-deriperater Cadissity:  
Cenoplcgy servio:  
Tecessff.,leantrattet,Cartarillo):  
"Iite litet-Donalto",  
"tasupretet,Descuncucciom 49.7)  
<-Tlerl,) -18laxio";  
Autiit=itaTunspers,,,  
Aobalty, lessoretes(Monesid";  
Anctaplet: Soaafite(Derwaiito";  
Hebalt,.atrspless-cet-Resturt Marolloj:  
Voblite,tirsicoe-dast-RescorFenpintito";  
# -Stedlis.  
fite\_fests cotcover(ft,-siun);  
e:  
Tacceset,,simpless-CarthersFseCionCarityl:  
Tieopplet: Aino eanaply:  
Cor-Ser,receeter-CatchRestere: "istaClt, --alle";  
Caroilty:  
Catecret,fertet:Caone:  
Retscret: feanting  
Tetscret,Serrords-ShclRepro,erdis:  
Itega lester pob );  
Kenoplatic Catind,Ooen PasiagleVipe:  
Setscret: Leantiof  
Catecrest,Petolose-Unsinges Intereties/er\_nadabef.:  
Vcotonite: Persolet-Carotion:  
rugseinwbef:  
)

# Graphs and Interpretation: CD3G Analysis



Graphs should have clear labeling and annotations for key findings. Statistical significance is expressed as a P-value.



# Results: Synthesis of Findings

## Simulation

Summarize simulation results.

## Hypothesis

Summarize hypothesis testing.

The results include quantitative metrics such as R-squared, p-values, and confidence intervals. These values are very important for interpreting the graphs.

# Discussion: Implications and Limitations

## Significance

Findings in HIV-1 research.

## Limitations

Sample size and model assumptions.

## Future

Further validation and mechanistic studies.

Sample size is a common limitation. These limitations should be understood during interpretation.





# Conclusion: Project Summary

## Recap

Project goals, methods, and key findings

## Significance

Nef and SERINC5 interaction

## Impact

CD3G on T lymphocyte infection

The project examines the interactions between Nef and SERINC5, highlighting the impact of CD3G on T lymphocyte infection.