

# Agglutination Concentration Calculator



Gabrielle Xia

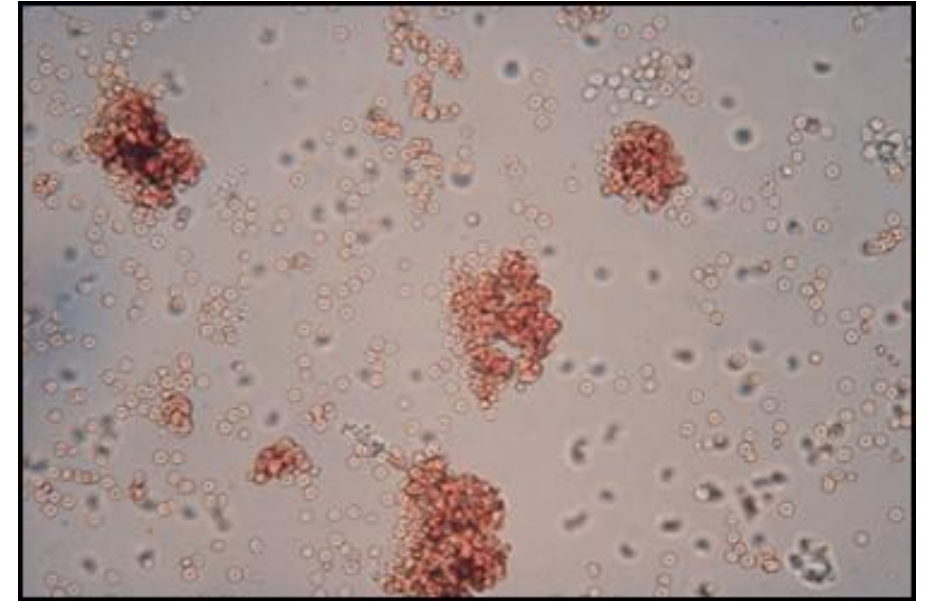
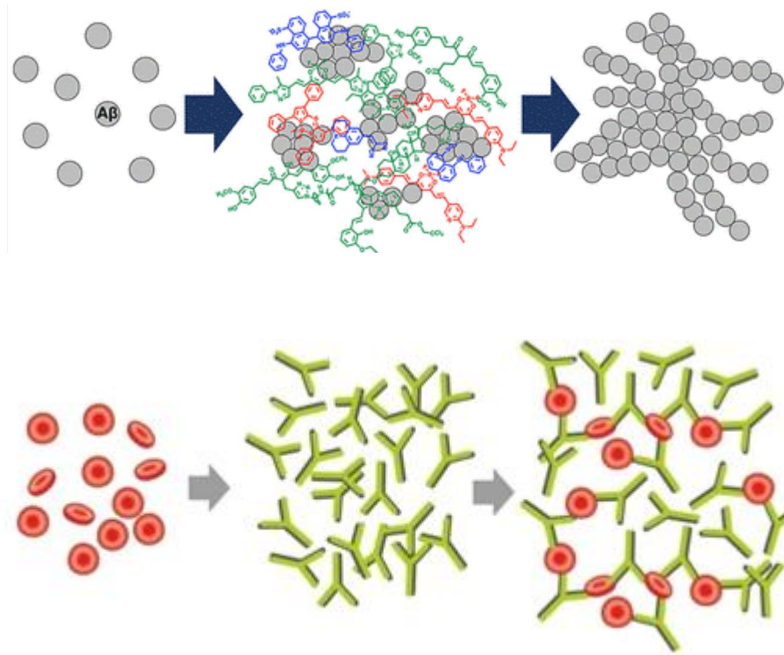
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## CONTENT

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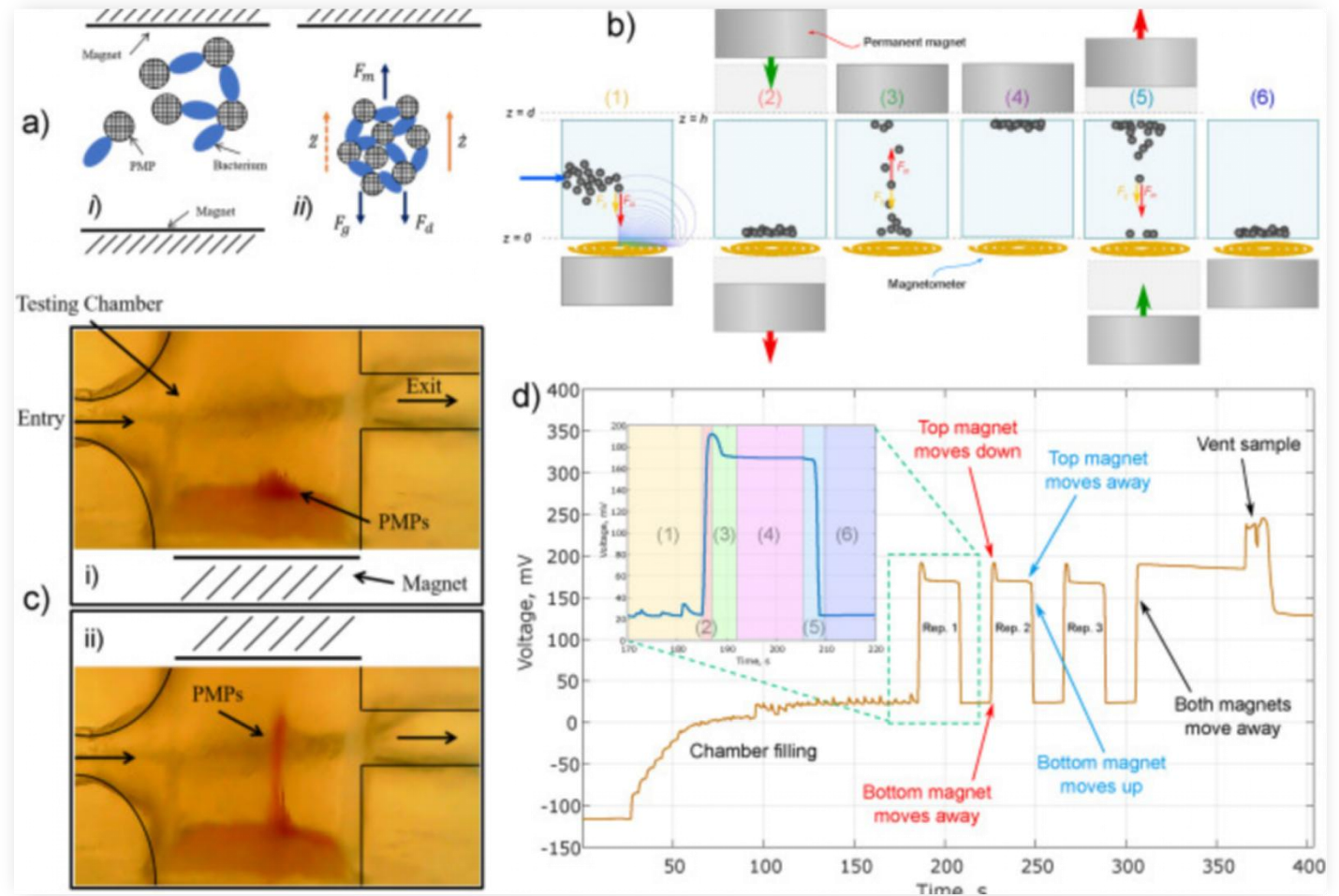
- Background
- Problem Statement
- Methodology
- Results
- Challenges & Limitations

# Background - Agglutination

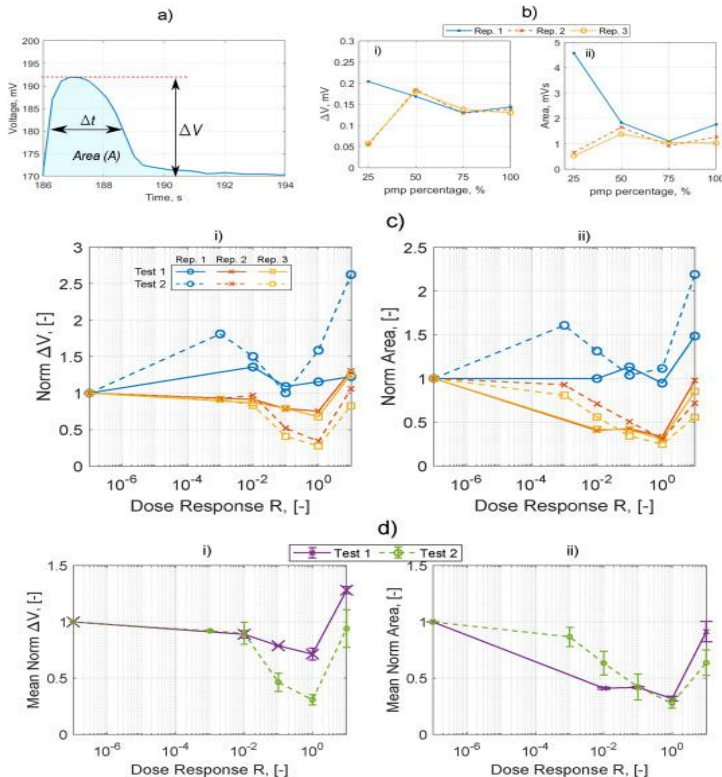


# Background - Current Challenges

- Traditional manual analysis
- Time-consuming process
- Subjective interpretation



Hughes R, Fishman A, Lamb-Riddell K, Sleigh Muñoz V, Champneys A, Kiely J, Luxton R. Modelling a dynamic magneto-agglutination bioassay. Biosens Bioelectron. 2023 Feb 15;222:114745. doi: 10.1016/j.bios.2022.114745. Epub 2022 Sep 28. PMID: 36502714.

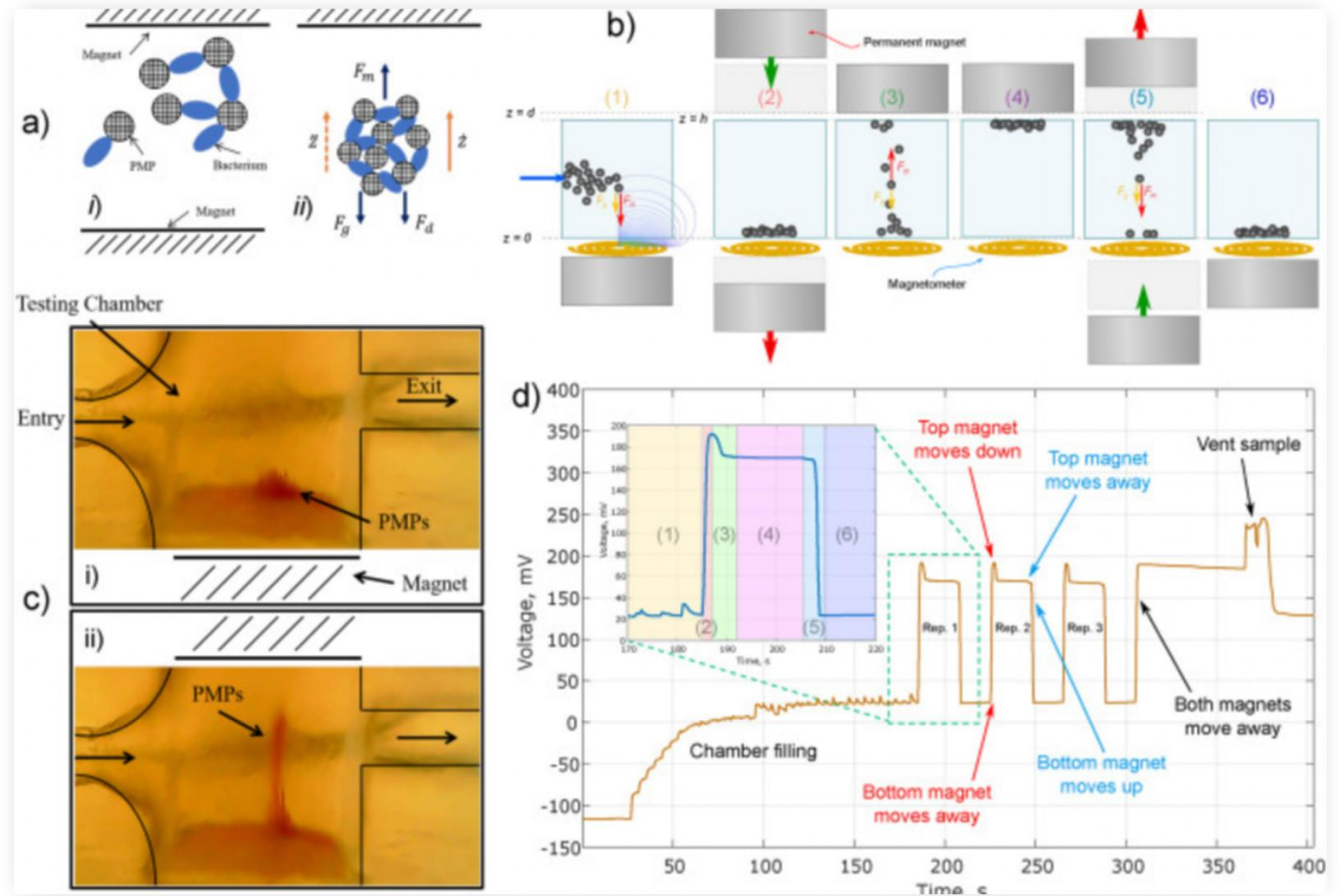


**Question:**

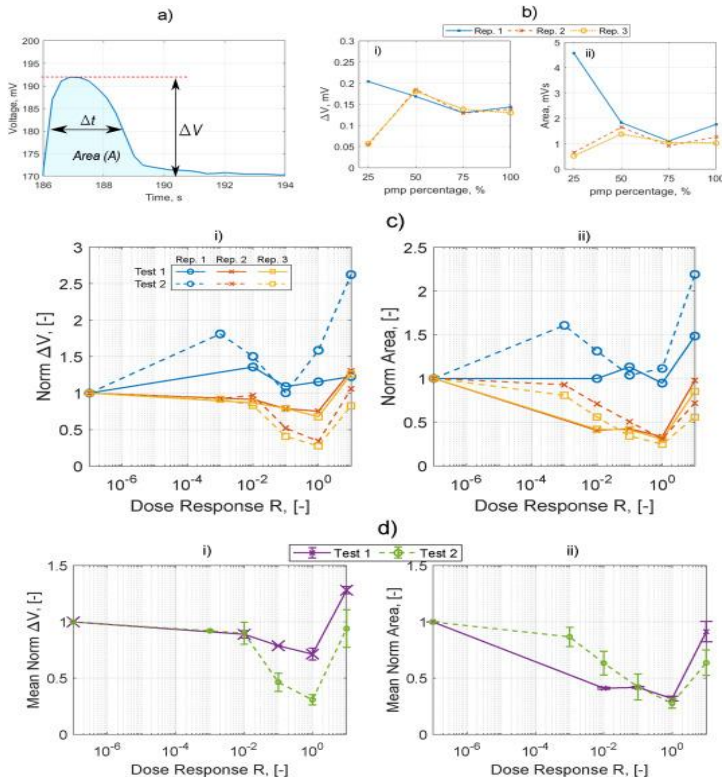
**Can we develop an automated method  
for accurate recognition and  
quantification of agglutination  
patterns?**

# Background - Current Challenges

- Traditional manual analysis
- Time-consuming process
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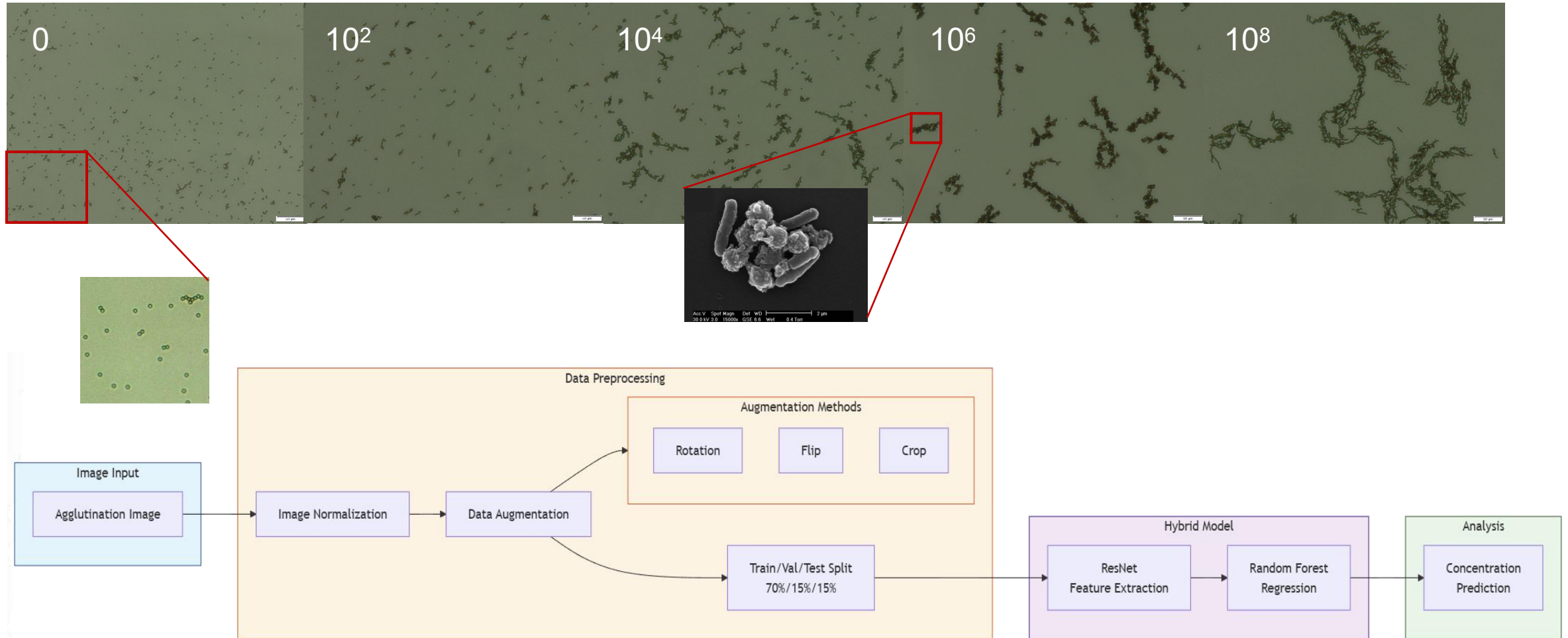


Hughes R, Fishman A, Lamb-Riddell K, Sleigh Muñoz V, Champneys A, Kiely J, Luxton R. Modelling a dynamic magneto-agglutination bioassay. Biosens Bioelectron. 2023 Feb 15;222:114745. doi: 10.1016/j.bios.2022.114745. Epub 2022 Sep 28. PMID: 36502714.



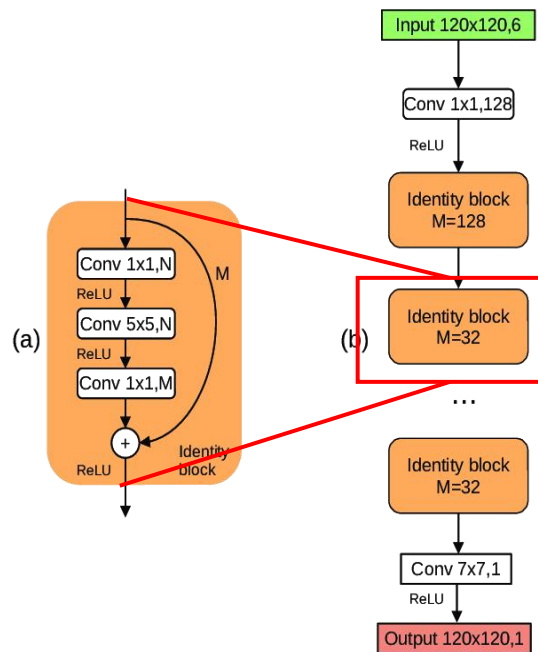


# Methodology - Data

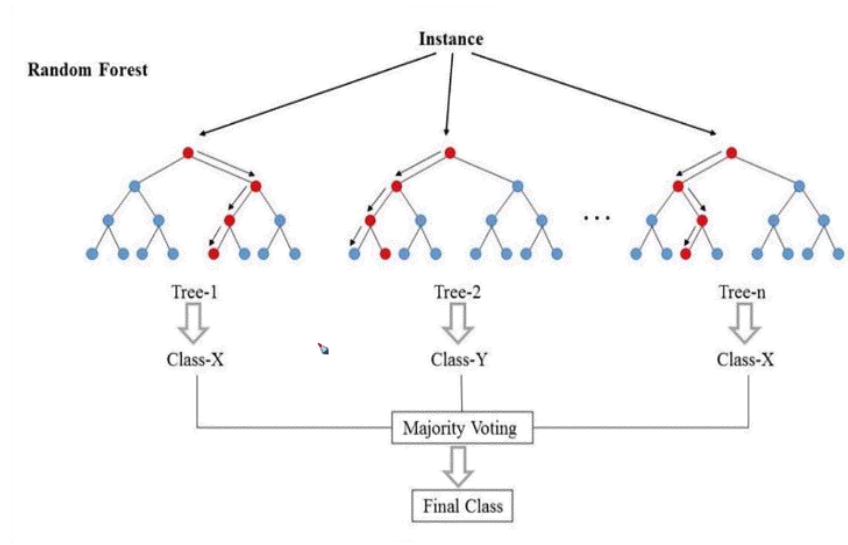


# Methodology

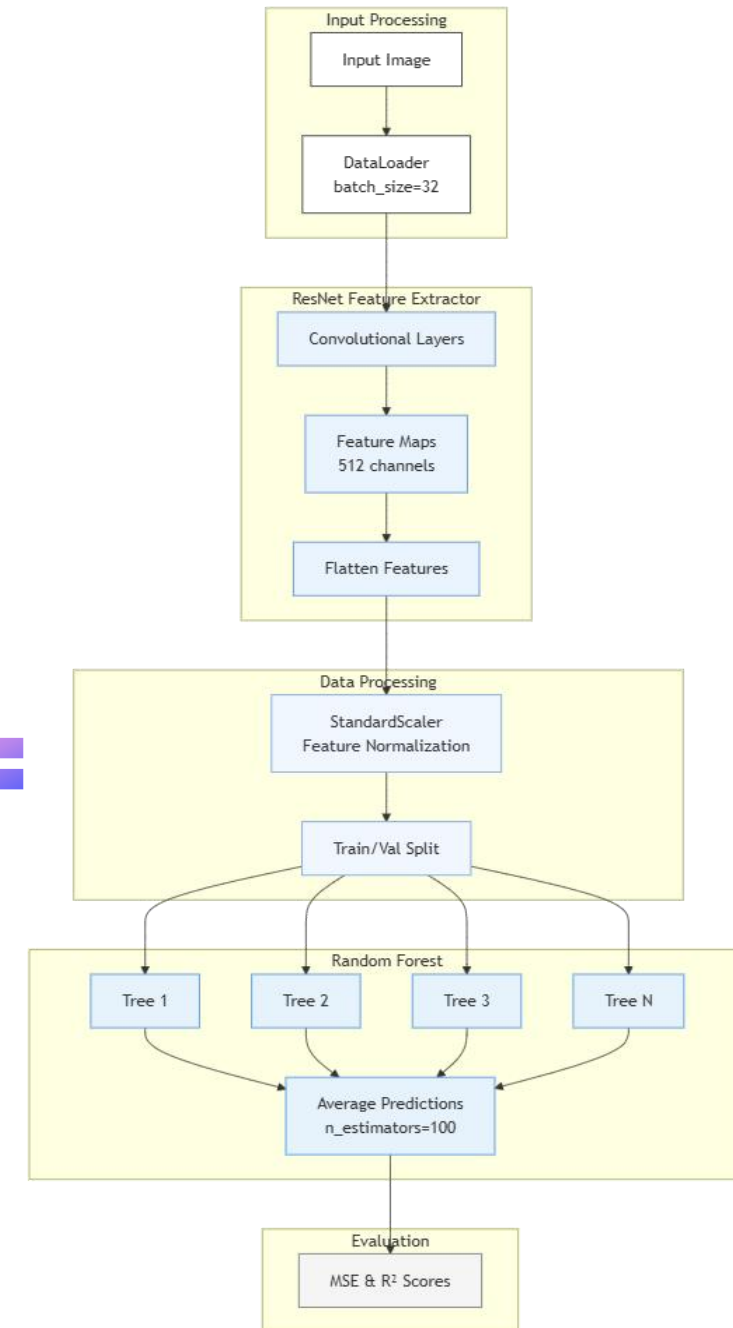
- Hybrid Model Architecture: ResNet-RF Model



Extract image feature

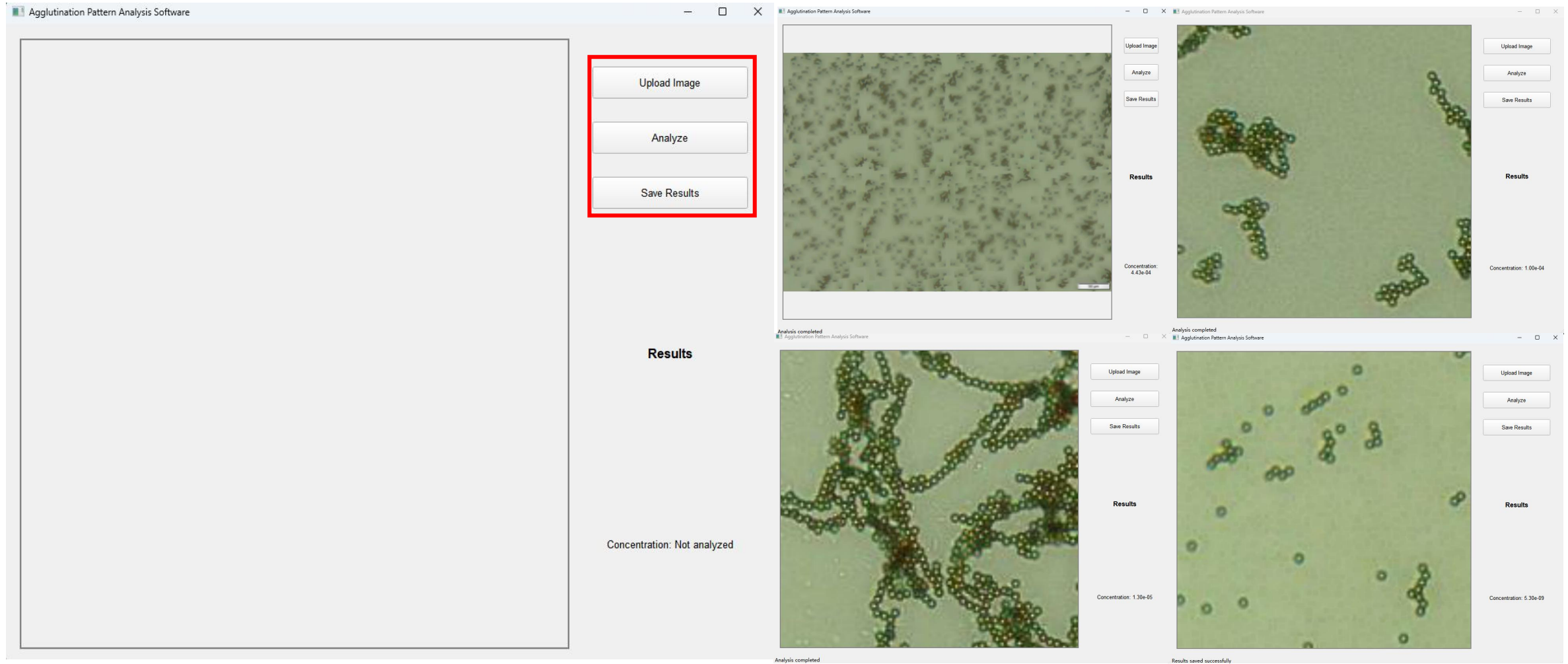


Robust to overfitting  
Handles limited data well



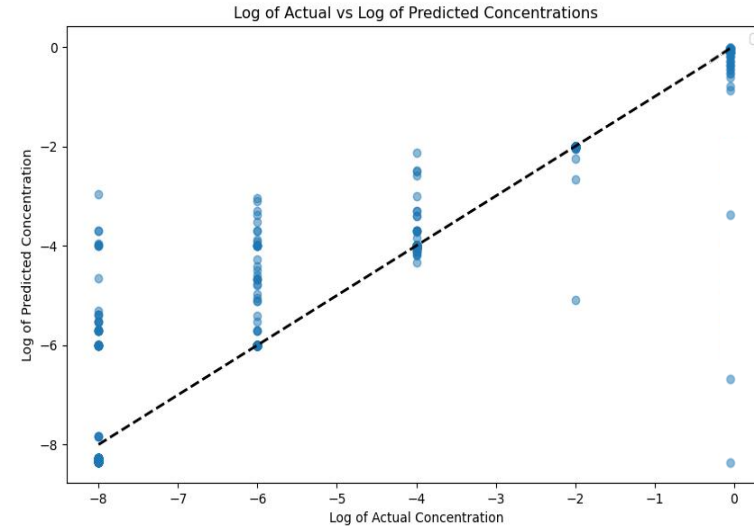


# Results Demo - GUI Development



# Results

- Superior agglutination pattern analysis
- Successful detection across various concentrations
- Effective with limited training data through augmentation



# Challenges & Limitations

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- Dataset limitations
- Pattern complexity
- Integration challenges
- More portable



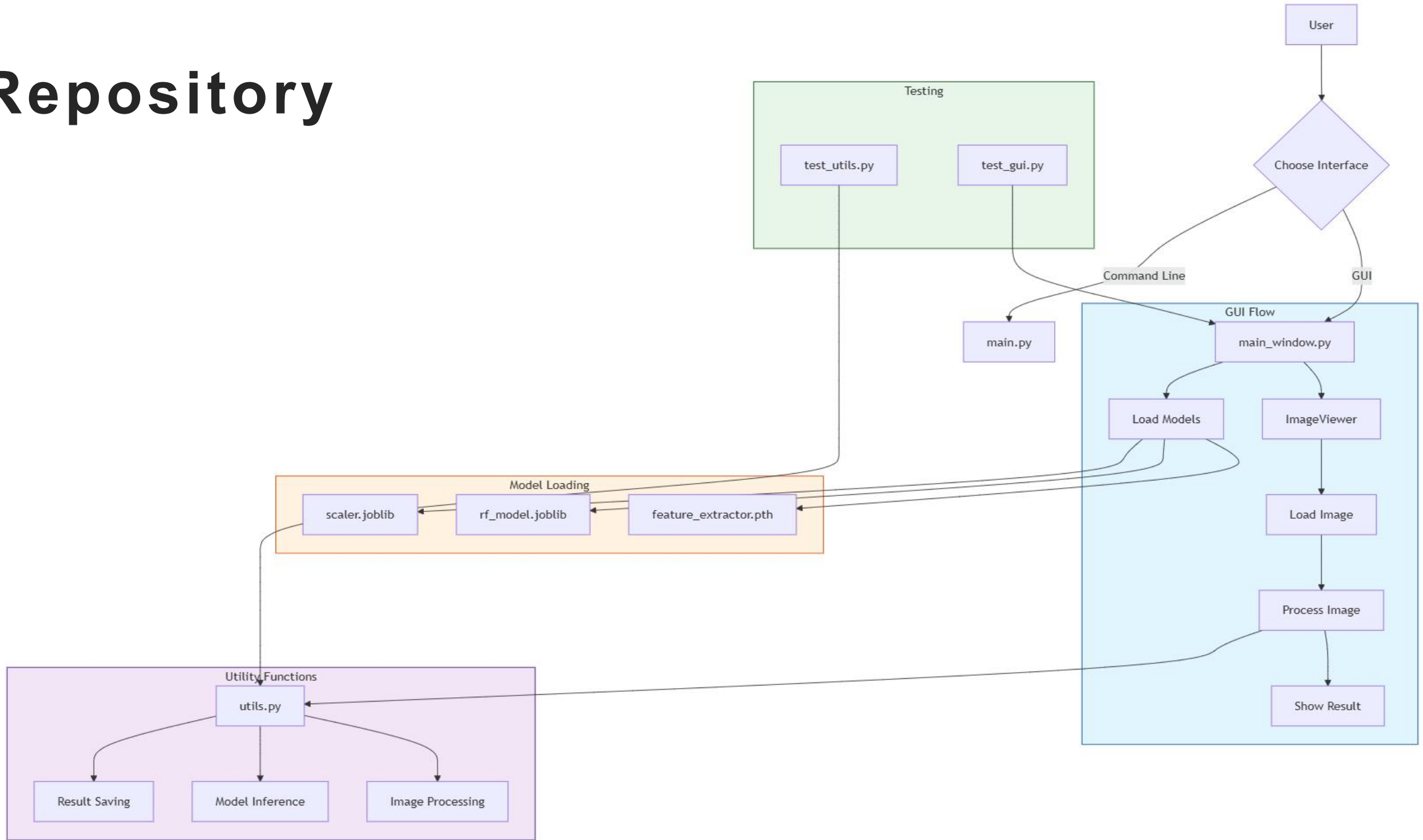
# Repository

📁	AgglutinationConcentrationCaculator
└─ 📁	src
└─ 📁	AgglutinationConcentrationCaculator
└─ 📄	init.py
└─ 📄	main.py
└─ 📄	utils.py
└─ 📁	models
└─ 📁	models
└─ 📁	GUI
└─ 📄	init.py
└─ 📄	main_window.py
└─ 📁	components
└─ 📄	init.py
└─ 📄	image_viewer.py
└─ 📄	test.py
└─ 📄	setup.py
└─ 📄	requirements.txt
└─ 📄	README.md
└─ 📄	LICENSE

Main structure

🔗 JM-Xia	Delete saved_results directory	
📁	.idea	package
📁	src	package
📁	trained_models	package
📄	Component Specification.pdf	code
📄	Functional Specification.pdf	code
📄	README.md	package
📄	Requirements.txt	code
📄	setup.py	package
📄	test.py	package

# Repository





**Thank  
you!!**