

An Offline End-to-End Platform for Unified DICOM Archiving, BIDS Standardization and AI Driven Pediatric MRI Neuroimaging Analysis

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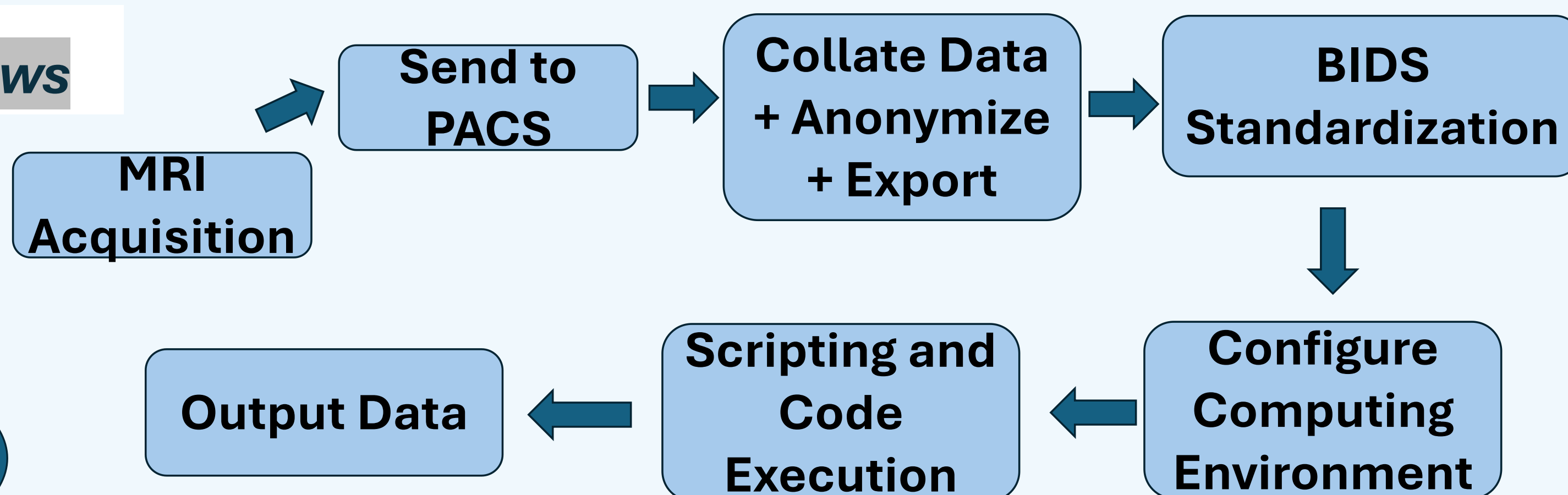
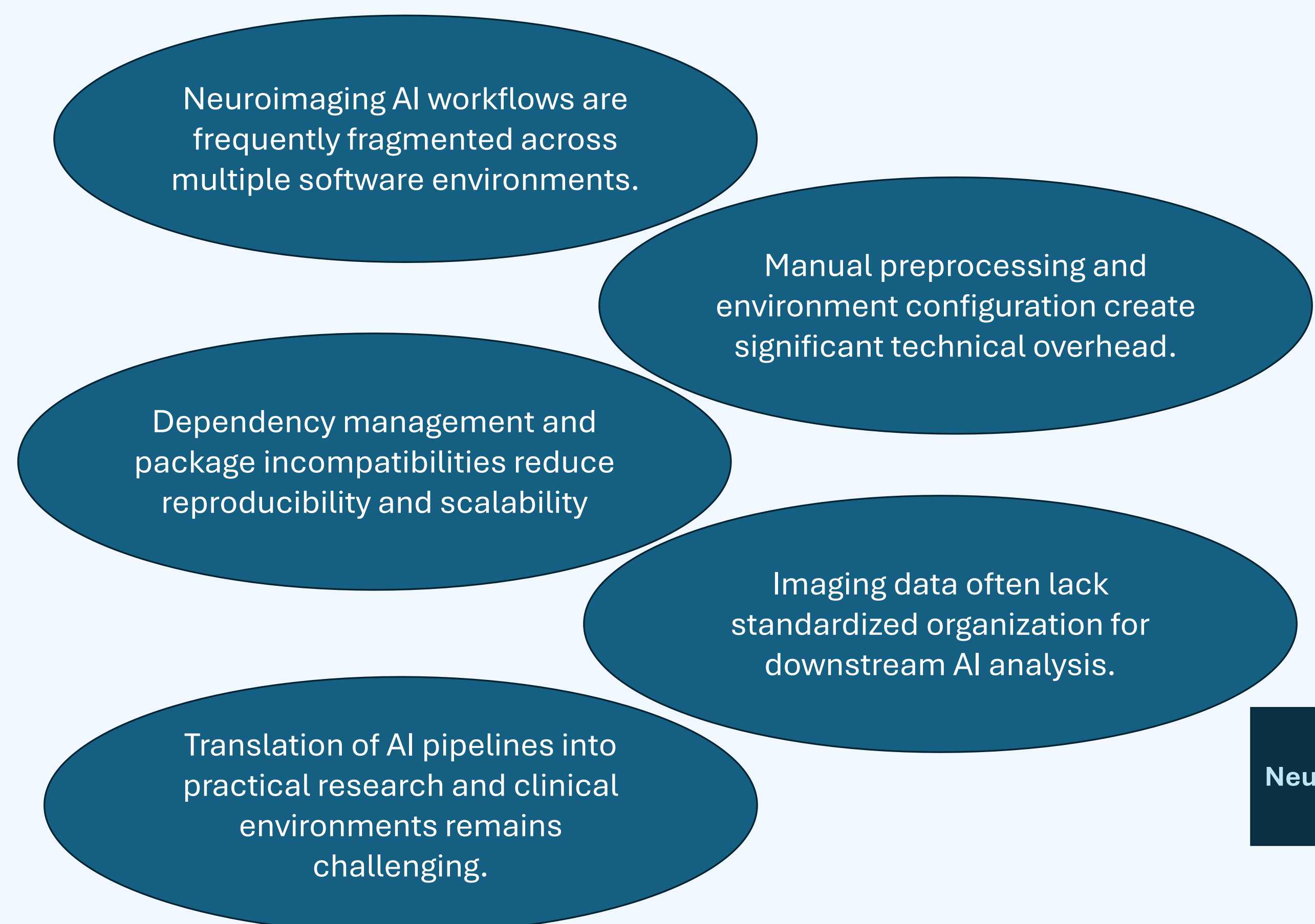
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Overview

Neuroimaging workflows are often fragmented across multiple infrastructures, software tools, and skill sets, leading to inefficient and labour-intensive processes. **Aesclepien Vision** is a proof-of-concept platform designed to unify these components into a single, streamlined system. Written in streamlit and python integrated with a Linux (Debian) operating system and hosted on our radiology network, Aesclepien Vision integrates DICOM archiving from PACS and research scanners, automated BIDS standardization, and a user-friendly interface that seeks to enable on-site radiologists to run neuroimaging and AI-driven workflows through simple click-and-submit interactions. By consolidating established pipelines and custom segmentation tools for our compute restraints, Aesclepien Vision lays the groundwork for scalable, future-ready neuroimaging analysis.

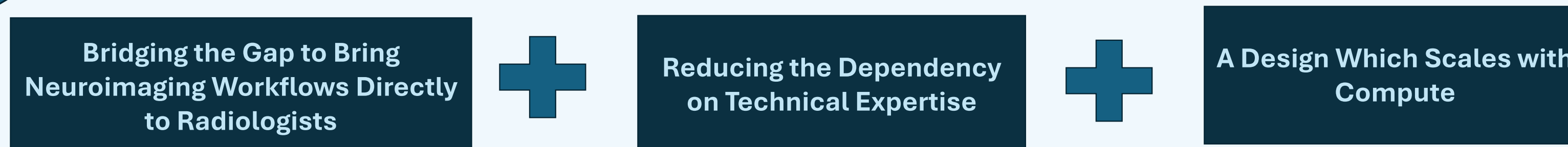
Motivation

The Problems with Traditional Neuroimaging Workflows

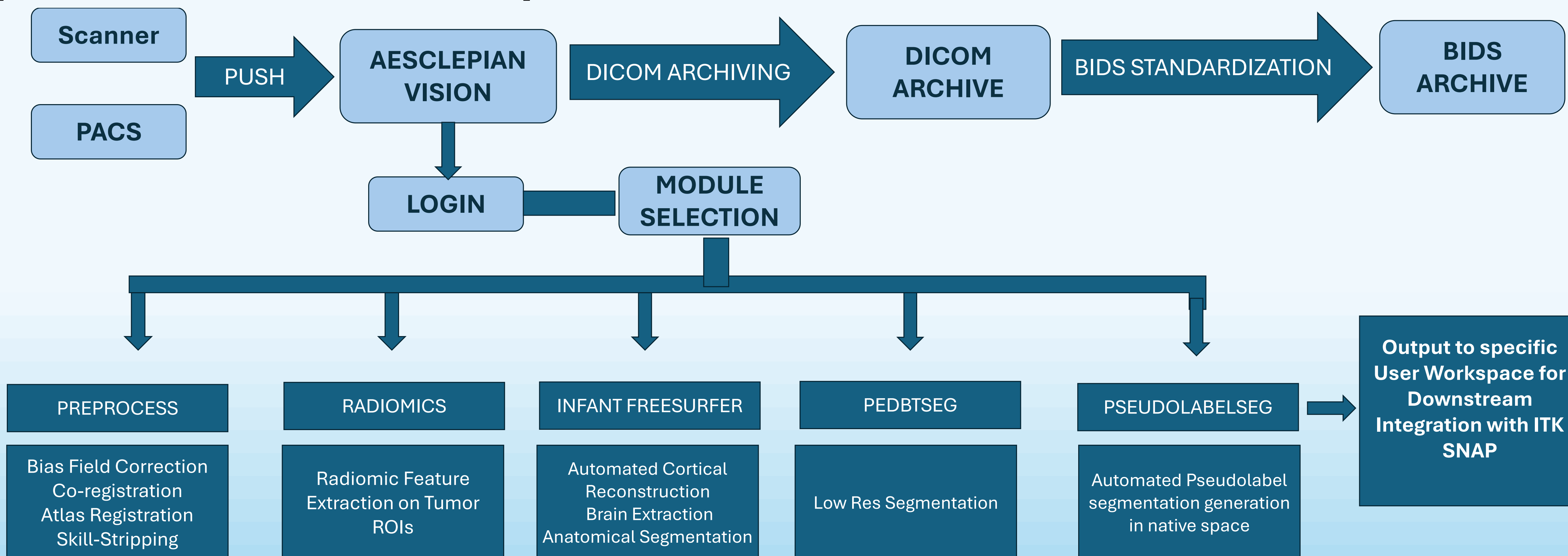


Example Neuroimaging Workflow

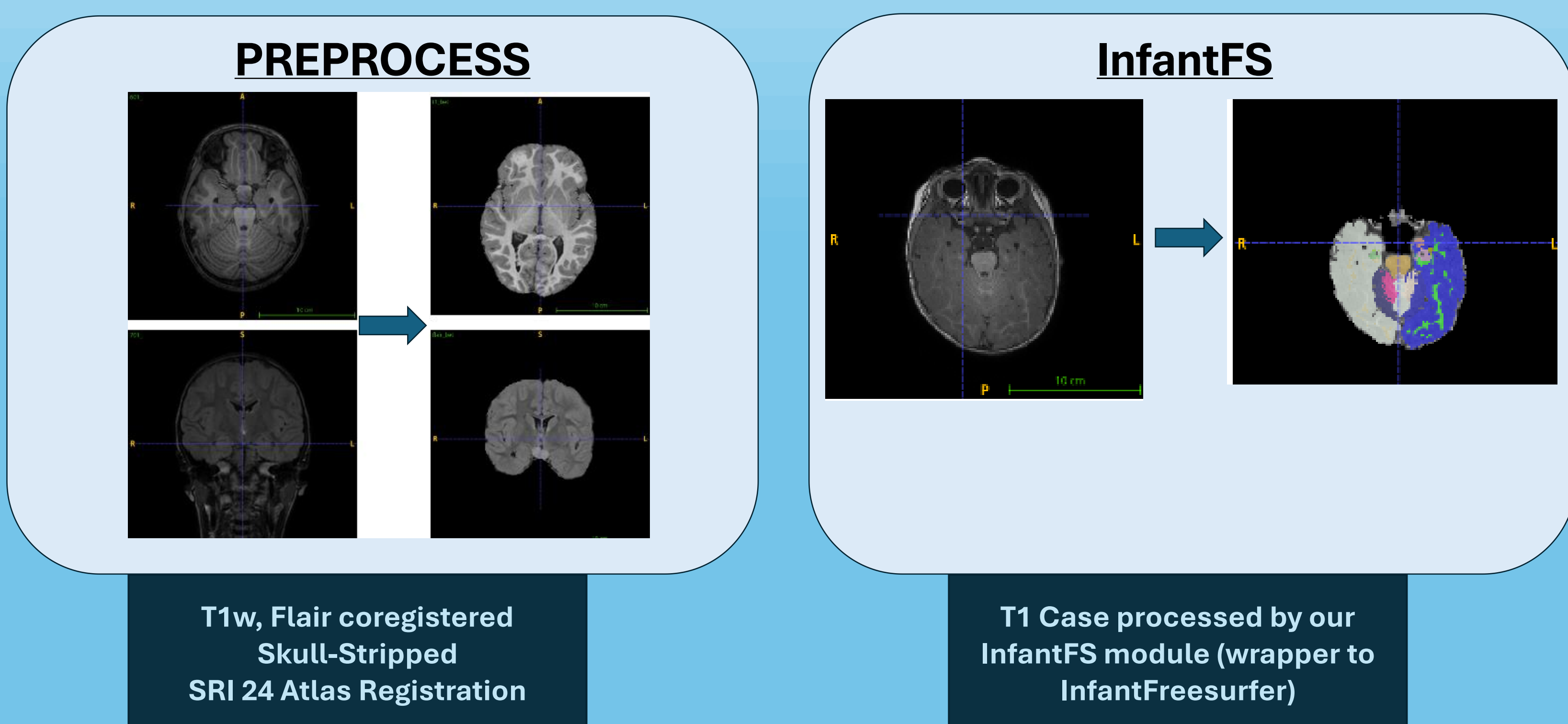
What We Require – Bringing AI Directly to the Radiologist



Proposed Solution – Aesclepien Vision



Results and Example Outputs



Module:	Built on:	Processing Time (per case):
InfantFreesurfer	Freesurfer [1]	22m
Preprocess	Brainles-Preprocessing [4]	8m
Radiomics	Pyradiomics [3] + custom	28m
PEDBTSEG	BraTS Data [2] + custom	11.5m
PSEUDOLABELSEG	BraTS-PEDs [2] Data + custom	17m

Conclusion and Future Work

Aesclepien Vision demonstrates a unified neuroimaging platform integrating DICOM ingestion, BIDS standardization, preprocessing, radiomics and proof-of-concept AI workflows within a scalable “click-and-submit” infrastructure designed for resource-constrained research environments. Though currently operating with low-resolution AI models due to compute restraints, future development will focus on deployment on higher-capacity GPU infrastructure, integration of validated high-performance public AI models on clinical data, expanded pseudo-labelling workflows and rigorous validation on private on-site datasets

References

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- [3] van Griethuysen, J. J. M., Fedorov, A., Parmar, C., Hosny, A., Aucoin, N., Narayan, V., Beets-Tan, R. G. H., Filion-Robin, J. C., Pieper, S., Aerts, H. J. W. L. (2017). Computational Radiomics System to Decode the Radiographic Phenotype. *Cancer Research*, 77(21), e104–e107. <https://doi.org/10.1158/0008-5472.CAN-17-0339>
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