Leopard-EM: An extensible Python package for 2DTM

Matthew Giammar

FrostByte

11 June 2025

Wolfram Seifert Davila

Lab Members

Prof. Bronwyn Lucas
Josh Dickerson
Joshua Paul
Matthew Giammar
Wing Yan Wu
Clarence Ling
Kithmini Herath
Laina Hall
Shloka Jasignh
Ben Rose

Berkeley
UNIVERSITY OF CALIFORNIA

CCB | CENTER FOR COMPUTATIONAL BIOLOGY

NIH
National Institutes of Health

CHAN ZUCKERBERG INITIATIVE

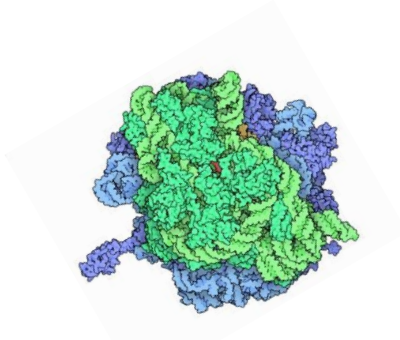
SEARLE SCHOLARS PROGRAM
FUNDING EXCEPTIONAL YOUNG SCIENTISTS

Shurl and Kay Curci Foundation

2DTM locates macromolecules *in situ*

- Two-dimensional template matching (2DTM) finds structures in cryo-EM images using a known reference template

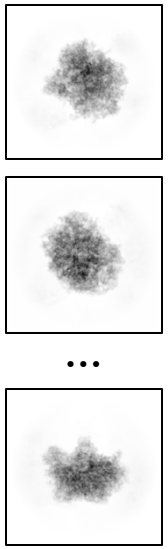
2DTM on *in situ* cryo-EM

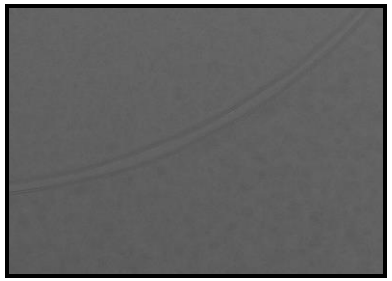


atomistic model

generate projections

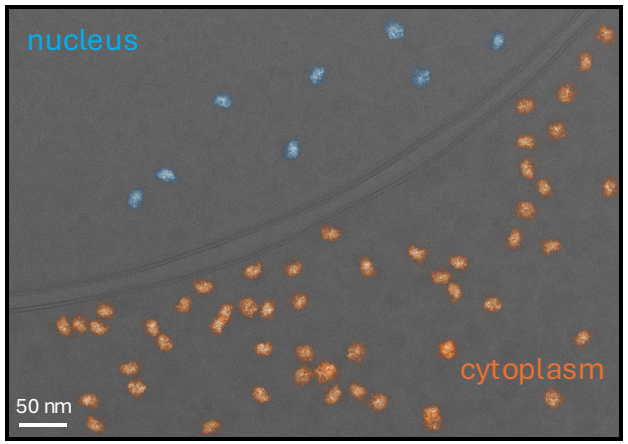
(~1.6 million)





cross-correlate with micrograph

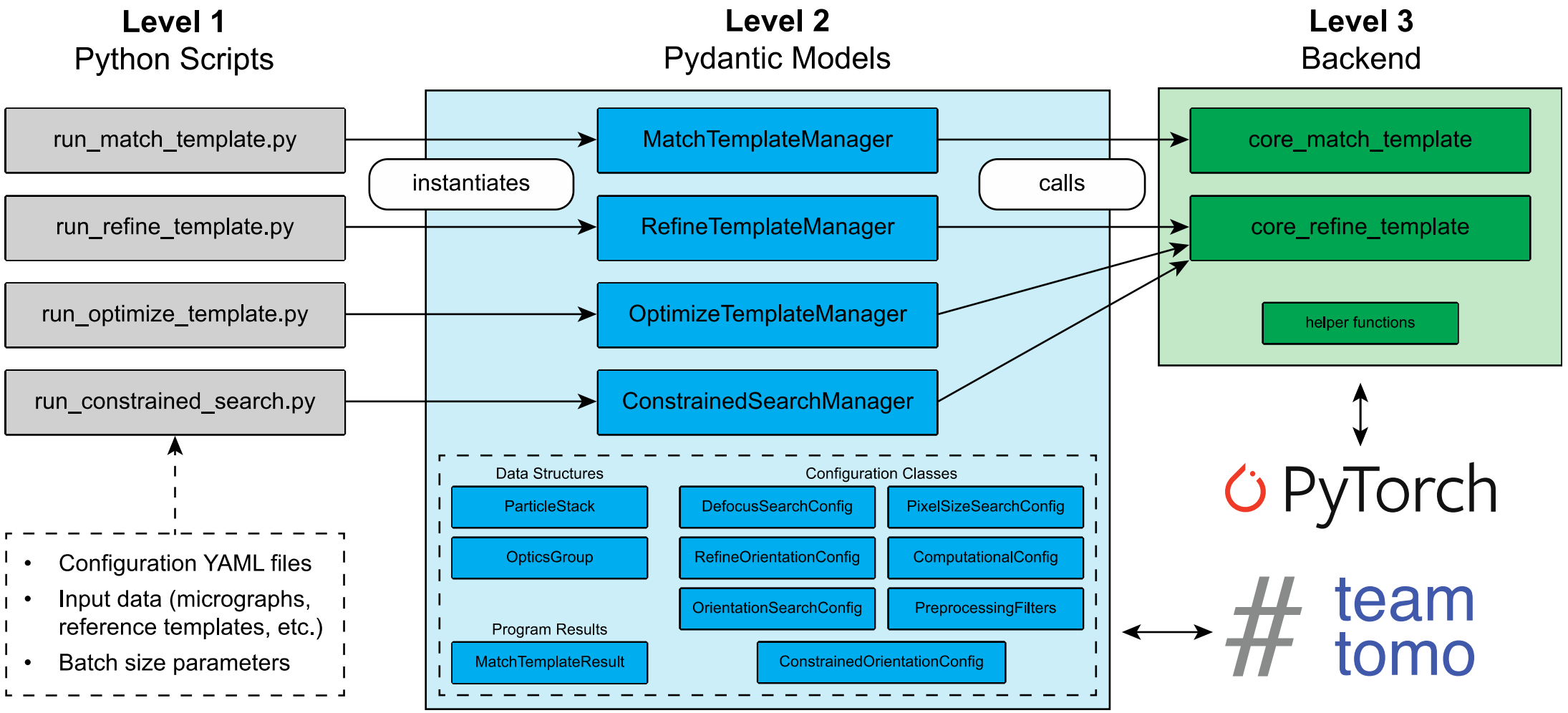
particle locations and orientations



What is Leopard-EM? Why a new package?

- Leopard-EM (**L**ocation & ori**E**ntati**O**n of **PAR**ticles found using two-dimensional t**E**mplate **M**atching) is an open-source, extensible Python package for running 2DTM
- Need a common (and easily installable) platform for developing and deploying tools using 2DTM
- Leopard-EM provides a framework for running GPU accelerated 2DTM while remaining flexible for creating more complex workflows and powerful tools

What is Leopard-EM? Why a new package?



Leopard-EM Demonstration

github.com/mgiammar/FrostByte_Leopard-EM_demo