

Grid Search Methods for Modeling Polymerization Kinetics

Katie Ziebarth

Landis Group, Department of Chemistry, UW-Madison

HTCondor Week, May 2019

Polymers

- Consist of long chains of monomers linked together
- >300 million tons of polymers produced per year
- Ubiquitous in modern society

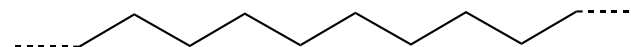
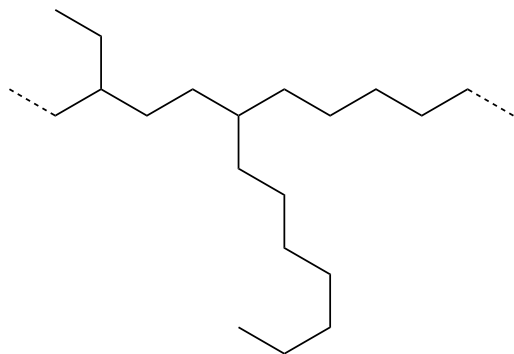
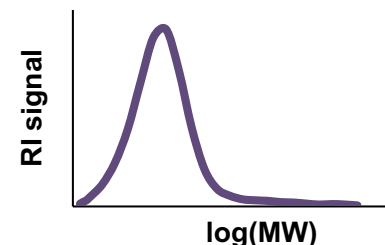


Plastics - the Facts 2017. PlasticsEurope 2018.

Images: <https://shop.crayola.com/color-and-draw/markers>, <https://www.watersandfarr.co.nz/product/imperial-low-density-polyethylene-pe-pipe/>, <https://www.amazon.com/American-Plastic-Toys-Assorted-Colors/dp/B002RQU3VQ>, https://www.uline.com/Cls_35/Food-Service-and-Packaging, <https://www.consumerreports.org/new-cars/best-and-worst-new-cars/>, <https://www.pinterest.com/pin/353321533236396447/>

Polymer Properties

- Bulk properties are determined by molecular level features, including
 - Microstructure
 - Molecular weight distribution
 - Nature and sequence of monomers
- Molecular properties are controlled by relative rates of reactions



Kinetic models:

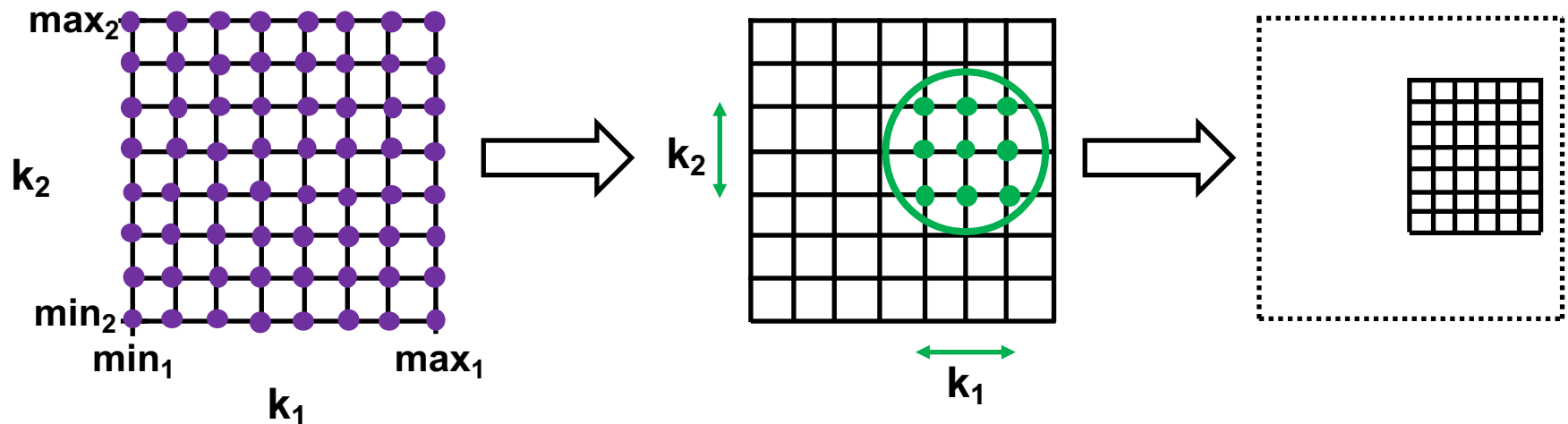
- Consist of a set of rate equations for every species in the system
 - Allows for simulations under any reaction conditions
 - Can predict molecular weight distribution, microstructure, etc.
- Account for the different possible reactions and their relative rates
- Require optimization of certain parameters (rate constants) to best fit the experimental data

Challenges:

- Typically involve 1000s of ODEs
- Iterative optimization procedures are slow and prone to getting stuck in local minima

Alternative Approach: Grid Searching

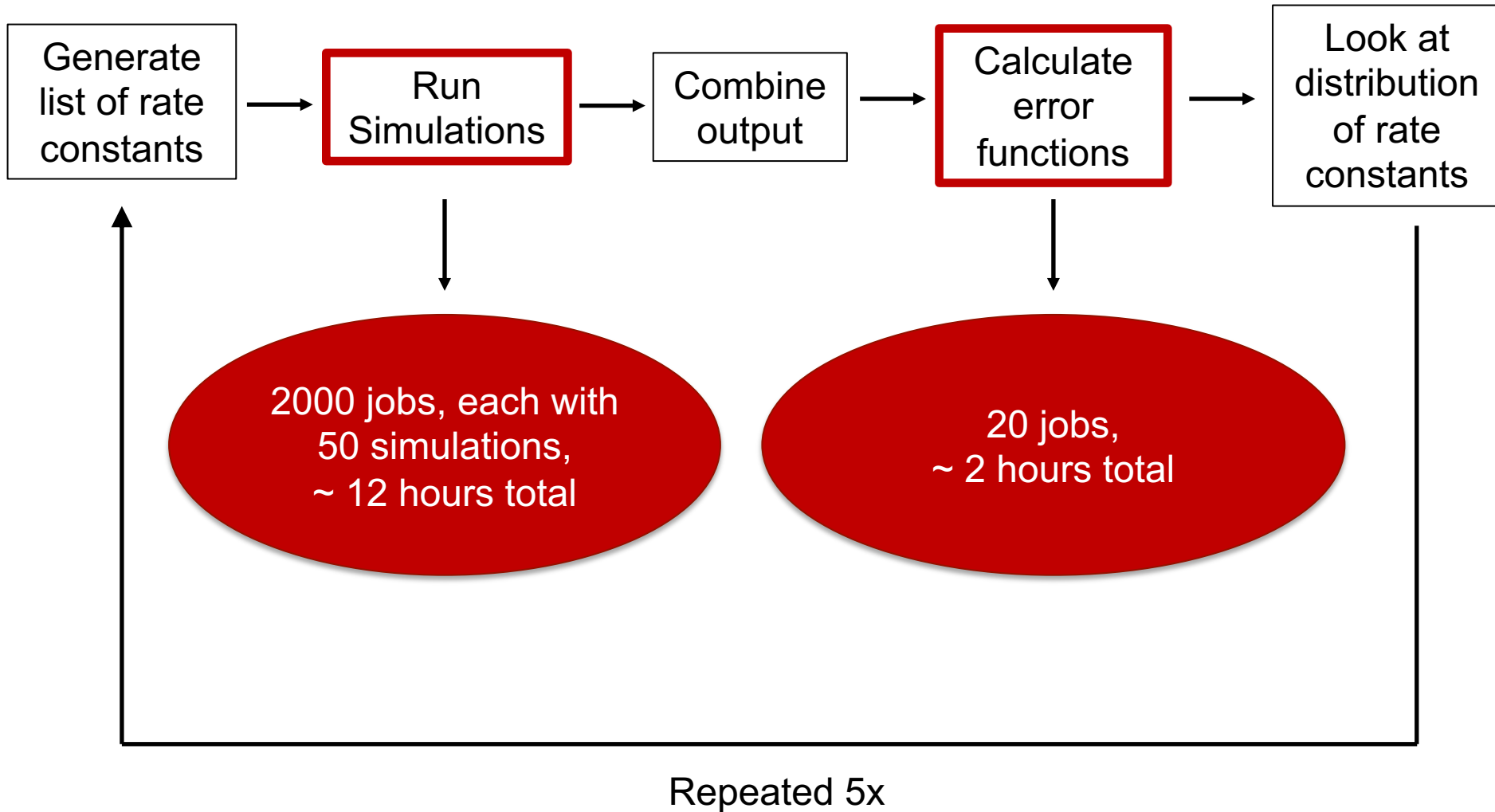
- Run simulations for many different combinations of parameters
- Compare simulations to experiment – look for best matches
- Use bootstrapping analysis to examine uncertainty
 - Get distribution of best matches
- Use results to guide selection of an adjusted set of parameters
 - Goal is to have an increasingly fine grid to improve precision of result



Calculation Set-Up

- Zr-catalyzed 1-hexene polymerization
 - 1658 ODEs
 - 5 parameters to optimize
 - 2443 data points to use for fitting
- Generate kinetic model using SimBiology toolbox in MATLAB
 - Provide chemical species, reactions, and experimental observables
- Perform grid search
 - Consider 10^5 possible combinations of parameters
 - Initially cover range of six orders of magnitude per parameter

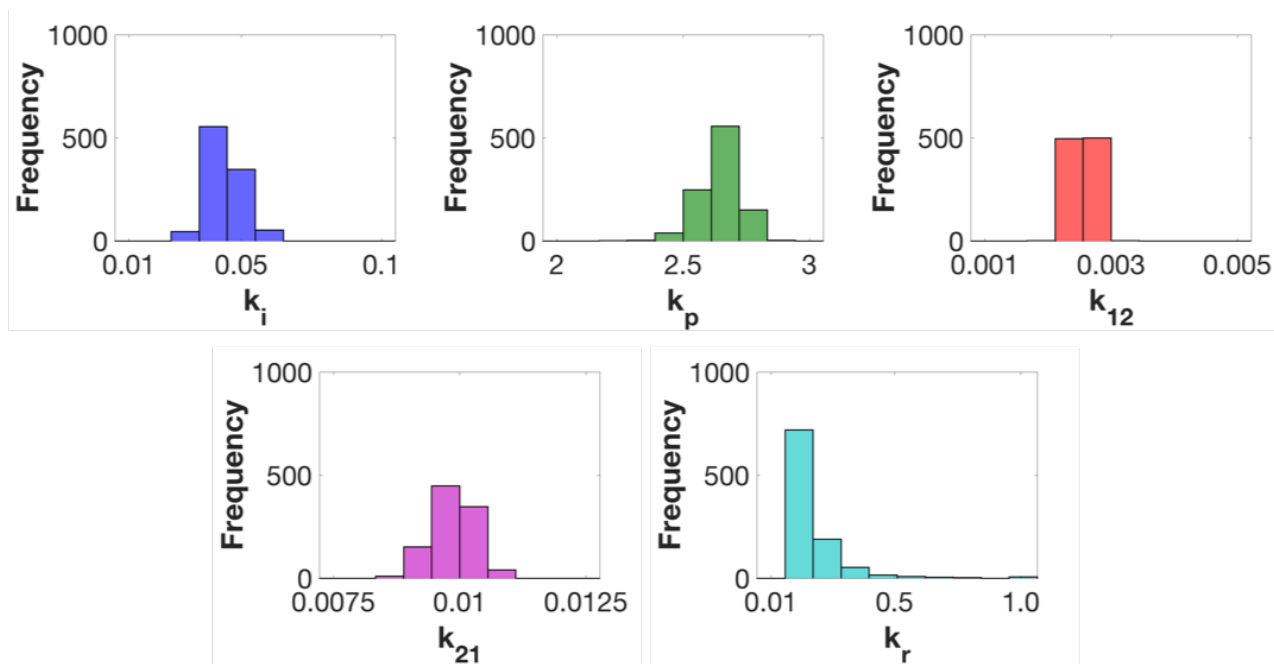
Workflow



- Submitting multiple jobs:
 - Use process number as input into MATLAB function
- Running MATLAB Calculations:
 - Use MATLAB runtime with compiled functions
- Expanding beyond CHTC:
 - Use UW Grid and Open Science Grid
- Other options:
 - “max_retries = 3” to automatically re-run failed jobs

Modeling Results

Rate constant	Median	95% Confidence Interval	Literature value ¹
k_i	0.04	0.03-0.06	0.029 ± 0.008
k_p	2.6667	2.444-2.7778	2.9 ± 0.3
k_{12}	0.0028	0.0023-0.0028	0.0027 ± 0.0006
k_{21}	0.0097	0.0092-0.0108	0.010 ± 0.0001
k_r	0.1211	0.1211-0.4544	0.11 ± 0.07



Power of parallelization:

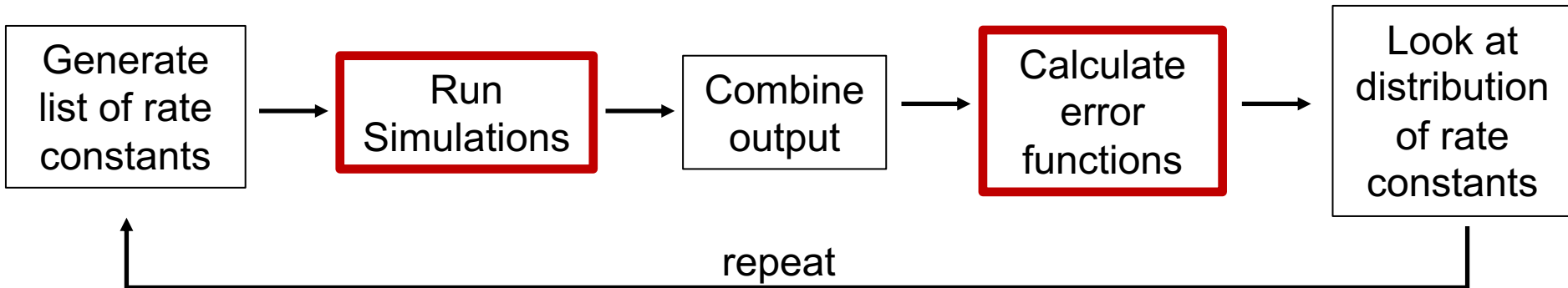
- 100,000 simulations estimated to take 2-3 months without parallelization
 - Corresponds to one iteration of grid searching process

Comparison to optimization:

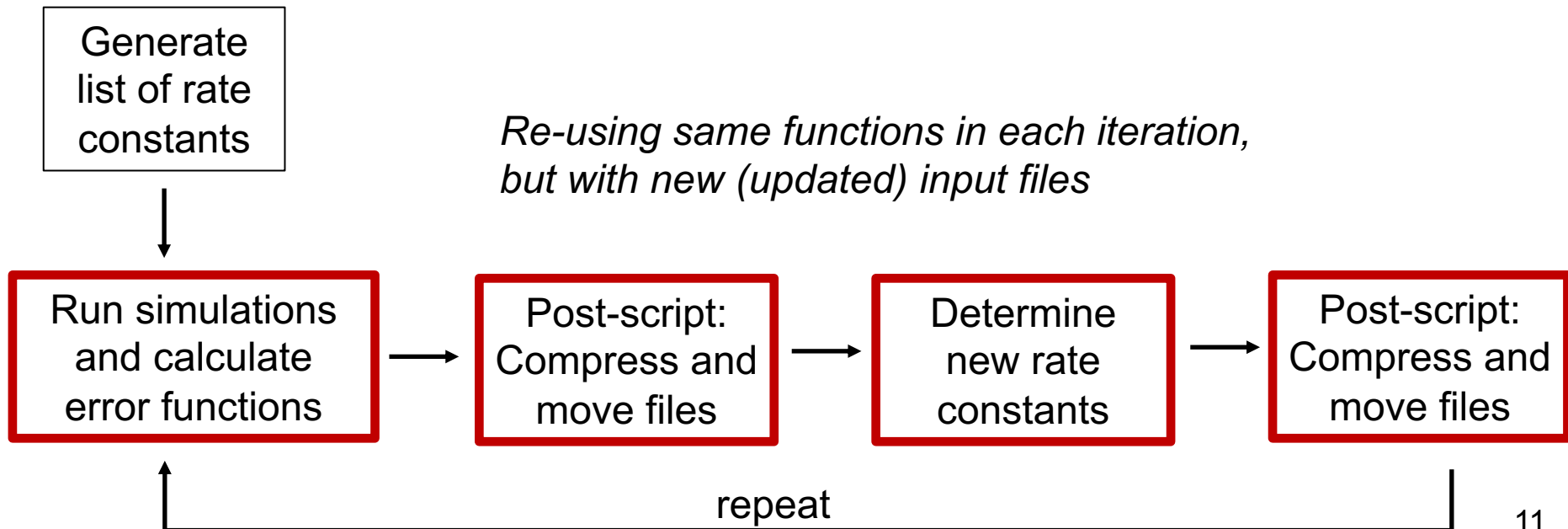
- ~4 days for 6 iterations of grid searching using HTCondor
- Ran 10 iterative optimizations with random starting points
 - Using Copasi (kinetic modeling software)
 - Running on department cluster
 - 8/10 finished in >8 days (fastest in 2.5 days)

Improving the Method

Before:



Now:



Challenges

- Jobs fail or get “stuck”
 - “max_retries = 3” to automatically re-run failed jobs
 - “condor_ssh_to_job” to check on job
 - “condor_hold” and “condor_release” to restart jobs when necessary
- Ideally automate using DAGMan
 - How do you address “stuck” jobs with DAGMan?
 - Avoid manually checking jobs
 - Slow jobs may be “stuck”, but could also involve stiff system of ODEs

Conclusions and Future Directions

The grid searching method is:

- More computationally efficient than iterative optimization
- More thorough in searching the parameter space than iterative optimization
- Capable of accurately reproducing results from iterative optimization
- Promising as a future kinetic modeling method

The next steps are to:

- Automate the modeling process using DAGMan
- Apply the modeling method to more complex polymerization systems

Acknowledgements

- Professor Clark Landis
- Landis Group Members
 - Eric Cueny
 - Andrew Maza
 - Dr. Tanner McDaniel
 - Megan Nieszala
 - Dr. Nick Staudaher
- CHTC
 - Christina Koch
 - Lauren Michael

