



# DAKOTA Advanced Topics: Interfacing and Parallelism

<http://dakota.sandia.gov>



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# Basic Steps to Using DAKOTA

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1. Define analysis goals; understand how DAKOTA helps and select a method to use
2. Access DAKOTA and understand help resources
3. **Workflow:** create an automated workflow so DAKOTA can communicate with your simulation (Advanced Topic)
  - Parameters to model, responses from model to DAKOTA
  - Typically requires scripting (Python, Perl, Shell, Matlab) or programming (C, C++, Java, Fortran)
  - Workflow usually crosscuts DAKOTA analysis types
4. **DAKOTA input file:** Jaguar GUI or text editor to configure DAKOTA to exercise the workflow to meet your goals
  - Tailor variables, methods, responses to analysis goals
5. Run DAKOTA: command-line; text input / output



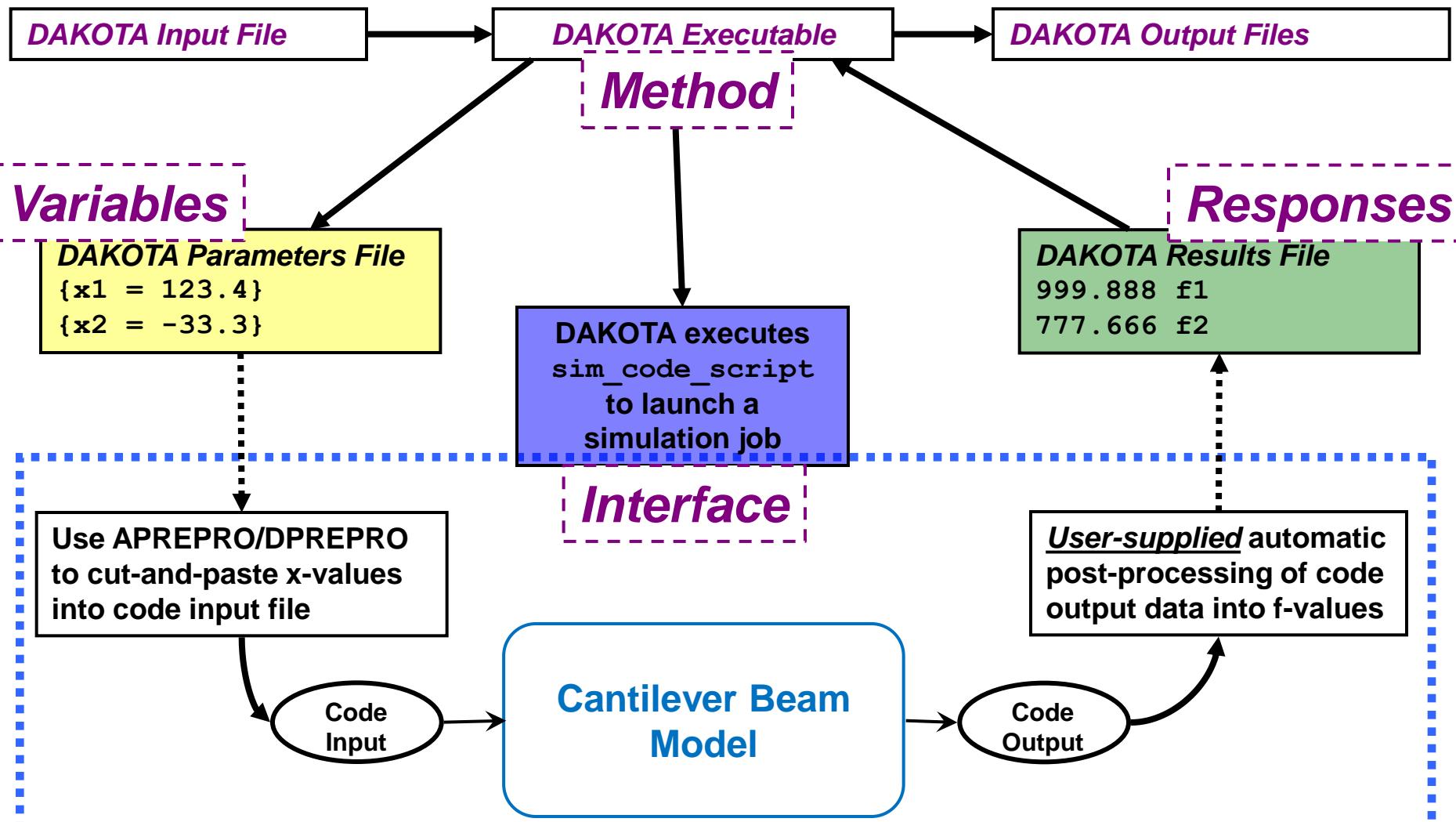
# Possible Directions

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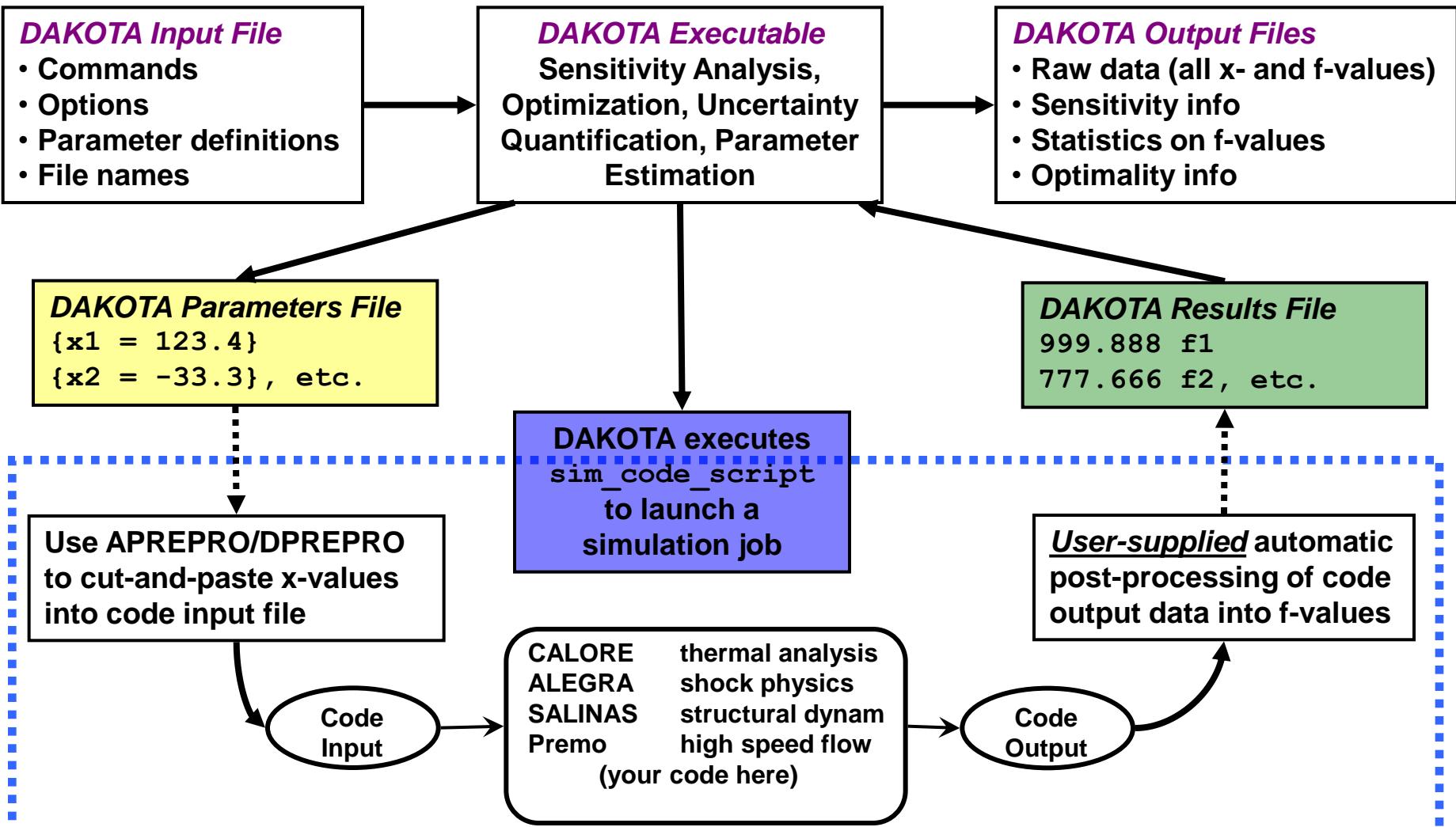


- See process of interfacing DAKOTA to a black-box application through file system
- See current state of DAKOTA library interface
- Understand MPI vs. local parallelism
- Understand modes of application parallelism (in queue, out of queue, serial, parallel apps)
- From DAKOTA 101:
  - Matlab, Python interfacing
  - DAKOTA as a library
  - Basics of HPC at SNL

# Interface communicates through file system and user-supplied script



# DAKOTA Execution & Info Flow



DAKOTA Application Interfacing Class



# Application Stand-in:

## Rosenbrock “Banana” Function

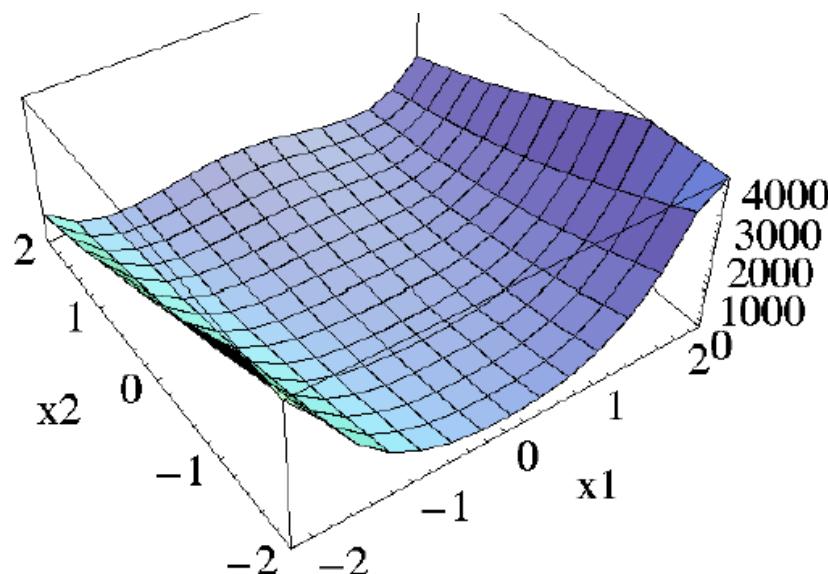
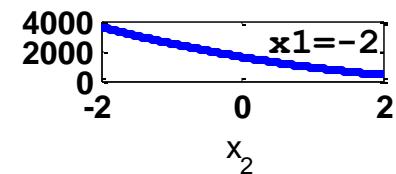
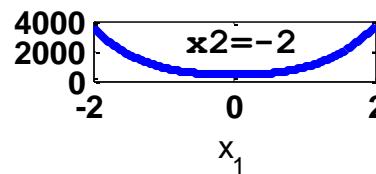
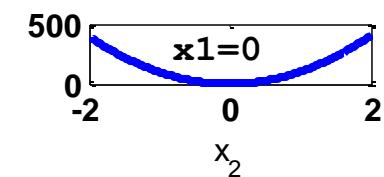
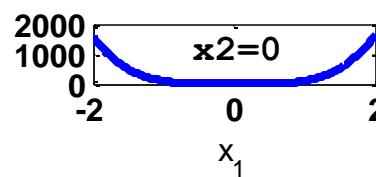
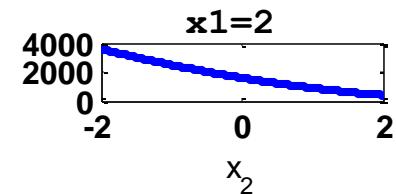
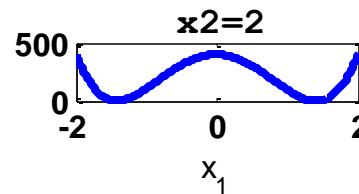
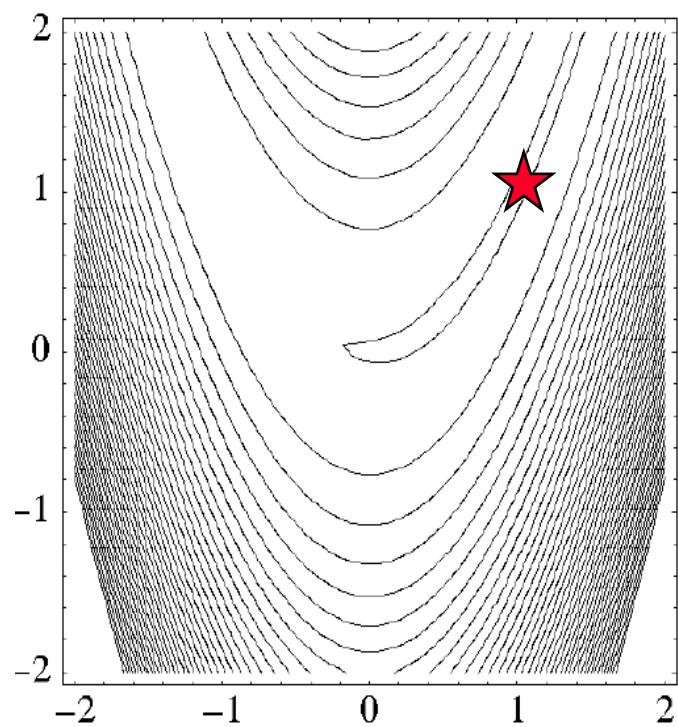


$$f(x_1, x_2) = 100*(x_2 - x_1^2)^2 + (1 - x_1)^2$$

$$-2 \leq x_1 \leq 2$$

$$-2 \leq x_2 \leq 2$$

$$\text{Minimum: } f(x_1, x_2) = f(1, 1) = 0.0$$





# Demo: Rosenbrock as a “black box”

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- Locate example in  
`Dakota/examples/script_interfaces/generic`
- Described in DAKOTA 5.2 User’s Manual 18.1
- Explore top-down (DAKOTA down to application and back)
- Since you’re familiar with your application, may want to build from application up



# Interfacing to Your Simulation (Assuming Text-based I/O)

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1. Annotate your input file to create template

```
{ stress }           { alpha1 }
```

2. Create a representative DAKOTA params.in file in aprepro format (see User's 11.6) and test:

```
dprepro params.in analysis.in.template analysis.in
```

3. Verify commands to run application with analysis.in

4. Determine how to automatically extract results of interest (direct application to export, shell commands, python, perl, visual basic, etc.) to create results.out (see User's 13.2)

5. Assemble into a script, e.g., run\_analysis.sh; test script with sample params.in:

```
./run_analysis.sh params.in results.out
```

6. Test with a simple DAKOTA input deck, e.g., parameter study



# Parallelism

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- See Application Parallelism slides shipped in Dakota/examples/parallelism

# Parallelism from a computing platform perspective

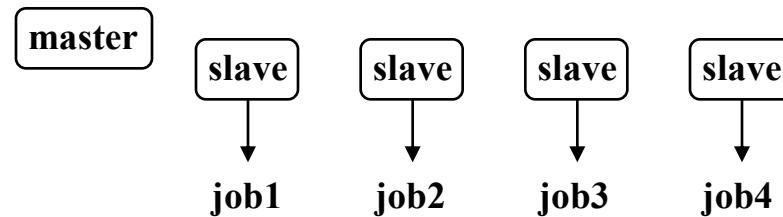


*Nested parallel models support large-scale applications and architectures.*

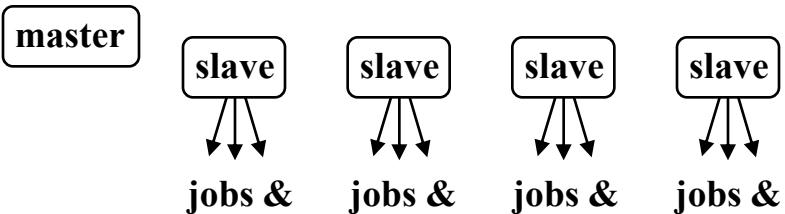
**1. SMP/multiprocessor workstations: Asynchronous (external job allocation)**



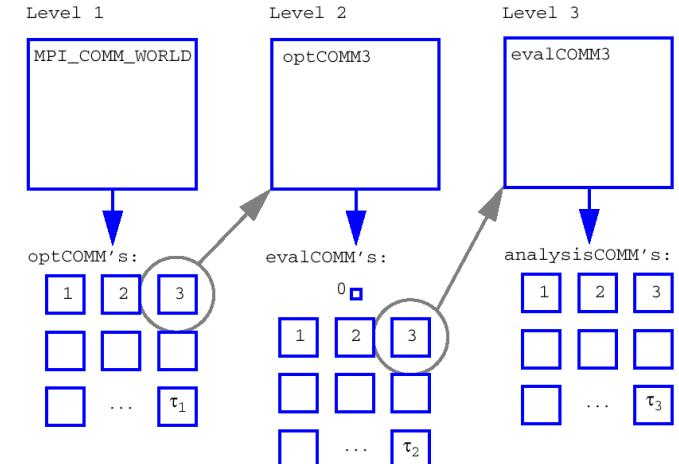
**2. Cluster of workstations: Message-passing (internal job allocation)**



**3. Cluster of SMP's: Hybrid (service/compute model)**



**4. MPP: Internal MPI partitions (nested parallelism)**





# Parallelism from an algorithmic perspective

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1. ***Algorithmic coarse-grained parallelism***: independent fn.

Evaluations performed concurrently:

- Gradient-based (e.g., finite difference gradients, speculative opt.)
- Nongradient-based (e.g., GAs, PS, Monte Carlo)
- Approximate methods (e.g., DACE)
- Concurrent-method strategies (e.g., parallel B&B, island-model GAs, OUU)

2. ***Algorithmic fine-grained parallelism***: computing the internal linear algebra of an opt. algorithm in parallel (e.g., large-scale opt., SAND)

3. ***Function evaluation coarse-grained parallelism***: concurrent execution of separable simulations within a fn. eval. (e.g., multiple loading cases)

4. ***Function evaluation fine-grained parallelism***: parallelization of the solution steps within a single analysis code (e.g., SALINAS, MPSalsa)