

The impact of noise on pipelined Krylov method performance

Hannah Morgan¹ | Patrick Sanan² | Matthew Knepley³ | Richard Mills¹

¹Mathematics and Computer Science,
Argonne National Laboratory, Argonne,
Illinois, USA

²Institute of Geophysics, ETH Zurich,
Zurich, Switzerland

³Computer Science in Engineering,
University of Buffalo, Buffalo, New York,
USA

Correspondence

Hannah Morgan, Mathematics and
Computer Science, Argonne National
Laboratory, Argonne, Illinois, USA
Email: hmorgan@anl.gov

Funding information

The authors were supported by the U.S.
Department of Energy, Office of Science,
Advanced Scientific Computing Research
under Contract DE-AC02-06CH11357.
This research used resources of the
Argonne Leadership Computing Facility,
which is a DOE Office of Science User
Facility supported under Contract
DE-AC02-06CH11357. PS acknowledges
financial support from the Swiss University
Conference and the Swiss Council of
Federal Institutes of Technology through
the Platform for Advanced Scientific
Computing (PASC) program.

In this work, we develop a performance model and study the impact of operating system, machine variance, and other factors on Krylov and pipelined Krylov method execution. We perform repeated runs and collect fine-grained data that shows the influence of variability on Krylov and pipelined Krylov methods. To succinctly describe the execution performance, we employ stochastic models based on the distribution of iteration times of each method. We test the models with collected data and suggest ways to improve and expand them in order to make a prior performance estimates.

KEYWORDS

Krylov, pipelining, noise, performance model, GMRES, PGMRES

1 | INTRODUCTION

Large-scale simulations often use Krylov methods [1] to solve sparse systems of equations in high performance computing (HPC) environments. As we move to more massively parallel computing the latency cost for global communication has skyrocketed [2], degrading the performance of Krylov methods because of the reduction operations used

in each iteration. To mitigate the latency associated with global communication, algebraically equivalent pipelined versions of Krylov methods have been introduced [3, 4, 5, 6, 7, 8]. Pipelined methods rearrange computations so that it is possible to hide some of the cost of global communication with local computation. This rearrangement typically incurs additional local computation and degrades numerical stability [9, 10]. We have included a GMRES algorithm (Algorithm 1) and a pipelined version by [4] (Algorithm 2) below for completeness.

The increasing complexity of HPC computing environments has introduced many sources of run-to-run variability at different levels of HPC systems. For example, operating systems can interrupt processors at any time for its activities, causing detours in computations and degrading performance [11, 12]. Inter-job contention for shared resources such as network bandwidth, routers, and links is another source of variability that can affect application performance [13, 14].

Highly synchronous applications such as those that use Krylov methods are vulnerable to performance degradation induced by variability at different machine levels. Because each iteration is performed in lockstep, an operating system interrupt that delays a single processor can cause others to be delayed as well. The variable amount of bandwidth available between iterations and runs can degrade Krylov methods because of the use of vector norms and orthogonalizations. It is important to understand and characterize the performance of applications in order to evaluate HPC systems and algorithms. However, developing coherent performance models is difficult in the presence of variability [15, 16] particularly between systems.

Employing stochastic performance models for algorithms that run on HPC systems could reflect a more realistic computing scenario since many detours and sources of variability are unpredictable. Some work has been done using stochastic models to predict performance in HPC environments. For example, [17] studied the impact of different

Algorithm 1 GMRES	Algorithm 2 PGMRES
1: $r_0 \leftarrow b - Ax_0$; $v_0 \leftarrow r_0 / \ r_0\ _2$	1: $r_0 \leftarrow b - Ax_0$; $v_0 \leftarrow r_0 / \ r_0\ _2$; $z_0 \leftarrow v_0$
2: for $i = 0, 1, \dots, m-1$ do	2: for $i = 0, 1, \dots, m+1$ do
3: $z \leftarrow Av_i$	3: $w \leftarrow Az_i$
4: $h_{j,i} \leftarrow \langle z, v_j \rangle, j = 0, 1, \dots, i$	4: if $i > 1$ then
5: $\tilde{v}_{i+1} \leftarrow z - \sum_{j=0}^i h_{j,i} v_j$	5: $v_{i-1} \leftarrow v_{i-1} / h_{i-1,i-2}$
6: $h_{i+1,i} \leftarrow \ \tilde{v}_{i+1}\ _2$	6: $z_i \leftarrow z_i / h_{i-1,i-2}$
7: $v_{i+1} \leftarrow \tilde{v}_{i+1} / h_{i+1,i}$	7: $w \leftarrow w / h_{i-1,i-2}$
8: # apply Givens rotations to $H_{:,i}$	8: for $j = 0, 1, \dots, i$ do
9: end for	9: $h_{j,i-1} \leftarrow h_{j,i-1} / h_{i-1,i-2}$
10: $y_m \leftarrow \operatorname{argmin} \ (H_{m+1,m} y_m - \ r_0\ _2 e_1)\ _2$	10: end for
11: $x \leftarrow x_0 + V_m y_m$	11: $h_{i-1,i-1} \leftarrow h_{i-1,i-1} / h_{i-1,i-2}^2$
	12: end if
	13: $z_{i+1} \leftarrow w - \sum_{j=0}^{i-1} h_{j,i-1} z_{j+1}$
	14: if $i > 0$ then
	15: $v_i \leftarrow z_i - \sum_{j=0}^{i-1} h_{j,i-1} v_j$
	16: $h_{i,i-1} \leftarrow \ v_i\ _2$
	17: end if
	18: $h_{j,i} \leftarrow \langle z_{i+1}, v_j \rangle, j = 0, 1, \dots, i$
	19: end for
	20: $y_m \leftarrow \operatorname{argmin} \ (H_{m+1,m} y_m - \ r_0\ _2 e_1)\ _2$
	21: $x \leftarrow x_0 + V_m y_m$

noise distributions on a single collective operation and [18] modeled operating system “jitter” as random variables in order to compute computational slowdown in the presence of noise. In [19], we introduced stochastic performance models that described the performance of Krylov and pipelined Krylov methods in the presence of noise using random variables to model iteration times.

In this work, we are interested in characterizing the performance of Krylov and pipelined Krylov methods on HPC systems in the presence of variability using experimental data and refining the performance model introduced in [19]. We detail the results of experiments performed at the Argonne Leadership Computing Facility (ALCF) and the Swiss National Supercomputing Center and find that, using these results, our stochastic performance models can accurately describe runtimes and suggest a way to perform a priori estimates.

This paper is organized into several sections. Section 2 reviews the performance models introduced in [19] for Krylov and pipelined Krylov methods in the presence of system noise. In Section 3 we present experimental data and refine these performance models in Section 4. In Section 5 we employ our stochastic performance models for a specific problem and show that they are in close agreement with reality. In Sections 6 we suggest a way to perform a priori performance estimates and in Section 7 we present more experimental data and use our performance models in more extensive circumstances. Finally, we conclude our work in Section 8.

2 | STOCHASTIC MODEL REVIEW

We model a Krylov method as a set of P processes repeatedly performing some local computation and global communication. Because of the synchronizations in each iteration, the processors perform in lockstep so that the total time for each iteration is the time given by the slowest processor. Then the total time T for a Krylov method is

$$T = \sum_k \max_p T_p^k, \quad (1)$$

where T_p^k is the time for iteration k on process p . Since this work can be interrupted by operating system noise interference, the iteration times T_p^k might fluctuate over steps and processors. To model this nondeterministic behavior, we let the iterates be random variables and ask for the expected total runtime

$$E[T] = \sum_k E[\max_p T_p^k]. \quad (2)$$

If the iterates T_p^k are identical and independent of processor (p) and stationary in time (k), then we can compute the expected runtime of a Krylov method using the integral expression

$$E[T] = KP \int_{-\infty}^{\infty} x F(x)^{P-1} f(x) dx, \quad (3)$$

where the random variables T_p^k are drawn from a distribution with probability density function (pdf) $f(x)$ and cumulative distribution function (cdf) $F(x)$.

Similarly, we model a pipelined Krylov method as a set of P communicating processors. Pipelined methods employ split-phase collectives that do not require global synchronizations. Rather, the collective operation is first initialized, say with `MPI_Ibcast()`, and later finalized with `MPI_Wait()` so that useful work can continue between initialization and finalization. Provided no processor falls too far behind, the total time for a pipelined method T' is the time it take

the slowest processor to perform all the given work

$$T' = \max_p \sum_k T_p^k. \quad (4)$$

Because of detours, we do not expect the iteration times to be constant. Again we ask for the expected total run time

$$E[T'] = E[\max_p \sum_k T_p^k], \quad (5)$$

letting the iterates be random variables drawn from a distribution. If the iterates T_p^k are identical and independent of process (p) and stationary in time (k), then, in the limit of large K , $T_p^k \rightarrow \mu$ where μ is the mean of the underlying iteration time distribution with pdf $f(x)$ and cdf $F(x)$. So we have an expression to compute the expected total time for a pipelined method

$$E[T'] \rightarrow K\mu. \quad (6)$$

In the next section we present fine-grained data collected from runs of Krylov and pipelined Krylov methods. This gives us insight into how detours affect these simulations, which assumptions above are realistic, and how the models might be refined. For a more thorough explanation of the arguments presented in this section, see [19].

3 | EXPERIMENTAL RESULTS

Here we present the results from a set of experiments run on the Cray XC40 Theta at the Argonne Leadership Computing Facility. Theta contains Xeon Phi Knights Landing (KNL) compute nodes [20] with 64 CPU processors per node connected by a Cray Aries dragonfly topology [21]. We use the Portable, Extensible Toolkit for Scientific Computation (PETSc) [22, 23] software package to simulate the solution to problems with varying characteristics such as sparsity pattern. One MPI rank per core is used throughout and we boot the nodes in quadrant clustering mode with flat memory mode. We collect iteration times T_p^k by inserting calls to `MPI_Wtime()` at the beginning and end of each Krylov cycle in PETSc's scalable linear equation solvers (KSP) component's GMRES (generalized minimal residual method) and PGMRES (pipelined GMRES) methods. Since changes and upgrades to HPC machines can affect performance, we note that experiments presented in this paper were performed in autumn 2018.

3.1 | One-dimensional Laplacian

PETSc tutorial ex23 is a one-dimensional discretization of the Laplacian, resulting in a simple tridiagonal system. We run ex23 with GMRES and PGMRES on 8192 processors with 10^6 unknowns and a Jacobi preconditioner. Throughout these simulations we force 5000 iterations of the Krylov method.

The stochastic model expressions (3) and (6) place assumptions on the iterates T_p^k . We check them here to examine the actual performance of the algorithms and to justify use of the models. In Figure 1 we graph normed histograms of the iterates T_p^k to represent probability distribution functions for select processors identified by their MPI ranks. The distributions look similar between ranks, implying that the iterations might be identical with respect to process. We make use of the two sample Kolmogorov–Smirnov test to check whether two samples (e.g. iterations from rank 0 and rank 1) are drawn from the same underlying distribution. The Kolmogorov–Smirnov test calculates

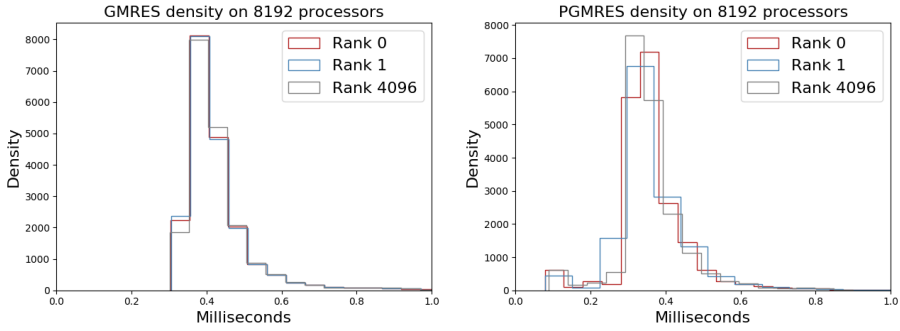


FIGURE 1 Distribution of iterates \mathcal{T}_p^k for fixed processors.

the distance between the empirical distributions of two samples with empirical distribution functions F_1 of size n and F_2 of size m with

$$D = \sup_x |F_1(x) - F_2(x)|.$$

We reject the hypothesis that the samples come from the same distribution with significance level α if

$$D > c(\alpha) \sqrt{\frac{n+m}{nm}}$$

where $c(\alpha)$ is a tabulated value. For GMRES, $n = m = 5000$ and $n = m = 5334$ for PGMRES. We use significance level $\alpha = 0.05$ and SciPy's `stat.ks_2samp` function to calculate the test statistic D . For GMRES ranks 0 and 1, we do not reject that the iterates come from the same distribution with significance level $\alpha = 0.05$ since $D = 0.002 < 0.024$, the threshold. For PGMRES ranks 0 and 1, $D = 0.088 > 0.023$, so we reject the hypothesis that the iterates follow the same distribution. We compare rank 1 with the $P - 1$ other ranks and do not reject that any of the GMRES pairs come from the same distribution. However, we reject 54.5% of the PGMRES pairs.

Because it is inefficient to orthogonalize against a very big basis, GMRES methods are often implemented to restart after R iterations. When a Krylov method restarts, the basis for the Krylov space is thrown out and the current solution is used as the initial guess for the next cycle. Since the PETSc default restart value $R = 30$ and each cycle of PGMRES uses two additional iterations to “fill the pipeline,” 5334 iterations are actually employed instead of 5000. Some of these are very quick and easily identifiable as the bump of very short iterations in Figure 1 (right).

Figure 2 shows the time for iterations $k = 44$ (GMRES) and $k = 48$ (PGMRES) on process p for the first 1000 processors in order of MPI rank. Iterates are drawn with grey bars. GMRES iterates are nearly constant on a node, so that each KNL node of 64 processors is clearly visible in Figure 2 (left) so that the iterations are not really independent in p as we claimed above. The variance of iteration times on node 0 (with MPI ranks 0-63) is $9.7 \cdot 10^{-13}$. This could be due to the synchronizations in each iteration of GMRES, forcing processors on a node to perform in lockstep. There is a significant difference between the performance of the nodes. Conversely, PGMRES iterations appear to contain more variability on a node ($1.8 \cdot 10^{-9}$ on the node with MPI ranks 0-63, four orders of magnitude greater than GMRES).

Figure 3 is a colormap of the iterates \mathcal{T}_p^k for the first 5000 processors. Graphed are the iterations that perform the “average” amount of work during each GMRES cycle (GMRES iteration $14 \bmod 30$ and PGMRES $16 \bmod 32$) so that each iteration shown performs the same computation. Horizontal lines are highly visible, implying that processors

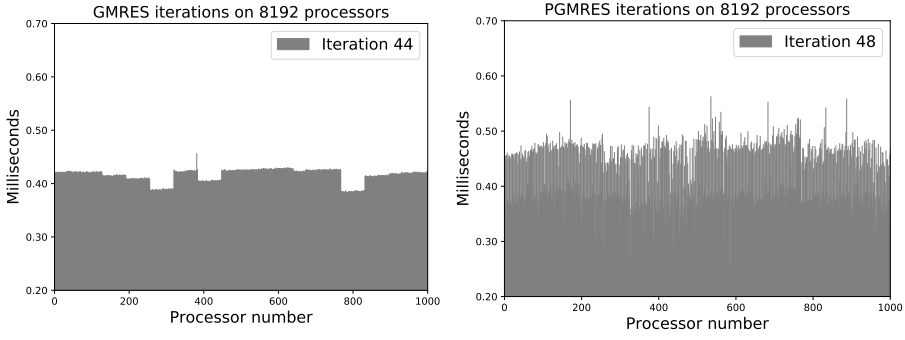


FIGURE 2 Time for iterations $k = 44, 48$ on process p .

perform similarly within a given iteration. The difference between different iterations is also clear so that the iterates seem to jump around in time without an obvious pattern. There are some groups of iterations (GMRES iterations $k \approx 1700 - 2300$ or PGMRES $k \approx 640 - 740$) that overall take longer than other iterations. This could be explained by some longer operating system interruption.

The derivations in Section 2 made the simplifying assumption that the iterates were stationary in time so that the sum in (2) could become a product in (3). We account for this non-stationary behavior when we refine the performance model in Section 4.

3.2 | Blatter-Pattyn equations

PETSc ex48 solves the hydrostatic equations for ice sheet flow, where the ice uses a power-law rheology with Glen exponent 3. This generates a much denser system of equations with about 10 times more nonzeros per row than ex23. Again we choose our problem size so that there are 10^6 unknowns, use a Jacobi preconditioner, and force 5000 iterates of the Krylov method. We stop after one nonlinear iteration.

We repeat the analysis from Section 3.1 and find qualitatively similar results, shown in Figure 4. Using the Kolmogorov-Smirnov test again we find that we do not reject the assumption that GMRES iterates from ranks 0 and 1 come from the same distribution since $D = 0.003 < 0.024$ and we reject that PGMRES iterates come from the same

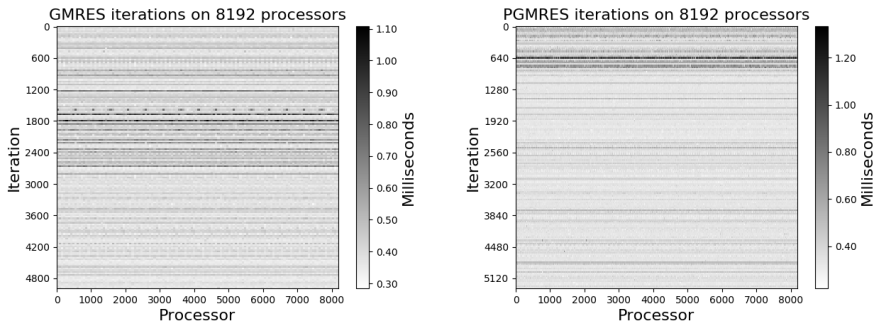


FIGURE 3 Colormap of iterates \mathcal{T}_p^k for the first 5000 processors.

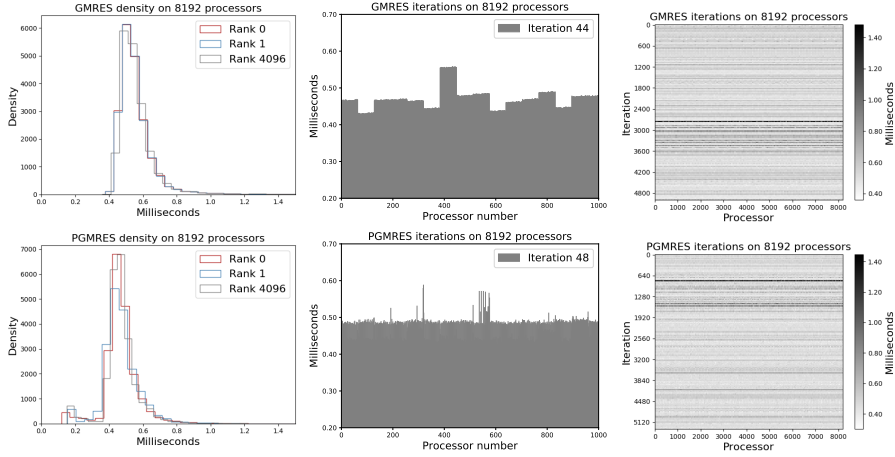


FIGURE 4 GMRES (top) and PGMRES (bottom) iterations for PETSc ex48.

distribution since $D = 0.078 > 0.023$. The iterates on a fixed process p look like they could be from the same family of distributions with different parameters as those in the previous subsection.

GMRES iterates again look highly dependent on the node with node 0 variance $1.4 \cdot 10^{-12}$. The variance on PGMRES node 0 is $5.2 \cdot 10^{-10}$. This could be explained by the communication induced by the matrix sparsity pattern. While certain nodes appear to take much longer, the colormap (bottom right) shows that overall processors perform similarly within an iteration. Again, the computation is not stationary in time.

4 | NON-STATIONARY PERFORMANCE MODEL

Based on the results from the last section, we move to a non-stationary performance model where the iterates \mathcal{T}_p^k can fluctuate in time. The expected total time for a Krylov method is still given by

$$E[T] = \sum_k E[\max_p \mathcal{T}_p^k]$$

but we relax the claim that the iterates are stationary in time. In iteration k , the random variables \mathcal{T}_p^k are drawn from a distribution with cdf $F_k(x)$ and pdf $f_k(x)$, which can now fluctuate across steps. Then the expected runtime of a Krylov method is given by

$$\widehat{E}[T] = \sum_k P \int_{-\infty}^{\infty} x F_k(x)^{P-1} f_k(x) dx, \quad (7)$$

We call this the “non-stationary” performance model and distinguish between $E[T]$ in (3) and $\widehat{E}[T]$ here.

Similarly for a pipelined method, we use (5) as before and drop the assumption that the iterates are stationary in time, so that

$$\widehat{E}[T'] \rightarrow \sum_k \mu_k, \quad (8)$$

where μ_k is the mean of the underlying distribution in iteration k .

The original Krylov model (3) benefits from slight alteration as well. Since the iterates on each node are nearly constant, shown in Figure (2) (left) and Figure 4 (top middle), they are more suitably modeled by $\hat{P} = P/64$ independent random variables than P independent processors. We make use of this substitution in the next section but it does not seem to affect (7) much.

5 | PERFORMANCE MODELING

In this section, we will deploy our performance models and test them against collected data.

5.1 | Computing expected runtimes

The expressions for $E[T]$ and $E[T']$ say that the iterates come from some underlying distribution with pdf $f(x)$, cdf $F(x)$, and mean μ . We will use “bulk statistics” with these performance models, taking all iterations for all processors in aggregate, for the underlying distribution to characterize the iteration times and machine variation.

To find the functions $f(x)$ and $F(x)$ and mean μ , we use Scipy’s `stats` package to fit various analytical distributions to our collected data. For a given continuous distribution and data, the `fit` function returns the maximum likelihood estimation for the shape, location, and scale parameters by maximizing a log-likelihood function. We pick the distributions that minimize the sum of squared error between the data and the fit distribution. For the pipelined methods, we disregard the two iterations in each cycle that “fill the pipeline” to avoid distribution fitting complications.

Using these good fitting distributions (e.g. Johnson SU shown in Figure 5), we can calculate $E[T]$ and $E[T']$ and compare the expected results to the actual KSPSolve times (the time spent inside the Krylov solver) provided by PETSc’s `-log_view` option. For integration in (3) we use Python’s `quad` function and integrate over the bounds of the data.

To employ the updated models $\hat{E}[T]$ and $\hat{E}[T']$, we again perform distribution fitting using `scipy`, this time for each iteration to find $f_k(x)$, $F_k(x)$, and mean μ_k . We claim that the runtimes \mathcal{T}_p^k for each iteration k are from the same family with possibly different parameters. Not all iterations resemble the same distribution family, so we use a uniform distribution to model the iterations, shown fitted to two GMRES iterations in Figure 6. The distribution parameters vary by iteration. In (7), integration is performed in each iteration again using `quad` and the calculated expected total

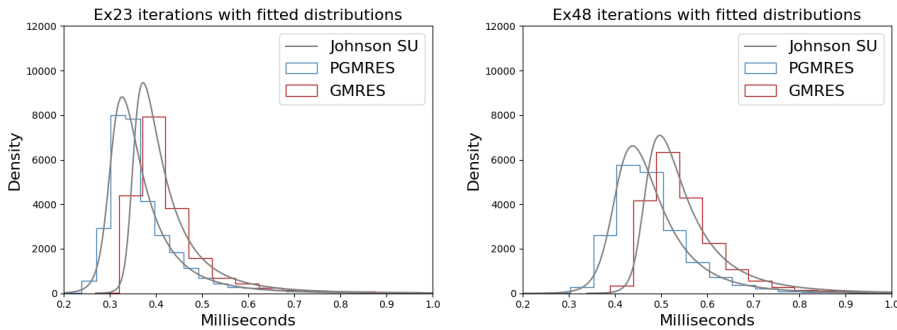


FIGURE 5 GMRES and PGMRES bulk statistics with fitted distributions for PETSc ex23 (left) and ex48 (right).

times are compared to the KSPSolve time.

Analytical expressions have been used [18] to bound the maximum of a set of random variables using the sample mean μ_X and standard deviation σ_X . Cramer [24, 25] bound the maximum of N identical and independent random variables with

$$E[X_{\max(N)}] \leq \mu_X + \frac{\sigma_X(N-1)}{\sqrt{2N-1}} \quad (9)$$

and Bertsimas [26] bound the maximum of N identical, but not independent random variables by

$$E[X_{\max(N)}] \leq \mu_X + \sigma_X \sqrt{N-1}. \quad (10)$$

We will use these to compare with our Krylov performance models.

5.2 | Results

Distribution fitting alone gives some insight into algorithm execution. In Figure 5, we show bulk data from Section 3 with the Johnson SU distribution. Note that there were some other good fitting distributions, including Non-central Student's T. The bulk data show that in a given method, the iterates \mathcal{T}_p^k are mostly clustered and fairly quick with a fewer, longer, giving the distribution a small tail. In general, PGMRES runtimes were faster than GMRES, consistent with faster overall execution in these examples. Ex48 runtimes are shifted to the right of ex23 and more spread out, implying longer iterations with more variation.

Results for the data presented in Section 3 are shown in Table 1 for PETSc ex23 and ex48. We see that the original model for the expected time of a Krylov method $E[T]$ overestimates the actual runtimes and is not a particularly good estimate, nor is any bulk distribution best in all cases. On the other hand, the updated Krylov model $\hat{E}[T]$ is a big improvement for traditional Krylov methods and makes a reasonable prediction. Using a uniform distribution to model each iteration is a simplification that could account for some of the discrepancy between the KSPSolve time and $\hat{E}_{\text{Unif}}[T]$. Not all iterations resembled the same distribution, however, so we will keep this simplification. The analytical bounds are very loose and not particularly helpful. $E[T']$ and $\hat{E}[T']$ are both good estimates for the pipelined method, suggesting that modeling a method without explicit synchronization is more flexible. In one case, the non-stationary model $\hat{E}[T']$ is not as good a predictor for PGMRES, but it is more representative of the actual process. The results show that when we have available iteration data, the updated performance models (7) and (8) are good performance predictors and we will use them from here on.

6 | PREDICTING RUNTIMES

In the previous section, we showed that our performance models $\hat{E}[T]$ and $\hat{E}[T']$ can reasonably predict execution time when we have the time for iteration k on process p for all k and p .

Bulk statistics appear to be enough to succinctly describe the performance of a pipelined method, they are not a sufficient way to describe a traditional Krylov method. Instead, we used non-stationary uniform distributions to model each iteration, shown in Figure 6. Here we see how non-stationary the iterations actually are, in this case they are almost non-overlapping, and how the parameters change over time. That is, for each iteration k , the random variables

TABLE 1 Performance model results and bounds for ex23 and ex48 with good fitting distributions.

ex23	KSPSolve	$E_{\text{JohnSU}} [T]$	$E_{\text{NCT}} [T]$	$\hat{E}_{\text{Unif}} [T]$	Cramer bound	Bertsimas bound
GMRES	2.217	4.831	4.365	2.432	6.35	8.102
PGMRES	2.006	1.865	1.868	1.857		
ex48						
GMRES	2.943	5.716	10.88	3.189	20.59	27.99
PGMRES	2.656	2.413	2.413	2.455		

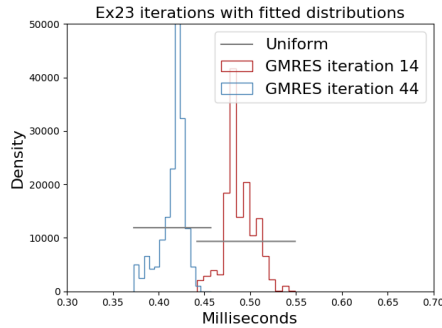
\mathcal{T}_p^k follow a uniform distribution with pdf f_k and cdf F_k given by

$$f_k(x) = \frac{1}{b_k - a_k}, \quad F_k(x) = \frac{x - a_k}{b_k - a_k}. \quad (11)$$

The uniform distribution can be described with two parameters: the minimum a_k and the span $s_k = b_k - a_k$. We model a Krylov method with K uniform distributions where in each iteration the uniform parameters a_k and s_k are random variables drawn from some distribution. Figure 7 show histograms of the uniform parameters from PETSc ex48 using GMRES and PGMRES with fitted Johnson SU distribution. Johnson SU, a transformation of the normal distribution, is described by two shape parameters a and b and location and scale parameters `loc` and `scale` in Scipy.

The location and scale parameters shift the distribution left and right (`loc`) and stretch and shrink horizontally (`scale`) so that standardizing the distribution with `loc = 0` and `scale = 1` involves the transformation $y = (x - \text{loc})/\text{scale}$. Table 2 shows Johnson SU parameters for the uniform distribution parameters from Figure 7 and PETSc ex23. In general, they show that, in a given iteration, the fastest processor is generally faster in a PGMRES run, but the runtimes are more spread out. All Johnson SU distributions are shaped such that they lean left with a tail, some longer than others.

To simulate a Krylov computation, we assume that each iteration time \mathcal{T}_p^k is uniformly distributed with parameters

**FIGURE 6** GMRES iterations $k = 14, 44$ with fitted uniform distributions.

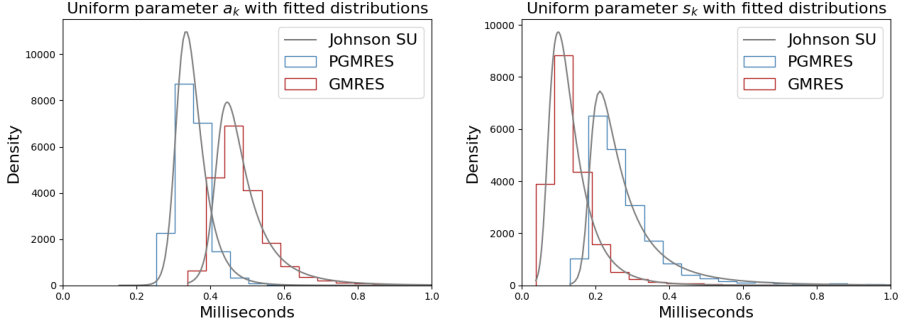


FIGURE 7 Uniform parameters a_k and s_k from PETSc ex48 with fitted distributions.

a_k and s_k in iteration k

$$\mathcal{T}_p^k \sim \text{Uniform}(a_k, s_k).$$

We further assume that the parameters a_k and s_k are themselves random variables drawn from a Johnson SU distribution with parameters a , b , loc , and scale .

We draw random variables a_k and s_k using Scipy's `rvs` function, which generates random variates from a distribution and compute the expected time for iteration k , $\widehat{E}[T_k]$, given by

$$\widehat{E}[T_k] = \widehat{P} \int_{-\infty}^{\infty} x F_k(x)^{\widehat{P}-1} f_k(x) dx. \quad (12)$$

Repeating for K iterations, we get $\widehat{E}[T]$. We simulate a pipelined Krylov computation in the same way, pulling random variables a_k and s_k and computing

$$\widehat{E}[T'_k] = \mu_k \quad (13)$$

where μ_k is the mean of $\text{Uniform}(a_k, s_k)$. Table 3 shows the results of this simulation using the Johnson SU parameters from Table 2. The results are good when we have the Johnson SU parameters. The challenge in general will be to reason about these parameters so that we can make a priori performance estimates for Krylov and pipelined Krylov methods.

7 | EXTENSION TO OTHER ALGORITHMS AND COMPUTING PLATFORMS

In the last section, we saw that we can reasonable simulate the execution time of a Krylov method given Johnson SU parameters to model uniformly distributed iterations. Many factors can influence performance such as algorithm and matrix pattern, as we've seen. In this section, we expand our experiments to study other factors including problem size and computing platform in an effort to test our non-stationary model in other scenarios and suggest ways to perform a priori runtime estimates. Again, these experiments were performed in autumn 2018.

TABLE 2 Johnson SU parameters for uniform parameters a_k and s_k .

ex23	Uniform a_k				Uniform s_k			
	a	b	loc	scale	a	b	loc	scale
GMRES	-5.86e-01	3.35	3.97e-04	1.07e-21	-7.40e-01	3.21	8.06e-04	1.86e-23
PGMRES	2.84	6.74	3.10e-04	2.26e-19	-6.18e-02	2.42	2.21e-03	6.47e-19
ex48								
GMRES	6.74e-01	2.09	2.22e-02	2.24e-24	6.69e-01	2.10	1.71e-03	9.23e-26
PGMRES	-6.02e-01	3.34	4.07e-04	3.05e-23	1.24	1.84	1.36e-02	1.66e-18

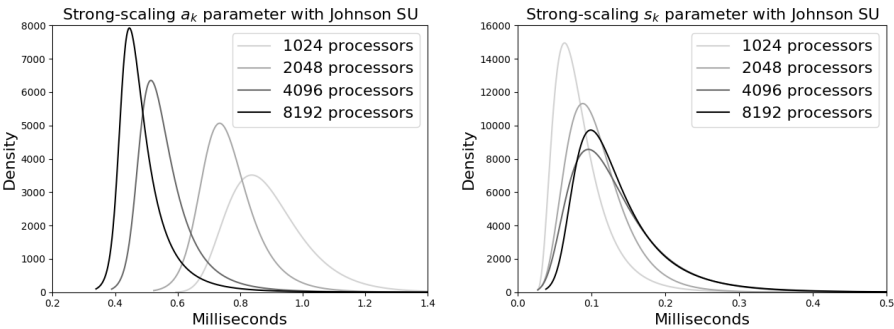


FIGURE 8 GMRES ex48 strong-scaling results on $P = 1024 - 8192$ processors.

7.1 | Scaling experiments

Our experiments so far have been performed on 8192 processors with 10^6 unknowns. To see how changing processor count and problem size affect the Krylov method performance and underlying uniform parameters, we run strong- and static-scaling experiments. Figures 8 and 9 show the Johnson SU distributions for the uniform parameters a_k and s_k for strong- and static-scaling experiments using GMRES.

With strong-scaling experiments, we see how varying the processor count affects Krylov method performance for a fixed problem. We repeat runs of ex48 with 10^6 unknowns on $P = 1024 - 8192$ processors. We see that, for a fixed number of unknowns, when we use fewer processors the Johnson SU distribution that models the uniform

TABLE 3 Actual and simulated runtimes in seconds on 8192 processors with 10^6 unknowns.

ex23	GMRES	PGMRES	ex48	GMRES	PGMRES
KSPSolve	2.217	2.006	KSPSolve	2.943	2.656
Simulated	2.416	1.908	Simulated	3.14	2.482

parameter a_k (the minimum) shifts to the right, which is unsurprising. The distribution of the uniform parameter s_k (the span) flattens slightly with more processors, but not much.

We also perform static-scaling results where we keep the number of processors fixed at $P = 8192$ and vary the number of unknowns to see how the amount of computation affects the underlying iteration distributions. Increasing the amount of computation per processor shifts the distribution of the uniform parameters a_k and s_k . Similar results were found for computations using PGMRES.

7.2 | BCGS

We solve PETSc ex23, the one-dimensional Laplacian problem, using the Stabilized biconjugate gradient method (BCGS) and a pipelined version (PIPEBCGS) with 5000 linear iterations and 10^6 unknowns on Theta.

Many aspects of the BCGS and PIPEBCGS computations were consistent with GMRES and PGMRES, such as non-stationary iterates and nearly constant BCGS runtimes on a given node of Theta. Figure 10 shows uniform parameter a_k and s_k histograms with GMRES and PGMRES for comparison. Although with different parameters, the BCGS and PIPEBCGS distributions look like they can be modeled by Johnson SU distribution family, suggesting that our performance model is applicable to Krylov methods outside of GMRES methods. GMRES and PGMRES outperform BCGS and PIPEBCGS and have quicker minimum iteration times (Johnson SU distributions shifted to the left for uniform parameter a_k), but runtimes are tightly grouped. Performance results for BCGS and PIPEBCGS using our non-stationary stochastic models are in shown Table 4.

7.3 | Piz Daint

We repeat experiments on the Cray XC40 Piz Daint supercomputer at the Swiss National Computing Center. Piz Daint and Theta both employ a Aries Dragonfly interconnect but Piz Daint contains Intel Xeon E5 Haswell processors [27] on compute nodes, so the differences we see are likely due to different processors or the shared use of a communication network. Figure 11 shows runs of ex48 with GMRES and PGMRES on 8192 processors and 10^6 unknowns. In a given iteration, the quickest processor can be much faster on Piz Daint than Theta, but both uniform parameters contain much more variation. Non-stationary performance model results from Piz Daint are in shown Table 4.

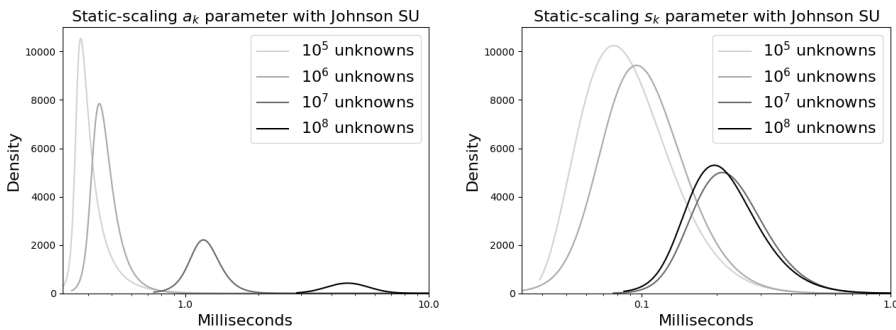


FIGURE 9 GMRES ex48 static-scaling results for $10^5 - 10^8$ unknowns.

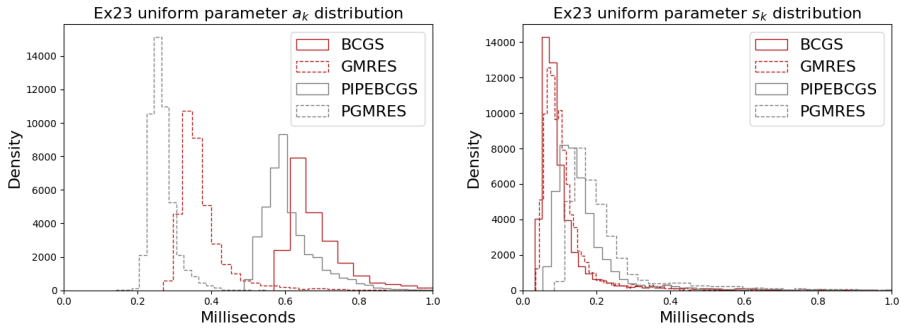


FIGURE 10 BCGS and PIPEBCGS uniform parameters compared to GMRES and PGMRES.

7.4 | Mira

We repeat ex48 experiments on Mira, an IBM Blue Gene/Q [28] at Argonne's ALCF. We expect a marked performance difference on Mira since nodes on Mira are connected by a 5D Torus Network with hardware to assist collective functions, where nodes on Theta are connected by a Cray Aries Network where neighboring workloads share network routes, increasing performance variability [29]. Each Blue Gene/Q node also contains a redundant processor that can soak up operating system interrupts, similar to Cray's core specialization feature where one core per node is dedicated to handling OS operations, which reduces core variability [14]. Figure 12 shows a bulk histogram for iterates from all processors and all iterations and histograms of iterations at different places in the GMRES cycle. GMRES iterations on Theta appear to be noisy enough that our simulation from Section 6 provided reasonable results even though we drew uniform parameters a_k and s_k from the same Johnson SU distributions regardless of k in the GMRES cycle. With Mira's quiet network, the GMRES iterates are much more distinct suggesting that a refined model that accounts for the amount of work done per iteration would be needed for a priori estimates. Furthermore, we see a jump in the time between iterations $k \bmod 30 = 13$ and $k \bmod 30 = 14$ probably due to cache effects and using more storage throughout a GMRES cycle. Similar results were found for PGMRES and performance results are in Table 4.

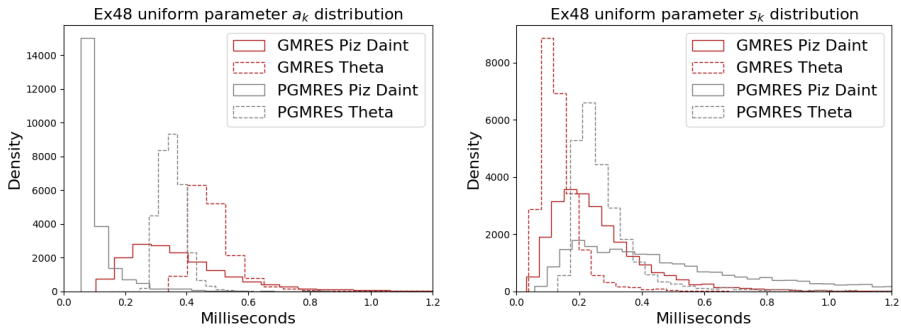


FIGURE 11 GMRES and PGMRES on Theta and Piz Daint.

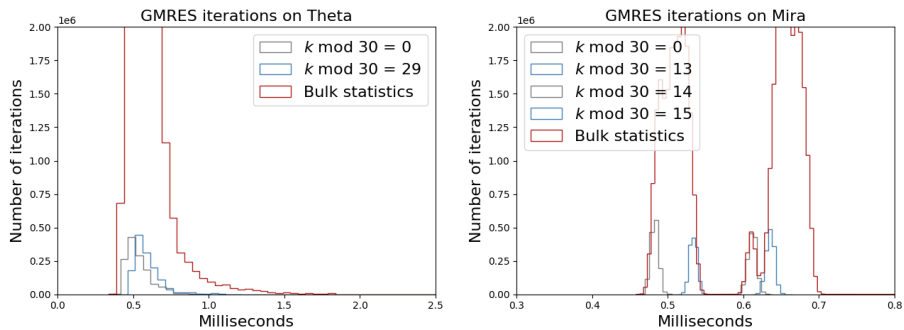


FIGURE 12 GMRES ex48 iterations and Theta and Mira.

8 | CONCLUSION AND FUTURE WORK

The goal of this work was to gather fine-grained iteration data from runs of Krylov and pipelined Krylov methods to develop a performance model and study the impact of machine interference on these methods. We used the data to develop and test stochastic performance models, which are in good agreement with reality. Variability during computation suggests that performance is not deterministic and could be better explained in a stochastic setting. With descriptive enough statistics we were also able to make a priori performance estimates.

Repeating similar analysis for different classes of problems on different machines will make HPC users better equipped to make good performance estimates in a variety of circumstances. Better performance estimates allow users to allocate an appropriate amount of time for jobs on HPC machines and eases the need to overestimate, which leads to idle, wasted machine time and energy.

In future work, nondeterministic performance models can be derived for other parallel algorithms where unpredictable system interference could impact performance. Insights from performance models can also be used to guide the development of new algorithms, particularly those we expect to be running in less predictable computing environments, such as heavily loaded machines or loosely coupled networks used in cloud computing or those with shared resources.

Acknowledgements

Thanks to everyone who offered insight and advice, including Todd Munson, Barry Smith, Ivana Marincic, Vivak Patel, Karl Rupp, and Oana Marin.

TABLE 4 Non-stationary performance model results for ex23 and ex48 for extended experiments.

			Piz Daint		Mira		
ex23	BCGS	PIPEBCGS	ex48	GMRES	PGMRES	GMRES	PGMRES
KSPSolve	3.957	3.53	KSPSolve	3.029	2.642	3.026	2.804
$\hat{E}_{\text{Unif}}[T]$	4.227	3.512	$\hat{E}_{\text{Unif}}[T]$	3.541	2.473	3.189	2.455

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