A Framework to Analyze the Performance of Load Balancing Schemes for Ensembles of Stochastic Simulations

Tae-Hyuk Ahn, *Student Member, IEEE,* Adrian Sandu, Layne T. Watson, *Fellow, IEEE,* Clifford A. Shaffer, *Senior Member, IEEE,* Yang Cao, and William T. Baumann, *Senior Member, IEEE*

Abstract—Ensembles of simulations are employed to estimate the statistics of possible future states of a system, and are widely used in important applications such as climate change and biological modeling. Ensembles of runs can naturally be executed in parallel. However, when the CPU times of individual simulations vary considerably, a simple strategy of assigning an equal number of tasks per processor can lead to serious work imbalances and low parallel efficiency. This paper presents a new probabilistic framework to analyze the performance of dynamic load balancing algorithms for ensembles of simulations where many tasks are mapped onto each processor, and where the individual compute times vary considerably among tasks. Four load balancing strategies are discussed: most-dividing, all-redistribution, random-polling, and neighbor-redistribution. Simulation results with a stochastic budding yeast cell cycle model is consistent with the theoretical analysis. It is especially significant that there is a provable global decrease in load imbalance for the local rebalancing algorithms due to scalability concerns for the global rebalancing algorithms. The overall simulation time is reduced by up to 25%, and the total processor idle time by 85%.

Index Terms—Dynamic load balancing (DLB), probabilistic framework analysis, ensemble simulations, stochastic simulation algorithm (SSA), high-performance computing (HPC), budding yeast cell cycle.

1 Introduction

Important scientific applications like climate and biological system modeling incorporate stochastic effects in order to capture the variability of the real world. For example, biological systems are frequently modeled as networks of interacting chemical reactions. At the molecular level, these reactions evolve stochastically and the stochastic effects typically become important when there are a small number of molecules for one or more species involved in a reaction [1]. Systems in which the stochastic effects are important must be described statistically.

The easiest way to generate statistics for complex systems is to run ensembles of simulations using different initial conditions and parameter values; their results sample the probability density of all possible future states [2], [3]. Taking advantage of the ideally parallel nature of ensembles, individual runs can be easily distributed to different processors. However, the inherent variability in compute times among individual simulations can lead to considerable load imbalances. For these simulations, load balancing among processors is necessary to avoid wasting computing resources and power.

A large body of research literature is available on static and dynamic load balancing (DLB) techniques [4], [5], [6], [7], [8]. Two classes of DLB methods are widely used: scheduling (work-sharing) schemes [9], [10], [11] and work-stealing schemes [12], [13], [14]. The factoring approach, one of the classical scheduling algorithms, allocates large chunks of iterations at the beginning of the computation to reduce scheduling overhead, and dynamically assigns small chunks towards the end of the computation to achieve good load balancing [10]. The work-stealing approach identifies and moves tasks from overloaded processors to idle processors. A simple yet powerful work-stealing scheme is random polling [15]. A processor that runs out of assigned work sends requests to randomly chosen processors, until a busy one is found. The requestee then sends part of its work to the requestor. Scheduling schemes usually take a centralized load balancing approach where the remaining tasks are stored in a central work queue [15], [16]. Work-stealing schemes, on the other hand, can employ both centralized and decentralized load balancing approaches [15]. In centralized DLB a master process distributes tasks to the workers (slave processes). In decentralized DLB, tasks are moved between peer processes.

This paper focuses on several work-stealing DLB methods and their application to stochastic biochem-

- *T.-H. Ahn, A. Sandu, L.T. Watson, C.A. Shaffer, and Y. Cao are with the Department of Computer Science, Virginia Polytechnic Institute and State University, Blacksburg, VA, USA. E-mail: {thahn, sandu, ltw, shaffer, ycao}@cs.vt.edu*
- *L.T. Watson is also with the Department of Mathematics, Virginia Polytechnic Institute and State University, Blacksburg, VA, USA.*
- *W.T. Baumann is with the Department of Electrical and Computer Engineering, Virginia Polytechnic Institute and State University, Blacksburg, VA, USA. E-mail: baumann@vt.edu*

ical simulations. In the most-dividing (MD) algorithm, the processor that finishes first receives new tasks from the most overloaded processor. In the all-redistribution (AR) algorithm, when one worker becomes idle, all remaining jobs are evenly redistributed among all processors. In the random-polling (RP) algorithm new tasks are received from a randomly chosen processor. In the neighbor-redistribution (NR) algorithm, the idle processor and its neighbors redistribute evenly all remaining jobs (on the neighbor processors). The Dijkstra-Scholten algorithm [17] and the Shavit-Francez algorithm [18] are adapted for detecting termination. MD and AR use a centralized DLB approach, whereas RP and NR employ a decentralized one.

Previous work has applied probabilistic analysis to investigate the performance of DLB strategies [10], [19], [20], [21], [22]. For example, the efficiency of the factoring scheme has been analyzed for the homogeneous (identical processors) case [10] as well as for the heterogeneous case [22] using order statistics [23]. A detailed analysis of random polling has been presented in [21].

The novelty of the work presented in this paper consists of a new *general framework* for analyzing *work-stealing dynamic load balancing algorithms* when applied to large ensembles of stochastic simulations. In this case the established deterministic analysis approaches are not appropriate, so a probabilistic analysis is developed. The times per task are assumed to be independent identically distributed random variables with a certain probability distribution. This is a natural assumption for ensemble computations, where the same model is run repeatedly with different initial conditions and parameter values. No assumption is made, however, about the shape of the underlying probability density function; the proposed analysis is very general. The level of load imbalance (defined by a given metric) is also a random variable. The analysis focuses on quantifying the decrease in the *expected value* of the random load imbalance. The probabilistic analysis reveals that the four applied DLB methods are effective for moderate parallelism; scalability is not investigated here. While the performance analysis is complex, the four DLB methods described here are easy to implement. Numerical results show that they achieve considerable savings in computation time for a computational biology application. The relative performance of the four DLB strategies is analyzed numerically for a biological problem in Section 5.

The proposed DLB analysis framework is relevant not only for distributed memory clusters, but also for cloud computing environments. Task scheduling optimization plays a key role in cloud computing systems to provide stable and elastic on-demand services with high efficiency [24]. For example, the Hadoop system — a widely used MapReduce cloud framework — adapts the centralized scheduler architecture with several scheduling policies such as FIFO, fair scheduler, and capacity scheduler [25]. Our proposed analysis framework can be applied to study the performance of these approaches.

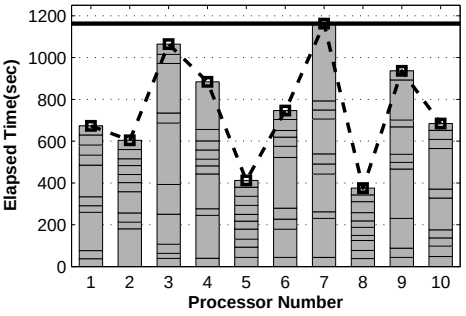


Fig. 1. Elapsed compute times for 100 prototype mutant multistage cell cycle simulations by static distribution across 10 worker processors. Dotted line represents different CPU times per processor and the solid line indicates the wall clock time.

The paper is organized as follows. The four load balancing algorithms are presented in Section 2. Section 3 explains the analysis framework, and Section 4 contains the probabilistic analysis of the load balancing algorithms. Section 5 shows theoretical and experimental results with a cell cycle model. Section 6 draws some conclusions.

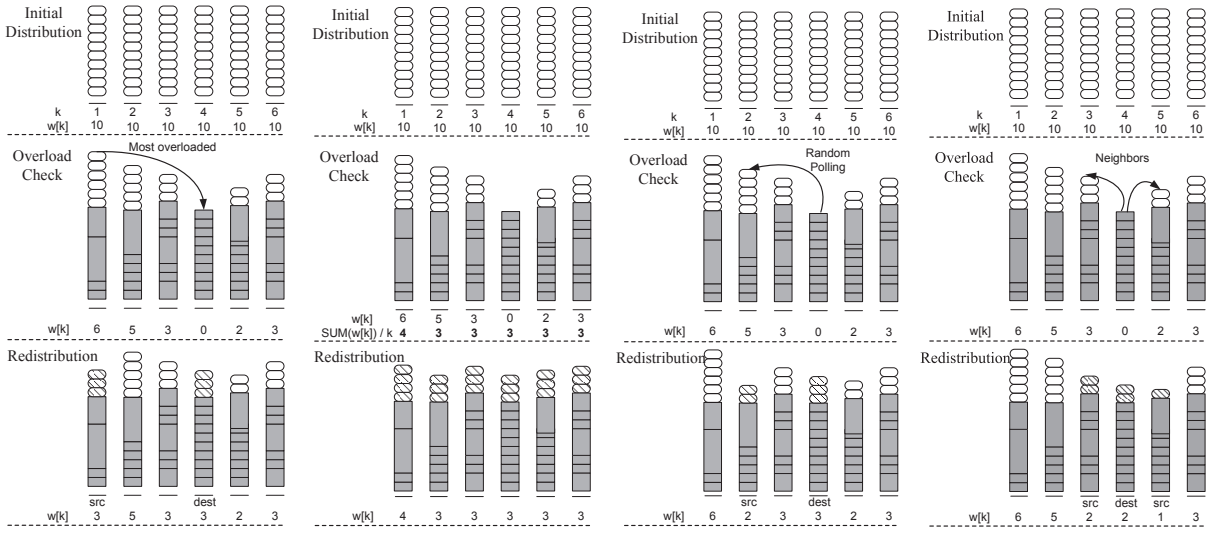
2 Load Balancing Algorithms

This section presents two centralized DLB strategies: most-dividing (MD) and all-redistribution (AR) and two decentralized DLB strategies: random-polling (RP) and neighbor-redistribution (NR).

2.1 Motivation

Each run of a stochastic simulation leads to different results. The goal of running an ensemble of stochastic simulations is to estimate the probability distribution of all possible outcomes. This typically requires thousands of simulations run concurrently on many CPUs. The stochastic nature of the system and the potentially dramatic differences running time per simulation can cause a severe load imbalance among processors that are running many simulations.

Consider, for example, stochastic simulations of the budding yeast cell. For certain mutants, a cell might never divide, or it might always divide, with some probability. Therefore, the CPU time to run the simulation is quite different from one case to another. Fig. 1. shows 100 prototype mutant multistage cell lineage simulations assigned statically to 10 worker processors. The results reveal a considerable load imbalance, with the CPUs being idle for approximately 40% of the aggregate compute time. This results in poor utilization of computer resources, longer time to



(a) MD load balancing idea. (b) AR load balancing idea. (c) RP load balancing idea. (d) NR load balancing idea.

Fig. 2. Adaptive load balancing strategies. Ellipses represent tasks to be done and gray rectangles represent completed tasks. Right diagonal patterned ellipses indicate tasks to be done on processors whose load has been adjusted by an adaptive load balancing algorithm.

results, and reduced scientific productivity. Dynamic load balancing strategies are required to improve the parallel efficiency. The stochastic simulation algorithm and budding yeast cell cycle model are explained in detail in Section 5.

2.2 Most-Dividing (MD) Algorithm

The most-dividing (MD) algorithm is based on the *central redistribution* work of Powley [26] and Hillis [27]. The idea of the MD algorithm is presented in Fig. 2 (a). First, the tasks (cell simulations) are evenly distributed to every worker processor in the system. Workers concurrently execute their jobs. Due to different CPU times per task, other processors may be well behind the first processor to finish its tasks. The processor that finishes its jobs becomes idle. The processor with the largest number of remaining jobs is considered to be the most overloaded processor. At this time the most overloaded processor sends out half of its remaining jobs to the idle processor. This sequence of steps is executed repeatedly until there is no remaining work.

To implement the MD algorithm, the idle processor has to receive new work from the highest load processor. Therefore, the highest load processor stops its work, and reduces its remaining work when another processor has completed all of its work. Stopping the computation when all the tasks are completed is called *termination*. The Dijkstra-Scholten algorithm [17] and the Shavit-Francez algorithm [18] are adapted for detecting terminations using requests and acknowledgement messages. Initially, each processor is in one of two states: inactive and active. Upon receiving a task from the master, slave processors are active. Slave processors send a message to the master whenever they finish a job, and receive messages setting their state to continue activity or become inactive once the termination condition is satisfied. When any processor finishes its assigned jobs, the highest load processor receives a suspend message. It suspends execution after finishing the currently active job, reduces its tasks to half of its remaining jobs, and then resumes execution where it left off.

2.3 All-Redistribution (AR) Algorithm

The all-redistribution (AR) method is also a centralized load balancing scheme. The idea of the AR algorithm is presented in Fig. 2 (b). The initial step of the AR algorithm is similar to that of the MD algorithm. The processor that finishes its jobs first becomes idle, and notifies the master of its idle status. Then, the master directs all workers to suspend execution, redistributes all remaining jobs in the workers' queues evenly among all workers, and finally directs the workers to resume execution.

2.4 Random-Polling (RP) Algorithm

Centralized schemes are inherently limited in terms of scalability. Due to finite communications resources, bottlenecks appear when many worker processors request jobs simultaneously from the same master. One approach to solve the scalability issue is to organize the system into multiple master/worker partitions, which are supervised by a dedicated supermaster process. Another approach, the decentralized scheme, is to fully distribute and execute tasks on all processors without any master supervision.

The random-polling (RP) method is a receiver-initiated decentralized load balancing algorithm [16]. Fig. 2 (c) illustrates the idea. When a worker processor becomes idle, it randomly polls other processors until it finds a busy one. The busy worker becomes a donor and sends out half of its remaining jobs to the idle processor. Each processor is selected as a donor with equal probability, ensuring that work requests are evenly distributed.

The implementation of the RP algorithm associates with each processor one of the following three states: available, idle, and locked. A processor with remaining jobs beyond the active one is in the available state. A processor that finishes its jobs becomes idle. A processor with one (active) job is locked. An idle processor randomly polls other processors to request jobs. Upon receiving the request, an available processor agrees to become a donor. The state of the donor processor(s) changes from available to locked in order to avoid overlaps (i.e., to become a donor for multiple idle processors that happened to randomly poll it). After the RP load balancing step ends, a locked processor is released and becomes available if there are remaining jobs besides the currently active one.

2.5 Neighbor-Redistribution (NR) Algorithm

The idea of the neighbor-distribution (NR) decentralized load balancing scheme is presented in Fig. 2 (d). A processor that finishes its jobs informs its neighbors of its idle status. The set of neighbors is predefined based on the network topology of the system (in this paper a 2-D torus topology is considered for the numerical experiments). From the algorithmic perspective, the sets of neighbors can be arbitrarily defined; assume that each processor has $k-1$ neighbors. The idle processor and its neighbors redistribute evenly all their remaining jobs (i.e., apply the AR algorithm on the subset of k processors).

The NR load balancing step performs a local redistribution of jobs, and therefore is suitable for parallel architectures where groups of nodes are linked directly. In this case the NR method is related to the dimension exchange algorithm, where a dimension corresponds to a fully connected subset [6], [19], [28]. Similar to RP, the NR algorithm uses three states (available, idle, and locked) to avoid overlaps (i.e., participation by the same processor in the balancing steps performed by two distinct groups of neighbors).

3 The Analysis Framework

This section presents a probabilistic framework for load balancing analysis. The assumptions needed for the analysis and the metrics used to measure load imbalance are considered in detail.

3.1 Assumptions for the Analysis

The computational goal is to run an ensemble of n stochastic (biochemical) simulations. Each individual simulation is referred to as a "task". Due to the stochastic nature of each simulation, the execution time t associated with a particular task cannot be estimated in advance. (The same situation occurs with deterministic adaptive models where the grid or time step adaptation depends on the data, and the chosen grid and step sizes greatly affect the total compute time.) The task compute times are modeled by random variables.

ASSUMPTION 1. *The compute times associated with different tasks are independent identically distributed (i.i.d.) random variables.*

The mean and the standard deviation of the random variable task compute time T are denoted by μ_T and σ_T, respectively. The exact shape of the probability density function for T is not relevant for the analysis; thus, the analysis results are very general.

Assumption 1 naturally covers the case where the ensemble is obtained by running the same model multiple times, with different initial conditions, different parameter values, or different seeds of the pseudo random number generator. New model runs are independent of the results of previous runs. Assumption 1 is also appropriate where multiple models are being run, and where each model of the batch is chosen with a specified frequency.

Next, the mapping of the n tasks of the ensemble onto the p processors is considered. Processor i has R_i tasks, such that $R_1 + \ldots + R_p = n$. Let t_{ij} denote the compute time of the jth task on the ith processor where $i = 1, \ldots, p$, $\quad j = 1, \ldots, R_i$. Note that all t_{ij} are i.i.d. random variables according to Assumption 1. The total compute time $X_i = \sum_{j=1}^{R_i} t_{ij}$ of processor i is also a random variable. In probability theory, the central limit theorem (CLT) states that the normalized sum of a sufficiently large number of independent identically distributed random variables, each with finite mean and variance, will be approximately standard normally distributed [29]. Therefore, using Assumption 1, if R_i is large enough, then

$$\frac{X_i - R_i\,\mu_T}{\sqrt{R_i}\,\sigma_T}$$

will be approximately normally distributed with

$$\mathrm{E}\left[X_i\right] = R_i \cdot \mu_T \ , \quad \mathrm{V}ar\left[X_i\right] = R_i \cdot \sigma_T^2 \ .$$

It is therefore assumed that

ASSUMPTION 2. *The number of tasks mapped onto each processor is sufficiently large such that the probability density function of the total compute time per processor is approximately Gaussian.*

Assumption 2 allows the analysis to work with Gaussian distributions of the total compute times per processor regardless of the underlying distribution of individual task times. Thus a very general setting for the analysis is possible. Assumption 2 is invalid during the winddown period (when there are only a few tasks left per processor), but that is a small fraction of the total ensemble computation time. Even during winddown load balancing continues to be beneficial, but the theoretical analysis cannot be directly applied.

3.2 Metrics of Load Imbalance

The algebraic mean of the compute times per processor is defined as

$$\eta_X = \frac{1}{p}\sum_{i=1}^{p} X_i = \frac{1}{p}\sum_{i=1}^{p}\sum_{j=1}^{R_i} t_{ij}.$$

Note that η_X is itself a random variable with $\mathrm{E}[\eta_X] = (n/p)\,\mu_T$. The algebraic variance of the compute times among processors is defined by

$$\xi_X^2 = \frac{1}{p-1}\sum_{i=1}^{p}\left(X_i - \eta_X\right)^2$$

and is also a random variable. The square root of the algebraic variance (RAV), $\sqrt{\xi_X^2}$, is also considered. The basic premise of variance is that larger variance between the compute times on different processors is a symptom of larger load imbalance. The first measure of the degree of load imbalance is therefore the expected value of the algebraic variance,

$$\mathrm{E}\left[\xi_X^2\right] = \frac{1}{p-1}\sum_{i=1}^{p}\mathrm{E}\left[\left(X_i - \eta_X\right)^2\right], \qquad (1)$$

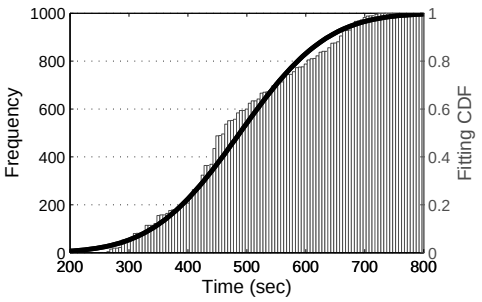
or more conveniently the square root $\sqrt{\mathrm{E}\left[\xi_X^2\right]}$.

Consider now the minimum and the maximum computation times among all processors, $Y_1 = \min\{X_1, \ldots, X_p\}$ and $Y_p = \max\{X_1, \ldots, X_p\}$. These are both random variables. The idle time spent by processor i is the difference between the maximum time and the compute time on the processor, $Y_p - X_i$. The second measure of load imbalance is the expected value of the largest idle time, i.e., the difference between the largest and the smallest compute times across all processors,

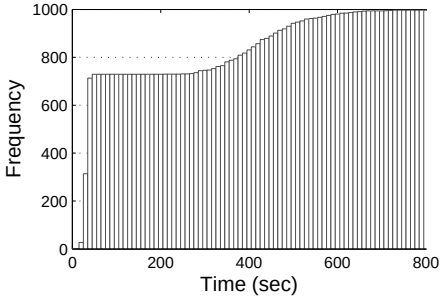
$$\mathrm{E}\left[Y_p - Y_1\right] = \mathrm{E}\left[\max\{X_1, \ldots, X_p\}\right] - \mathrm{E}\left[\min\{X_1, \ldots, X_p\}\right]. \qquad (2)$$

Finally, the third measure of load imbalance is the expected value of the average idle compute time across all processors,

$$\mathrm{E}\left[\frac{1}{p}\sum_{i=1}^{p}\left(Y_p - X_i\right)\right] = \mathrm{E}\left[Y_p - \eta_X\right]. \qquad (3)$$



(a) Wild-type 1,000 simulations.



(b) Prototype mutant 1,000 simulations.

Fig. 3. Discrete cumulative histogram of compute times per cell (bar) for wild-type and mutant simulations. The solid line represents the best-fit Gaussian CDF.

3.3 Variability in Compute Times per Cell

The wild-type cell lineage simulation time distribution from a simulation experiment is plotted in Fig. 3. (a). This distribution is based on 1,000 budding yeast multistage cell tracking simulations with 25 processors. The best continuous Gaussian CDF approximation to the discrete cumulative histogram is also shown; it is clear that the cell cycle simulation times are not normally distributed [30]. The wild-type simulation data from Fig. 3. (a) has the mean and standard deviation

$$\mu_T = 488.1 \text{ sec.} \quad \text{and} \quad \sigma_T = 116.6 \text{ sec.} \qquad (4a)$$

Fig. 3. (b) shows the cumulative discrete histogram of 1,000 prototype budding yeast mutant simulations. Approximately 75% of the cells never divide and the remaining 25% divide very irregularly. For the mutant simulation results

$$\mu_T = 152.0 \text{ sec.} \quad \text{and} \quad \sigma_T = 191.1 \text{ sec.} \qquad (4b)$$

4 Analysis of the Dynamic Load Balancing Algorithms

The probabilistic framework proposed here models compute times per task as i.i.d. random variables. Level of load imbalance is measured by three well-defined metrics (1)–(3). The analysis approach quantifies the *expected value* of the load imbalance metrics

before and after each work redistribution step, and assess the reduction in the expected load imbalance.

This analysis framework is useful for a considerably more general class of problems, beyond stochastic cell cycle modeling. The proposed analysis approach is applicable to any parallel ensemble calculations where the compute times per task follow the same probability distribution.

4.1 Order Statistics

Let $X_1, \ldots, X_p$ be p independent identically distributed random variables with a probability density function (PDF) $f_X(x)$, and cumulative distribution function (CDF) $F_X(x)$. The variables $Y_1 \le Y_2 \le \cdots \le Y_p$, where the Y_i are the X_i arranged in order of increasing magnitudes, are called *order statistics* corresponding to the random sample $X_1, \ldots, X_p$. Therefore, $Y_1 = \min\{X_1, \ldots, X_p\}$ and $Y_p = \max\{X_1, \ldots, X_p\}$. Some useful facts about order statistics [23] follow. The CDF of the largest order statistic Y_p is given by

$$\begin{aligned} F_{Y_p}(y) &= \Pr[\, Y_p \le y \,] = \Pr[\, X_1 \le y; \ldots; X_p \le y \,] \\ &= \prod_{j=1}^{p} \Pr[\, X_j \le y \,] = \prod_{j=1}^{p} F_{X_j}(y) = [\, F_X(y) \,]^p \end{aligned}$$

because the X_js are independent. Likewise

$$F_{Y_1}(y) = \Pr[\, Y_1 \le y \,] = 1 - [\, 1 - F_X(y) \,]^p.$$

These are important special cases of the general formula for $F_{Y_r}(y)$,

$$\begin{aligned} F_{Y_r}(y) &= \Pr[\, Y_r \le y \,] \\ &= \sum_{i=r}^{p} \binom{p}{i} [F_X(y)]^i \, [1 - F_X(y)]^{p-i}. \end{aligned}$$

The probability density function for the rth order variable Y_r from X is

$$f_{Y_r}(y) = \frac{[F_X(y)]^{r-1}[1 - F_X(y)]^{p-r}}{\mathrm{B}(r, p-r+1)} f_X(y),$$

where $\mathrm{B}(a,b) = \dfrac{\Gamma(a)\Gamma(b)}{\Gamma(a+b)}$ is the Euler beta function. $\Gamma(r) = \displaystyle\int_0^\infty x^{r-1} e^{-x}\, dx$ is the gamma function. Thus, the special probability density function for the maximum Y_p and the minimum Y_1 are

$$f_{Y_p}(y) = p\,[F_X(y)]^{p-1}\, f_X(y), \tag{5a}$$

$$f_{Y_1}(y) = p\,[1 - F_X(y)]^{p-1}\, f_X(y). \tag{5b}$$

Numerical evaluation of expected order statistics is complex. Chen and Tyler [31] show that the expected value, standard deviation, and complete PDF of the extreme order distributions can be accurately approximated when the samples X_i are i.i.d. Gaussian. The formulas use the expression $\Phi^{-1}\left(0.5264^{1/p}\right)$, where p is the sample size and $\Phi^{-1}(y) = \sqrt{2}\,\mathrm{erfinv}(2y-1)$ is the inverse function of the standard Gaussian CDF Φ, and erfinv is the inverse of the error function $\mathrm{erf}(x) = \dfrac{2}{\sqrt{\pi}} \displaystyle\int_0^x e^{-t^2}\, dt$. Specifically, the expected values of the largest and the smallest order statistics of i.i.d. Gaussian samples are, respectively,

$$\mathrm{E}[Y_p] \approx \mu_X + \sigma_X\, \Phi^{-1}\left(0.5264^{1/p}\right), \tag{6a}$$

$$\mathrm{E}[Y_1] \approx \mu_X - \sigma_X\, \Phi^{-1}\left(0.5264^{1/p}\right). \tag{6b}$$

Numerical evidence presented in [31] indicates that the relative approximation errors are of the order of a few percent for moderately large values of p ($p \ge 20$). Note that the compute times X_i here are not identically distributed (unless all the R_i are the same), and thus in general (6) does not apply to the min and max compute times Y_1 and Y_p. (6) is used only for initially equal R_i followed by AR, and in that case experimental results presented in Section 5 indicate that the approximations (6a) and (6b) are very close to the experimentally determined expected values.

4.2 Some Useful Results for Load Balancing

Consider the moment right after one processor (say, P_1) finishes all its jobs. Define R_i to be the number of remaining jobs outstanding (including the one currently executing) on the processor P_i. Since the analysis is carried out at a given moment in time, the R_i are known and are not random variables. Let t_{ij} be the execution time for the remaining job j on processor P_i. Let X_i be the execution time of all the remaining jobs on P_i.

Consider a load balancing step that redistributes (nonexecuting) jobs among processors. Since the total number of jobs is not changed, the algebraic mean of compute times remains the same.

LEMMA 1. *Let $X = [X_1, \ldots, X_p]$ be the remaining compute times when the first processor finishes its tasks, and before the load balancing is performed. Let $X' = [X'_1, \ldots, X'_p]$ be the vector of compute times after the load balancing step. The algebraic mean of compute times per processor is the same random variable for all configurations,*

$$\eta_X = \frac{1}{p}\sum_{i=1}^{p} X_i = \eta_{X'} = \frac{1}{p}\sum_{i=1}^{p} X'_i,$$

since X' contains the same tasks, therefore the same execution times t_{ij}, as X (just distributed differently). A load balancing step does not change the expected algebraic mean time $\mathrm{E}[\eta_X] = \mathrm{E}[\eta_{X'}]$.

In what follows, the algebraic mean and the algebraic variance of the remaining number of jobs per processor are denoted by

$$\mathrm{M}(R) = \frac{1}{p}\sum_{\ell=1}^{p} R_\ell,\ \mathrm{V}(R) = \frac{1}{p-1}\sum_{i=1}^{p}\big(R_i - \mathrm{M}(R)\big)^2. \tag{7}$$

Lemma 2 estimates the time left to completion.

LEMMA 2. *Consider a task that has started but not yet finished. There is no information about how far along the computation is. The total execution time t of the task is a random variable from a distribution with mean μ_T and variation σ_T^2. Then the total remaining execution time τ is a random variable with*

$$\mathrm{E}[\tau] = \frac{1}{2}\,\mu_T, \quad \mathrm{Var}[\tau] = \frac{\sigma_T^2}{3} + \frac{\mu_T^2}{12}.$$

Proof: Consider that a fraction $f \in [0,1]$ of the task still needs to run, while a fraction $(1-f)$ of the task has completed. Since there is no information about the part that is done, f is a uniformly distributed random variable, $f \in \mathcal{U}([0,1])$. It is important to notice that t and f are independent random variables.

The time left to completion $\tau = f\,t$ is a random variable. Due to the independence of t and f,

$$\mathrm{E}[\tau] = \mathrm{E}[f\,t] = \mathrm{E}[f]\;\mathrm{E}[t] = \frac{1}{2}\mu_T.$$

For the variance,

$$\mathrm{E}\left[\left(f\,t - \frac{1}{2}\,\mu_T\right)^2\right] = \frac{\sigma_T^2}{3} + \frac{\mu_T^2}{12}.$$

□

Define adjusted numbers $\widehat{R}_i$ of tasks per processor such that $\mathrm{E}[X_i] = \widehat{R}_i\,\mu_T$. The definition must account for the fact that one task may be running. When all processors are still working, one task on each processor is running. The adjusted number of tasks is defined as

$$\widehat{R}_i = R_i - \frac{1}{2} \quad \text{for } i = 1, \ldots, p. \tag{8a}$$

Assume, without loss of generality, that P_1 is the first processor that finishes its jobs and becomes idle. All other processors have one running task, and therefore

$$\widehat{R}_1 = 0 \quad \text{and} \quad \widehat{R}_i = R_i - \frac{1}{2} \;\text{ for } i = 2, \ldots, p. \tag{8b}$$

Right after the load balancing step the processor P_i has R_i' tasks to execute. On processors $P_2, \ldots, P_p$ the first task is the one being executed, but all the R_1' tasks on P_1 are newly assigned and queued: none has started yet. This leads to

$$\widehat{R}_1 = R_1' \quad \text{and} \quad \widehat{R}_i = R_i' - \frac{1}{2} \;\text{ for } i = 2, \ldots, p. \tag{8c}$$

The following lemma is a useful ingredient in proving the main results of the paper.

LEMMA 3. *The expected value of the algebraic variance of the compute times (1) depends on both the algebraic variance of the number of tasks, and the variance of the individual compute times, and is given by*

$$\mathrm{E}\left[\xi_X^2\right] = \mathrm{V}(\widehat{R})\,\mu_T^2 + \mathrm{M}(\widehat{R})\,\sigma_T^2 + \frac{p-1}{p}\left(-\frac{1}{6}\,\sigma_T^2 + \frac{1}{12}\,\mu_T^2\right), \tag{9}$$

where the $\widehat{R}_i$ represent the adjusted numbers of tasks per processor (8). The algebraic mean $\mathrm{M}(\widehat{R})$ and the algebraic variance $\mathrm{V}(\widehat{R})$ are defined in (7).

Proof: Redefine t_{ij} to be the time remaining for job j on processor P_i; the (random) compute times per processor and their average are

$$X_i = \sum_{j=1}^{R_i} t_{ij}, \quad \eta_X = \frac{1}{p}\sum_{\ell=1}^{p}\sum_{m=1}^{R_\ell} t_{\ell m}.$$

Each processor P_i, $i \geq 2$, has one task in progress with expected completion time $\mu_T/2$ when P_1 finishes its tasks. Note that if P_1 is idle (right before load balancing) then $R_1 = 0$. If P_1 is not idle (right after load balancing step) then none of the tasks assigned to it has started and $\mathrm{E}[t_{1j}] = \mu_T$ for $j = 1, \ldots, R_1$. Consequently, the mean compute time of the first job is different on P_1 than it is on other processors;

$$\mathrm{E}[t_{ij}] = \begin{cases} \mu_T/2, & i = 2, \ldots, p \text{ and } j = 1, \\ \mu_T, & i = 2, \ldots, p \text{ and } 2 \leq j \leq R_i, \\ \mu_T, & i = 1 \text{ and } R_1 \geq 1, \\ 0\,, & i = 1 \text{ and } R_1 = 0. \end{cases}$$

Now

$$\begin{aligned} X_i - \eta_X &= \sum_{j=1}^{R_i} t_{ij} - \frac{1}{p}\sum_{\ell=1}^{p}\sum_{m=1}^{R_\ell} t_{\ell m} \\ &= \left(1 - \frac{1}{p}\right)\sum_{j=1}^{R_i} t_{ij} - \frac{1}{p}\sum_{\ell=1,\ell\neq i}^{p}\sum_{m=1}^{R_\ell} t_{\ell m} \qquad (10) \\ &= \left(1 - \frac{1}{p}\right)\sum_{j=1}^{R_i}(t_{ij} - \mathrm{E}[t_{ij}]) + \left(1 - \frac{1}{p}\right)\sum_{j=1}^{R_i}\mathrm{E}[t_{ij}] \\ &\quad - \frac{1}{p}\sum_{\substack{\ell=1\\ \ell\neq i}}^{p}\sum_{m=1}^{R_\ell}(t_{\ell m} - \mathrm{E}[t_{\ell m}]) - \frac{1}{p}\sum_{\substack{\ell=1\\ \ell\neq i}}^{p}\sum_{m=1}^{R_\ell}\mathrm{E}[t_{\ell m}]. \end{aligned}$$

Recall $\widehat{R}_i$ was defined so that $\displaystyle\sum_{j=1}^{R_i}\mathrm{E}[t_{ij}] = \widehat{R}_i\,\mu_T$, and

$$\left(1 - \frac{1}{p}\right)\sum_{j=1}^{R_i}\mathrm{E}[t_{ij}] - \frac{1}{p}\sum_{\substack{\ell=1\\ \ell\neq i}}^{p}\sum_{m=1}^{R_\ell}\mathrm{E}[t_{\ell m}] = \left(\widehat{R}_i - \mathrm{M}(\widehat{R})\right)\mu_T.$$

Note that $\mathrm{E}\left[\displaystyle\sum_{j=1}^{R_i}(t_{ij} - \mathrm{E}[t_{ij}])\right] = 0$. $\mathrm{E}[(X_i - \eta_X)^2]$ will be determined from (10). First apply Lemma 2 to get

$$\mathrm{E}\left[(t_{ij} - \mathrm{E}[t_{ij}])^2\right] = \begin{cases} \frac{\sigma_T^2}{3} + \frac{\mu_T^2}{12}, & i = 2, ..., p \text{ and } j = 1, \\ \sigma_T^2, & i = 2, ..., p \text{ and } j \geq 2, \\ \sigma_T^2, & i = 1 \text{ and } R_1 \geq 1, \\ 0\,, & i = 1 \text{ and } R_1 = 0. \end{cases}$$

In compact notation

$$\sum_{j=1}^{R_i} \mathrm{E}\left[(t_{ij} - \mathrm{E}[t_{ij}])^2\right] = \widehat{R}_i\,\sigma_T^2 + \left(-\frac{1}{6}\,\sigma_T^2 + \frac{1}{12}\,\mu_T^2\right)(1-\delta_{i1}),$$

where δ_{i1} is the Kronecker delta. Due to the independence of individual compute times,

$$\mathrm{E}\left[(t_{ij} - \mathrm{E}[t_{ij}])\,(t_{\ell m} - \mathrm{E}[t_{\ell m}])\right] = 0 \text{ for } j \neq m \text{ or } i \neq \ell.$$

Hence $\mathrm{E}[(X_i - \eta_X)^2] =$

$$\left(\widehat{R}_i - \mathrm{M}(\widehat{R})\right)^2 \mu_T^2 + \frac{1}{p}\left(\mathrm{M}(\widehat{R}) + (p-2)\,\widehat{R}_i\right)\sigma_T^2 + \left(-\frac{1}{6}\,\sigma_T^2 + \frac{1}{12}\,\mu_T^2\right)\left(\frac{p^2 - p - 1 - (p^2-2p)\,\delta_{i1}}{p^2}\right).$$

Finally the expected value of the algebraic variance

$$\mathrm{E}\left[\xi_X^2\right] = \frac{1}{p-1}\sum_{i=1}^{p}\mathrm{E}[(X_i - \eta_X)^2] = \mathrm{V}(\widehat{R})\,\mu_T^2 + \mathrm{M}(\widehat{R})\,\sigma_T^2 + \frac{p-1}{p}\left(-\frac{1}{6}\,\sigma_T^2 + \frac{1}{12}\,\mu_T^2\right).$$

□

Lemma 3 provides insight into how the load balancing algorithms reduce the algebraic variance of compute times per processor. Any redistribution of tasks does not change the total number of tasks, and therefore does not change the algebraic mean $\mathrm{M}(\widehat{R})$. The second and the third terms in (9) are invariant with any load balancing algorithm. However, a reduction in the algebraic variance $\mathrm{V}(\widehat{R})$ of the number of tasks will decrease the expected algebraic variance of the compute times by reducing the first term in (9). Therefore the following corollary can be derived.

LEMMA 4. *Let R and R' be the number of tasks per processor before and after a load redistribution step, respectively. Let X and X' be the compute times per processor before and after a load redistribution step, respectively. The decrease in the expected value of the algebraic variance of the compute times (1) is*

$$\mathrm{E}\left[\xi_X^2\right] - \mathrm{E}\left[\xi_{X'}^2\right] = \left(\mathrm{V}(\widehat{R}) - \mathrm{V}(\widehat{R}')\right)\mu_T^2, \tag{11}$$

where the $\widehat{R}_i$ represent the adjusted numbers of tasks per processor (8).

4.3 Analysis of Static Distribution

Let X_i be total job execution time for processor i and t_{ij} be the jth job time of X_i in the static (no dynamic load balancing) approach. Assume the total number n of jobs is a multiple of the number p of processors. Processor i is assigned $R = \lceil n/p \rceil = n/p$ jobs, so that $X_i = \sum_{j=1}^{R} t_{ij}$ for $i = 1, \ldots, p$. From the analysis in the previous section, the total times per processor are i.i.d. approximately Gaussian random variables $X_1, \ldots, X_p$ with mean and variance given by

$$\mu_X = R\,\mu_T, \quad \sigma_X^2 = R\,\sigma_T^2. \tag{12}$$

The expected value of the algebraic variance (1) is given by Eq. (9) where all $\widehat{R}_i = R$,

$$\mathrm{E}\left[\xi_X^2\right] = R\sigma_T^2 + \frac{p-1}{p}\left(-\frac{1}{6}\sigma_T^2 + \frac{1}{12}\mu_T^2\right). \tag{13}$$

Let Y be the order distribution of $X : Y_1 \leq Y_2 \leq \cdots \leq Y_p$. From (5a)–(5b),

$$\mathrm{E}[Y_p] = \int_{-\infty}^{\infty} y\; p\,[F_X(y)]^{p-1} f_X(y)\; dy, \tag{14a}$$

$$\mathrm{E}[Y_1] = \int_{-\infty}^{\infty} y\; p\,[1 - F_X(y)]^{p-1} f_X(y)\; dy \tag{14b}$$

with the Gaussian probability density function

$$f_X(y) = \frac{1}{\sigma_X\sqrt{2\pi}} e^{-(y-\mu_X)^2/(2\sigma_X^2)}, \tag{15}$$

and the Gaussian cumulative distribution function

$$F_X(y) = \frac{1}{2}\left[1 + \mathrm{erf}\left(\frac{y-\mu_X}{\sigma_X\sqrt{2}}\right)\right]. \tag{16}$$

From (14a)–(16) together with the simulation data (4a), the probabilistic load imbalance measures (2)–(3) can be evaluated by numerical integration.

Alternatively, the approximations (6) can be used together with (12) to obtain

$$\mathrm{E}[Y_p - Y_1] \approx 2\,\sqrt{R}\,\sigma_T\,\Phi^{-1}\left(0.5264^{1/p}\right),$$

$$\mathrm{E}[Y_p - \eta_Y] \approx \sqrt{R}\,\sigma_T\,\Phi^{-1}\left(0.5264^{1/p}\right).$$

4.4 Analysis of MD Dynamic Load Balancing

Call P_1 the first processor that finishes its jobs and becomes idle. At this time each processor P_i, $i > 1$, has R_i outstanding jobs and a total remaining execution time X_i. By the CLT, each of $X_2, \ldots, X_p$ is approximately normally distributed if all R_i are large. The first (running) job on $P_2, \ldots, P_p$ has a different PDF and a negligible effect on compute time statistics, assuming that $R_i \gg 1$ for $i \geq 2$.

In the MD algorithm the highest loaded processor sends half of its unfinished jobs to the idle processor. Assume, without loss of generality, that and P_p has the highest load of R_p unfinished jobs. The MD load balancing step moves $\lfloor R_p/2 \rfloor$ jobs from the processor P_p to P_1. The loads for $P_2, \ldots, P_{p-1}$ are not changed. Therefore, the number of jobs per processor after redistribution is

$$R_1' = \left\lfloor \frac{R_p}{2} \right\rfloor,\; R_2' = R_2, \ldots,\; R_{p-1}' = R_{p-1},\; R_p' = \left\lceil \frac{R_p}{2} \right\rceil.$$

Let X_i' be the remaining compute time for processor P_i after the MD load balancing step. From the above $X_i' = X_i$ for $i = 2, \ldots, p-1$. For the first and last processors the expected values of the compute times are

$$\mathrm{E}[X_1'] = R_1' \, \mu_T = \left\lfloor \frac{R_p}{2} \right\rfloor \mu_T,$$
$$\mathrm{E}[X_p'] = \left(R_p' - \frac{1}{2} \right) \mu_T = \left(\left\lceil \frac{R_p}{2} \right\rceil - \frac{1}{2} \right) \mu_T.$$

The above expression accounts for the fact that P_p has one task in progress. Furthermore,

$$\mathrm{E}[X_p'] - \mathrm{E}[X_1'] = \left(R_p \bmod 2 - \frac{1}{2} \right) \mu_T.$$

The following propositions prove that each MD redistribution step decreases the level of load imbalance as measured by the metrics (1)–(3).

PROPOSITION 1. *The expected value of the algebraic variance of the compute times per processor (1) decreases after a MD DLB step by*

$$\mathrm{E}[\xi_X^2] - \mathrm{E}[\xi_{X'}^2] = \frac{R_p \, (R_p - 1)}{2 \, (p-1)} \, \mu_T^2.$$

Proof: The average adjusted number of tasks per processor is the same before and after MD load balancing, $\mathrm{M}(\widehat{R}) = \mathrm{M}(\widehat{R}')$. The decrease in the algebraic variance of the adjusted number of tasks is

$$\mathrm{V}(\widehat{R}) - \mathrm{V}(\widehat{R}') = \frac{1}{p-1} \Big((\widehat{R}_1 - \mathrm{M}(\widehat{R}))^2 - (\widehat{R}_1' - \mathrm{M}(\widehat{R}))^2 + (\widehat{R}_p - \mathrm{M}(\widehat{R}))^2 - (\widehat{R}_p' - \mathrm{M}(\widehat{R}))^2 \Big) = \frac{R_p \, (R_p - 1)}{2 \, (p-1)}.$$

Lemma 4 provides the difference between the expected variances of compute times across processors before and after a MD load balancing step,

$$\mathrm{E}[\xi_X^2] - \mathrm{E}[\xi_{X'}^2] = \frac{R_p \, (R_p - 1)}{2 \, (p-1)} \, \mu_T^2 \ . \tag{17}$$

The MD algorithm can be meaningfully applied only when the number of tasks on the most overloaded processor is $R_p \geq 2$. The relation (17) then provides a strict decrease in the expected value of the algebraic variance of compute times. □

PROPOSITION 2. *The expected value of the largest idle time (2) is monotonically decreased after a MD DLB step, that is,* $\mathrm{E}\left[Y_p' - Y_1'\right] \leq \mathrm{E}\left[Y_p - Y_1\right]$.

Proof: Before the MD load balancing step, the expected maximum imbalance is

$$\mathrm{E}[Y_p] - \mathrm{E}[Y_1] = \mathrm{E}[Y_p] \geq \mathrm{E}[X_p] = \widehat{R}_p \, \mu_T.$$

After the MD load balancing step, the new expected maximum imbalance time is $\mathrm{E}[Y_p'] - \mathrm{E}[Y_1']$.

Consider the random variables

$$Z_{min} = \min\{X_2, \cdots, X_{p-1}\},$$
$$Z_{max} = \max\{X_2, \cdots, X_{p-1}\} \ \leq \ Y_p \ .$$

The smallest and the largest order statistics after MD balancing are $Y_1' = \min\{X_1', X_p', Z_{min}\}$ and $Y_p' = \max\{X_1', X_p', Z_{max}\}$. There are nine possible combinations of Y_1' and Y_p' values. Two of them lead to $Y_1' = Y_p'$, i.e., the maximum idle time is zero after the MD load balancing step. The remaining seven combinations are as follows:

(1) $Y_1' = Z_{min}$ and $Y_p' = Z_{max}$;
(2) $Y_1' = Z_{min}$ and $Y_p' = X_p'$;
(3) $Y_1' = Z_{min}$ and $Y_p' = X_1'$;
(4) $Y_1' = X_p'$ and $Y_p' = Z_{max}$;
(5) $Y_1' = X_p'$ and $Y_p' = X_1'$;
(6) $Y_1' = X_1'$ and $Y_p' = Z_{max}$;
(7) $Y_1' = X_1'$ and $Y_p' = X_p'$.

In Case (1) the balanced times fall between Z_{min} and Z_{max}. The expected maximum idle time reduction is

$$\begin{aligned} &\{\mathrm{E}[Y_p] - \mathrm{E}[Y_1]\} - \{\mathrm{E}[Y_p'] - \mathrm{E}[Y_1']\} \\ &\quad = \{\mathrm{E}[Y_p] - \mathrm{E}[Y_1]\} - \{\mathrm{E}[Z_{max}] - \mathrm{E}[Z_{min}]\} \\ &\quad = \{\mathrm{E}[Y_p] - \mathrm{E}[Z_{max}]\} + \{\mathrm{E}[Z_{min}]\} \ \geq \mathrm{E}[Z_{min}] \ \geq 0. \end{aligned}$$

The reductions of expected maximum idle times for Cases (2) to (7) are straightforward verification.

$$\begin{aligned} \text{Case (2)}: \ &\{\mathrm{E}[Y_p] - \mathrm{E}[Y_1]\} - \{\mathrm{E}[Y_p'] - \mathrm{E}[Y_1']\} \\ &= \mathrm{E}[Y_p] - \{\mathrm{E}[X_p'] - \mathrm{E}[Z_{min}]\} \ \geq \ \mathrm{E}[Y_p] - \mathrm{E}[X_p'] \\ &\geq \widehat{R}_p \, \mu_T - (\lceil R_p/2 \rceil - 0.5) \, \mu_T > 0. \\ \text{Case (3)}: \ &\{\mathrm{E}[Y_p] - \mathrm{E}[Y_1]\} - \{\mathrm{E}[Y_p'] - \mathrm{E}[Y_1']\} \\ &= \mathrm{E}[Y_p] - \{\mathrm{E}[X_1'] - \mathrm{E}[Z_{min}]\} \ \geq \ \mathrm{E}[Y_p] - \mathrm{E}[X_1'] \\ &\geq (R_p - 0.5 - \lfloor R_p/2 \rfloor) \ \mu_T \ > \ 0. \\ \text{Case (4)}: \ &\{\mathrm{E}[Y_p] - \mathrm{E}[Y_1]\} - \{\mathrm{E}[Y_p'] - \mathrm{E}[Y_1']\} \\ &= \mathrm{E}[Y_p] - \{\mathrm{E}[Z_{max}] - \mathrm{E}[X_p']\} \ \geq \ \mathrm{E}[X_p'] \\ &= (\lceil R_p/2 \rceil - 0.5) \ \mu_T \ > \ 0. \\ \text{Case (5)}: \ &\{\mathrm{E}[Y_p] - \mathrm{E}[Y_1]\} - \{\mathrm{E}[Y_p'] - \mathrm{E}[Y_1']\} \\ &= \mathrm{E}[Y_p] - \{\mathrm{E}[X_1'] - \mathrm{E}[X_p']\} \\ &\geq \left(\widehat{R}_p - \lfloor R_p/2 \rfloor + \lceil R_p/2 \rceil - 0.5 \right) \mu_T \ > \ 0. \\ \text{Case (6)}: \ &\{\mathrm{E}[Y_p] - \mathrm{E}[Y_1]\} - \{\mathrm{E}[Y_p'] - \mathrm{E}[Y_1']\} \\ &= \mathrm{E}[Y_p] - \{\mathrm{E}[Z_{max}] - \mathrm{E}[X_1']\} \ \geq \ \mathrm{E}[X_1'] \ > \ 0. \\ \text{Case (7)}: \ &\{\mathrm{E}[Y_p] - \mathrm{E}[Y_1]\} - \{\mathrm{E}[Y_p'] - \mathrm{E}[Y_1']\} \\ &= \mathrm{E}[Y_p] - \{\mathrm{E}[X_p'] - \mathrm{E}[X_1']\} \\ &\geq \left(\widehat{R}_p + 0.5 + \lfloor R_p/2 \rfloor - \lceil R_p/2 \rceil \right) \mu_T \ > \ 0. \end{aligned}$$

Therefore, after a MD load balancing step, the expected maximum time imbalance is always the same or reduced. If $R_2 \geq 1$ and $R_{p-1} \geq 1$, then $\mathrm{E}[Z_{min}] > 0$. Then expected maximum time is always decreased after a MD load balancing step. □

The third measure of load imbalance is the expected value of the average idle compute time across all

processors

$$\mathrm{E}\left[\frac{1}{p}\sum_{i=1}^{p}(Y_p - X_i)\right] = \mathrm{E}\left[Y_p - \eta_X\right].$$

PROPOSITION 3. *The expected value of the average idle time (3) does not increase after a MD DLB step, that is,* $\mathrm{E}\left[Y'_p - \eta_{X'}\right] \le \mathrm{E}\left[Y_p - \eta_X\right]$.

Proof: The decrease in the expected average idle time is (since $\eta_{X'} = \eta_X$)

$$\mathrm{E}\left[Y_p - \eta_X\right] - \mathrm{E}\left[Y'_p - \eta_{X'}\right] = \mathrm{E}\left[Y_p\right] - \mathrm{E}\left[Y'_p\right].$$

Consider each of the possible values of Y'_p separately.

(1) $Y'_p = Z_{max}$:
$\mathrm{E}\left[Y_p\right] - \mathrm{E}\left[Y'_p\right] = \mathrm{E}\left[Y_p - Z_{max}\right] \ge 0$;

(2) $Y'_p = X'_1$:
$\mathrm{E}\left[Y_p\right] - \mathrm{E}\left[Y'_p\right] \ge \left(\widehat{R}_p - \lfloor R_p/2 \rfloor\right)\mu_T > 0$;

(3) $Y'_p = X'_p$:
$\mathrm{E}\left[Y_p\right] - \mathrm{E}\left[Y'_p\right] \ge \left(R_p - \lceil R_p/2 \rceil - 0.5\right)\mu_T > 0$;

by assuming that $R_p > 1$. □

4.5 Analysis of AR Dynamic Load Balancing

In the AR algorithm, all remaining jobs on all processors are equitably redistributed among all processors right after P_1 finishes its jobs and becomes idle. At this time each processor P_i, $i = 2, \cdots, p$, has R_i remaining jobs and a remaining execution time X_i. One job is in progress with an expected completion time $\mu_T/2$ and $R_i - 1$ jobs are queued. R_i is known and not a random variable because the analysis is carried out at a given time. The total number of remaining jobs is $\sum_{i=1}^{p} R_i$. Let $b = \left(\sum_{i=1}^{p} R_i\right) \mod p$, and

$$r = \lfloor \mathrm{M}(R) \rfloor = \mathrm{M}(R) - \frac{b}{p}, \quad \widehat{r} = r - \frac{1}{2}.$$

The new number of jobs that the AR algorithm assigns to processor P_i is

$$R'_i = \begin{cases} r\,, & \text{if } b = 0 \text{ and } i = 1, \ldots, p\,, \\ r\,, & \text{if } b \neq 0 \text{ and } i = 1, \ldots, p-b\,, \\ r+1\,, & \text{if } b \neq 0 \text{ and} i = p-b+1, \ldots, p\,. \end{cases}$$

Let X'_i denote the execution time of the jobs on P_i after the AR step. The expected value of X'_i is

$$\mathrm{E}[X'_i] = \begin{cases} r\,\mu_T\,, & \text{if } i = 1\,, \\ \widehat{r}\,\mu_T\,, & \text{if } i = 2, \ldots, p-b\ , \\ (\widehat{r}+1)\,\mu_T\,, & \text{if } i = p-b+1, \ldots, p\,. \end{cases} \quad (18)$$

PROPOSITION 4. *The expected algebraic variance (1) of X' is smaller than the expected algebraic variance of X after an AR DLB step, that is,* $\mathrm{E}[\xi^2_{X'}] < \mathrm{E}[\xi^2_X]$, *assuming* $\mathrm{V}(\widehat{R}) > 1/4$.

Proof: According to Lemma 4 the expected decrease in the algebraic variance of the execution times is proportional to the decrease in the algebraic variance of the modified number of jobs. The AR algorithm redistributes the number of jobs equitably, such that after the load balancing step the algebraic variance of the number of tasks is the smallest among all possible distributions. Therefore the AR load balancing algorithm decreases the expected variability of execution times across processors by the maximum possible amount, and $\mathrm{E}[\xi^2_{X'}] < \mathrm{E}[\xi^2_X]$.

The algebraic variance after AR load balancing is

$$\begin{aligned} \mathrm{V}(\widehat{R}') &= \frac{1}{p-1}\sum_{i=1}^{p}\left(\widehat{R}'_i - \mathrm{M}(\widehat{R}')\right)^2 \\ &= \frac{p\,(4b+1) - (2b+1)^2}{4\,p\,(p-1)} \le \frac{1}{4} \end{aligned}$$

for $0 \le b \le p-1$. The decrease in the expected value of the algebraic variance of the compute times is

$$\mathrm{E}\left[\xi^2_X\right] - \mathrm{E}\left[\xi^2_{X'}\right] \ge \left(\mathrm{V}(\widehat{R}) - \frac{1}{4}\right)\mu_T^2\,.$$

□

For the remaining part of the analysis consider the case where the mean number of jobs is large, $\mathrm{M}(R) \gg 1$. In this case $r + 1 \approx r \approx \widehat{r}$, i.e., the jobs are nearly equally distributed to processors by the AR step. Moreover, the fact that one job has started on each of P_2 to P_p but not on P_1 has a negligible effect on the statistics of compute times (which are dominated by the large number of queued tasks). Therefore assume that $\mathrm{M}(R)$ is large, $b = 0$, and no jobs have started on any of the processors. The AR algorithm recursively returns to the initial circumstances of the previous AR step, but with a smaller number of jobs. The equal distribution of work and the CLT permit approximation of the compute times per processor $X'_1, \ldots, X'_p$ with i.i.d. Gaussian random variables.

PROPOSITION 5. *If R_p is sufficiently large, the expected value of the largest idle time (2) is decreased after an AR DLB step, that is,* $\mathrm{E}\left[Y'_p - Y'_1\right] < \mathrm{E}\left[Y_p - Y_1\right]$.

Proof: The maximum compute time before balancing is at least equal to the compute time on the processor with the largest number of remaining jobs (assumed to be P_p without loss of generality). This implies that $\mathrm{E}[Y_p] \ge \mathrm{E}[X_p] = R_p\,\mu_T$. Similarly, the minimum compute time is at most equal to the compute time on the processor with the smallest number of remaining jobs. Therefore

$$\mathrm{E}[Y_1] \le \mathrm{E}[X_1] = R_1\,\mu_T = 0\,, \quad R_p\,\mu_T \le \mathrm{E}[Y_p - Y_1],$$
$$\text{and } \left(R_p - M(R)\right)\mu_T \le \mathrm{E}[Y_p - \eta_Y].$$

The expected values of the greatest and the least order statistics in Gaussian samples can be accurately approximated using (6a)–(6b). Under the above sim-

plifying assumptions ($b = 0$ and no processes have started) all the X_i are (approximately) i.i.d. normal random variables. From (6a), (6b), and (18),

$$\mathrm{E}[Y'_p] = r\,\mu_T + \sqrt{r}\,\sigma_T\,\Phi^{-1}(0.5264^{1/p}) + \mathrm{err}_p(p),$$
$$\mathrm{E}[Y'_1] = r\,\mu_T - \sqrt{r}\,\sigma_T\,\Phi^{-1}(0.5264^{1/p}) + \mathrm{err}_1(p).$$

Assume that the relative approximation errors have an upper bound $\epsilon < 0.5$ for all $p \geq 20$:

$$|\mathrm{err}_\mathrm{p}(p)| \leq \epsilon \cdot \left| r\,\mu_T + \sqrt{r}\,\sigma_T\,\Phi^{-1}(0.5264^{1/p}) \right|,$$
$$|\mathrm{err}_1(p)| \leq \epsilon \cdot \left| r\,\mu_T - \sqrt{r}\,\sigma_T\,\Phi^{-1}(0.5264^{1/p}) \right|,$$

taking the relative errors with respect to the approximate values for convenience. Note that the results in [31] estimate $\epsilon \leq 0.04$. Consequently,

$$\mathrm{E}[Y'_p] - \mathrm{E}[Y'_1] = 2\sqrt{r}\,\sigma_T\,\Phi^{-1}(0.5264^{1/p}) + \mathrm{err}_\mathrm{p}(p) - \mathrm{err}_1(p).$$

For bounded numbers of processors $p \leq p_{\max}$ the inverse function $\Phi^{-1}(0.5264^{1/p})$ is bounded by $\Phi^{-1}(0.5264^{1/p_{\max}}) = C_{\max} \approx 4.4$ for $p_{\max} = 1,000,000$. Therefore,

$$\begin{aligned}\mathrm{E}[Y'_p] - \mathrm{E}[Y'_1] &\leq 2\,C_{\max}\,\sqrt{r}\,\sigma_T + |\mathrm{err}_\mathrm{p}(p)| + |\mathrm{err}_1(p)| \\ &\leq 2\,(1+\epsilon)\,C_{\max}\,\sqrt{r}\,\sigma_T + 2\,\epsilon\,r\,\mu_T.\end{aligned}$$

The decrease in expected maximum idle time is at least

$$\begin{aligned}&\mathrm{E}\left[Y_p - Y_1\right] - \mathrm{E}\left[Y'_p - Y'_1\right] \\ &\quad \geq (R_p - 2\,\epsilon\,r)\;\mu_T - 2\,(1+\epsilon)\,C_{\max}\,\sqrt{r}\,\sigma_T \\ &\quad > (1 - 2\,\epsilon\,)\;R_p\,\mu_T - 2\,(1+\epsilon)\,C_{\max}\,\sqrt{R_p}\,\sigma_T \geq 0\end{aligned}$$

for $r < R_p$ and

$$R_p \;\geq\; \frac{4\,(1+\epsilon)^2\,C_{\max}^2}{(1-2\,\epsilon)^2}\,\left(\frac{\sigma_T}{\mu_T}\right)^2.$$

This lower bound for R_p does not depend on p ($20 \leq p \leq p_{\max}$), but depends only on σ_T and μ_T.

□

PROPOSITION 6. *If $R_p > (1+\epsilon+g)\,r$ for some $g > 0$ and r is sufficiently large, the expected value of the average idle time (3) is decreased after an AR DLB step, that is, $\mathrm{E}\left[Y'_p - \eta_X\right] < \mathrm{E}\left[Y_p - \eta_X\right]$.*

Proof: Before an AR load balancing step, since $\mathrm{E}[Y_p] \geq \mathrm{E}[X_p] = R_p\,\mu_T$ as before, the mean load imbalance is $\mathrm{E}\left[Y_p - \eta_X\right] \geq (R_p - r)\,\mu_T$. After the AR step, and using ϵ from the proof of Proposition 5, the mean load imbalance becomes

$$\begin{aligned}&\mathrm{E}\left[Y'_p - \eta_X\right] \\ &\quad = r\,\mu_T + \sqrt{r}\,\sigma_T\,\Phi^{-1}(0.5264^{1/p}) + \mathrm{err}_\mathrm{p}(p) - r\mu_T \\ &\quad \leq (1+\epsilon)\,\left(r\,\mu_T + \sqrt{r}\,\sigma_T\,\Phi^{-1}(0.5264^{1/p})\right) - r\mu_T \\ &\quad \leq \epsilon\,r\mu_T + (1+\epsilon)\,C_{\max}\,\sqrt{r}\,\sigma_T\,.\end{aligned}$$

Therefore, the difference after the AR step is

$$\begin{aligned}&\mathrm{E}\left[Y_p - \eta_X\right] - \mathrm{E}\left[Y'_p - \eta_X\right] \\ &\quad \geq (R_p - r - \epsilon\,r)\;\mu_T - (1+\epsilon)\,C_{\max}\,\sqrt{r}\,\sigma_T \\ &\quad > \; g\,r\,\mu_T - (1+\epsilon)\,C_{\max}\,\sqrt{r}\,\sigma_T\,.\end{aligned}$$

The expected mean idle time decreases if R_p is sufficiently large, when

$$R_p > (1+\epsilon+g)\,r \geq (1+\epsilon+g)\,\left(\frac{(1+\epsilon)\,C_{\max}\,\sigma_T}{g\,\mu_T}\right)^2.$$

□

4.6 Analysis of RP Dynamic Load Balancing

Recall that P_1 is the first processor that finishes its tasks and becomes idle. In the RP algorithm, the idle processor sends requests to randomly chosen processors until a busy one is found. Assume, without loss of generality, that P_k is the busy processor that was chosen randomly. P_k has the load of R_k unfinished jobs. The RP load balancing step moves $\lfloor R_k/2 \rfloor$ jobs from the busy processor P_k to P_1. The loads of the processors other than P_1 and P_k are not changed. P_p has the highest load of R_p unfinished jobs as before. Let X'_i be the remaining compute time for processor P_i after the RP DLB step. From the above, $X'_i = X_i$ for $i = 2, \ldots, p$ and $i \neq k$. For the processors P_1 and P_k, the expected values of the compute times are

$$\mathrm{E}[X'_1] = R'_1\,\mu_T = \left\lfloor \frac{R_k}{2} \right\rfloor\;\mu_T\,,$$
$$\mathrm{E}[X'_k] = \left(R'_k - \frac{1}{2}\right)\,\mu_T = \left(\left\lceil \frac{R_k}{2} \right\rceil - \frac{1}{2}\right)\,\mu_T\,.$$

The above expression accounts for the fact that P_k has one task in progress. Furthermore,

$$\mathrm{E}[X'_k] - \mathrm{E}[X'_1] = \left(R_k \bmod 2 - \frac{1}{2}\right)\,\mu_T.$$

The following propositions prove that each RP redistribution step decreases the level of load imbalance as measured by the metrics (1)–(3).

PROPOSITION 7. *The expected value of the algebraic variance of the compute times per processor (1) decreases after a RP DLB step by*

$$\mathrm{E}[\xi_X^2] - \mathrm{E}[\xi_{X'}^2] = \frac{(\mathrm{M}(R))^2 - \mathrm{M}(R) + \mathrm{V}(R)}{2(p-1)}\,\mu_T^2\;.$$

Proof: Assume the probability that the P_k is randomly chosen as a donor processor is $1/(p-1)$. The average adjusted number of tasks per processor is the same before and after RP load balancing, $\mathrm{M}(\widehat{R}) = \mathrm{M}(\widehat{R}')$. The decrease in the algebraic variance of the

adjusted number of tasks is

$$\mathrm{V}(\widehat{R}) - \mathrm{V}(\widehat{R}') = \frac{1}{p-1}\Big((\widehat{R}_1 - \mathrm{M}(\widehat{R}))^2 - (\widehat{R}'_1 - \mathrm{M}(\widehat{R}))^2 + (\widehat{R}_k - \mathrm{M}(\widehat{R}))^2 - (\widehat{R}'_k - \mathrm{M}(\widehat{R}))^2\Big) = \frac{R_k\,(R_k-1)}{2\,(p-1)}.$$

Lemma 4 and the probability that P_k is randomly chosen as a donor processor provide the difference between the expected variances of compute times across processors before and after a RP DLB step

$$\begin{aligned}
\mathrm{E}[\xi_X^2] - \mathrm{E}[\xi_{X'}^2] &= \sum_{k=2}^{p} \frac{1}{p-1}\left(\frac{R_k\,(R_k-1)}{2\,(p-1)}\right)\mu_T^2 \\
&= \frac{\mu_T^2}{2(p-1)^2}\sum_{k=2}^{p}\left(R_k^2 - R_k\right) \\
&= \frac{\mu_T^2}{2(p-1)^2}\sum_{k=2}^{p}\Big\{\,(R_k - \mathrm{M}(R))^2 \\
&\quad + (2\mathrm{M}(R)-1)\,R_k - (\mathrm{M}(R))^2\,\Big\} \\
&= \frac{\mu_T^2}{2(p-1)^2}\Big\{(p-1)\mathrm{V}(R) \\
&\quad + (p-1)\left((\mathrm{M}(R))^2 - \mathrm{M}(R)\right)\Big\} \\
&= \frac{(\mathrm{M}(R)-1)^2 + (\mathrm{M}(R)-1) + \mathrm{V}(R)}{2(p-1)}\,\mu_T^2 > 0
\end{aligned}$$

for $\mathrm{M}(R) > 1$. □

PROPOSITION 8. *The expected value of the largest idle time (2) is not increased after a RP DLB step, that is,* $\mathrm{E}\left[Y'_p - Y'_1\right] \le \mathrm{E}\left[Y_p - Y_1\right]$.

Proof: Before the RP load balancing step, the expected maximum imbalance is

$$\mathrm{E}[Y_p] - \mathrm{E}[Y_1] = \mathrm{E}[Y_p] \ge \mathrm{E}[X_p] = \widehat{R}_p\,\mu_T.$$

After the RP load balancing step, the new expected maximum imbalance time is $\mathrm{E}[Y'_p] - \mathrm{E}[Y'_1]$. If $P_k = P_p$ has the highest load of R_p, the proof is the same as that for Proposition 2. Otherwise $1 < k < p$. Consider the random variables

$$\begin{aligned}
Z_{min} &= \min\{X_2, \cdots, X_{k-1}, X_{k+1}, \cdots, X_p\}, \\
Z_{max} &= \max\{X_2, \cdots, X_{k-1}, X_{k+1}, \cdots, X_p\} \;\le\; Y_p.
\end{aligned}$$

The smallest and the largest order statistics after the RP load balancing step are $Y'_1 = \min\{X'_1, X'_k, Z_{min}\}$ and $Y'_p = \max\{X'_1, X'_k, Z_{max}\}$. Seven possible combinations of Y'_1 and Y'_p values are considered as in the proof of Proposition 2.

(1) $Y'_1 = Z_{min}$ and $Y'_p = Z_{max}$;
(2) $Y'_1 = Z_{min}$ and $Y'_p = X'_k$;
(3) $Y'_1 = Z_{min}$ and $Y'_p = X'_1$;
(4) $Y'_1 = X'_k$ and $Y'_p = Z_{max}$;
(5) $Y'_1 = X'_k$ and $Y'_p = X'_1$;
(6) $Y'_1 = X'_1$ and $Y'_p = Z_{max}$;
(7) $Y'_1 = X'_1$ and $Y'_p = X'_k$.

In Case (1) the balanced times fall between Z_{min} and Z_{max}. That the expected maximum idle time reduction is greater than or equals to zero is proved the same as for Case (1) in Proposition 2. The reductions of expected maximum idle times for Cases (2) to (7) are shown by straightforward verification.

$$\begin{aligned}
&\text{Case (2):}\ \ \{\mathrm{E}[Y_p] - \mathrm{E}[Y_1]\} - \{\mathrm{E}[Y'_p] - \mathrm{E}[Y'_1]\} \\
&\quad = \mathrm{E}[Y_p] - \{\mathrm{E}[X'_k] - \mathrm{E}[Z_{min}]\} \;\ge\; \mathrm{E}[Y_p] - \mathrm{E}[X'_k] \\
&\quad \ge (R_p \;- \lceil R_k/2 \rceil)\,\mu_T > 0, \\
&\text{Case (3):}\ \ \{\mathrm{E}[Y_p] - \mathrm{E}[Y_1]\} - \{\mathrm{E}[Y'_p] - \mathrm{E}[Y'_1]\} \\
&\quad = \mathrm{E}[Y_p] - \{\mathrm{E}[X'_1] - \mathrm{E}[Z_{min}]\} \;\ge\; \mathrm{E}[Y_p] - \mathrm{E}[X'_1] \\
&\quad \ge (R_p - 0.5 - \lfloor R_k/2 \rfloor)\;\mu_T \;>\; 0, \\
&\text{Case (4):}\ \ \{\mathrm{E}[Y_p] - \mathrm{E}[Y_1]\} - \{\mathrm{E}[Y'_p] - \mathrm{E}[Y'_1]\} \\
&\quad = \mathrm{E}[Y_p] - \{\mathrm{E}[Z_{max}] - \mathrm{E}[X'_k]\} \;\ge\; \mathrm{E}[X'_k] \\
&\quad = (\lceil R_k/2 \rceil - 0.5)\;\mu_T \;>\; 0, \\
&\text{Case (5):}\ \ \{\mathrm{E}[Y_p] - \mathrm{E}[Y_1]\} - \{\mathrm{E}[Y'_p] - \mathrm{E}[Y'_1]\} \\
&\quad = \mathrm{E}[Y_p] - \{\mathrm{E}[X'_1] - \mathrm{E}[X'_k]\} \\
&\quad \ge (R_p - \lfloor R_k/2 \rfloor + \lceil R_k/2 \rceil - 1)\;\mu_T \;>\; 0, \\
&\text{Case (6):}\ \ \{\mathrm{E}[Y_p] - \mathrm{E}[Y_1]\} - \{\mathrm{E}[Y'_p] - \mathrm{E}[Y'_1]\} \\
&\quad = \mathrm{E}[Y_p] - \{\mathrm{E}[Z_{max}] - \mathrm{E}[X'_1]\} \;\ge\; \mathrm{E}[X'_1] \;\ge\; 0, \\
&\text{Case (7):}\ \ \{\mathrm{E}[Y_p] - \mathrm{E}[Y_1]\} - \{\mathrm{E}[Y'_p] - \mathrm{E}[Y'_1]\} \\
&\quad = \mathrm{E}[Y_p] - \{\mathrm{E}[X'_k] - \mathrm{E}[X'_1]\} \\
&\quad \ge (R_p + \lfloor R_k/2 \rfloor - \lceil R_k/2 \rceil)\,\mu_T \;\ge\; 0.
\end{aligned}$$

Therefore, after a RP load balancing step, the expected maximum time imbalance is always the same or reduced. Note that if $R_p \ge 2$ and $r \ge 1$, then the expected maximum time imbalance is always reduced. This condition is general in load balancing steps. □

PROPOSITION 9. *The expected value of the average idle time (3) is not increased after a RP DLB step, that is,* $\mathrm{E}\left[Y'_p - \eta_{X'}\right] \le \mathrm{E}\left[Y_p - \eta_X\right]$.

Proof: The decrease in the expected average idle time is (since $\eta_{X'} = \eta_X$)

$$\mathrm{E}\left[Y_p - \eta_X\right] - \mathrm{E}\left[Y'_p - \eta_{X'}\right] = \mathrm{E}\left[Y_p\right] - \mathrm{E}\left[Y'_p\right].$$

Consider each of the possible values of Y'_p separately.

(1) $Y'_p = Z_{max}$:
$\mathrm{E}\left[Y_p\right] - \mathrm{E}\left[Y'_p\right] = \mathrm{E}\left[Y_p - Z_{max}\right] \ge 0$;

(2) $Y'_p = X'_1$:
$$\mathrm{E}\left[Y_p\right] - \mathrm{E}\left[Y'_p\right] \ge \left[R_p - \left\lfloor \frac{R_k}{2} \right\rfloor - \frac{1}{2}\right]\mu_T > 0;$$

(3) $Y'_p = X'_k$:
$$\mathrm{E}\left[Y_p\right] - \mathrm{E}\left[Y'_p\right] \ge \left[R_p - \left\lceil \frac{R_k}{2} \right\rceil\right]\mu_T \ge 0.$$

In the first case $Y'_p = Z_{max}$, Z_{max} is the same as Y_p except when the donor processor P_k is randomly selected to be the most overloaded processor P_p. Therefore the expected value of the reduction in the average idle time is zero for most RP load balancing steps. □

4.7 Analysis of NR Dynamic Load Balancing

In the NR algorithm, the idle processor sends requests to neighbor processors to redistribute the remaining jobs on the neighbor processors and itself. Assume that the number of neighbor processors of the idle processor is $k-1$ and changes with different network topologies. Let P_1 be the idle processor that finishes its jobs with its neighbor processors $P_2, \ldots, P_k$.

Before the NR load balancing step, each processor P_i, $i = 2, \ldots, k$, has R_i remaining jobs and a remaining execution time X_i. One job is in progress with an expected completion time $\mu_T/2$ and $R_i - 1$ jobs are queued. Let $b = \left(\sum_{i=1}^{k} R_i\right) \bmod k$, $\widetilde{\mathrm{M}}(R) = \frac{1}{k}\sum_{i=1}^{k} R_i$ and

$$r = \left\lfloor \widetilde{\mathrm{M}}(R) \right\rfloor = \widetilde{\mathrm{M}}(R) - \frac{b}{k}, \quad \widehat{r} = r - \frac{1}{2}.$$

The new number of jobs that the NR algorithm assigns to processor P_i is

$$R'_i = \begin{cases} r\,, & i = 1, \ldots, k-b\,, \\ r+1\,, & i = k-b+1, \ldots, k\,, \\ R_i\,, & i = k+1, \ldots, p\,. \end{cases}$$

Let X'_i denote the execution time of the jobs on P_i after the NR step. The expected value of X'_i is

$$\mathrm{E}[X'_i] = \begin{cases} r\,\mu_T\,, & \text{if } i = 1\,, \\ \widehat{r}\,\mu_T\,, & \text{if } i = 2, \ldots, k-b\,, \\ (\widehat{r}+1)\,\mu_T\,, & \text{if } i = k-b+1, \ldots, k\,. \\ \widehat{R}_i\,\mu_T\,, & \text{if } i = k+1, \ldots, p\,. \end{cases}$$

Define

$$\widetilde{\mathrm{M}}(\widehat{R}) = \frac{1}{k}\sum_{i=1}^{k} \widehat{R}_i,\ \widetilde{\mathrm{V}}(\widehat{R}) = \frac{1}{k-1}\sum_{i=1}^{k} \left(\widehat{R}_i - \widetilde{\mathrm{M}}(\widehat{R})\right)^2.$$

PROPOSITION 10. *The expected algebraic variance (1) of X' is smaller than the expected algebraic variance of X after an NR DLB step, that is, $\mathrm{E}[\xi^2_{X'}] < \mathrm{E}[\xi^2_X]$, assuming $\widetilde{\mathrm{V}}(\widehat{R}) > 1/4$.*

Proof: Since $R'_i = R_i$ for $i = k+1, \ldots, p$,

$$\begin{aligned} \mathrm{V}(\widehat{R}) - \mathrm{V}(\widehat{R}') &= \frac{1}{p-1}\left\{\sum_{i=1}^{p}\left(\widehat{R}_i\right)^2 - \sum_{i=1}^{p}\left(\widehat{R}'_i\right)^2\right\} \\ &= \frac{1}{p-1}\left\{\sum_{i=1}^{k}\left(\widehat{R}_i\right)^2 - \sum_{i=1}^{k}\left(\widehat{R}'_i\right)^2\right\} \\ &= \frac{k-1}{p-1}\left(\widetilde{\mathrm{V}}(\widehat{R}) - \widetilde{\mathrm{V}}(\widehat{R}')\right). \end{aligned}$$

Proposition 4 provides the algebraic variance of the modified number of jobs after the NR load balancing step, since it is the same as the AR load balancing step for P_i where $i = 1, \ldots, k$.

$$\begin{aligned} \widetilde{\mathrm{V}}(\widehat{R}') &= \frac{1}{k-1}\sum_{i=1}^{k}\left(\widehat{R}'_i - \widetilde{\mathrm{M}}(\widehat{R}')\right)^2 \\ &= \frac{k\,(4b+1) - (2b+1)^2}{4\,k\,(k-1)} \le \frac{1}{4}. \end{aligned}$$

for $0 \le b \le k-1$. Finally the decrease in the expected value of the algebraic variance of the compute times is

$$\mathrm{E}\left[\xi^2_X\right] - \mathrm{E}\left[\xi^2_{X'}\right] \ge \frac{k-1}{p-1}\left(\widetilde{\mathrm{V}}(\widehat{R}) - \frac{1}{4}\right)\mu_T^2.$$

□

PROPOSITION 11. *The expected value of the largest idle time (2) is monotonically decreased after a NR DLB step, that is, $\mathrm{E}\left[Y'_p - Y'_1\right] \le \mathrm{E}\left[Y_p - Y_1\right]$.*

Proof: Before the NR load balancing step the expected maximum imbalance is

$$\mathrm{E}[Y_p] - \mathrm{E}[Y_1] = \mathrm{E}[Y_p] \ge \mathrm{E}[X_p] = \widehat{R}_p\,\mu_T.$$

After the NR load balancing step, the new expected maximum imbalance time is $\mathrm{E}[Y'_p] - \mathrm{E}[Y'_1]$.

Consider the random variables

$$\begin{aligned} Z_{min} &= \min\{X'_1, \cdots, X'_k\}\,, \\ Z_{max} &= \max\{X'_1, \cdots, X'_k\} \le \max\{X_1, \cdots, X_k\} \le Y_p\,, \\ W_{min} &= \min\{X'_{k+1}, \cdots, X'_p\} \ \ge\ Y_1 = 0\,, \\ W_{max} &= \max\{X'_{k+1}, \cdots, X'_p\} \ \le\ Y_p\,. \end{aligned}$$

The smallest and the largest order statistics after NR balancing are $Y'_1 = \min\{Z_{min}, W_{min}\}$ and $Y'_p = \max\{Z_{max}, W_{max}\}$. There are four possible combinations of Y'_1 and Y'_p values:

(1) $Y'_1 = Z_{min}$ and $Y'_p = W_{max}$;
(2) $Y'_1 = W_{min}$ and $Y'_p = W_{max}$;
(3) $Y'_1 = Z_{min}$ and $Y'_p = Z_{max}$;
(4) $Y'_1 = W_{min}$ and $Y'_p = Z_{max}$.

$$\begin{aligned} \text{Case (1)}: &\ \{\mathrm{E}[Y_p] - \mathrm{E}[Y_1]\} - \{\mathrm{E}[Y'_p] - \mathrm{E}[Y'_1]\} \\ &= \{\mathrm{E}[Y_p] - \mathrm{E}[W_{max}]\} + \mathrm{E}[Z_{min}] \ge \mathrm{E}[Z_{min}] \ge 0. \\ \text{Case (2)}: &\ \{\mathrm{E}[Y_p] - \mathrm{E}[Y_1]\} - \{\mathrm{E}[Y'_p] - \mathrm{E}[Y'_1]\} \\ &= \{\mathrm{E}[Y_p] - \mathrm{E}[W_{max}]\} + \mathrm{E}[W_{min}] \ \ge\ 0. \\ \text{Case (3)}: &\ \{\mathrm{E}[Y_p] - \mathrm{E}[Y_1]\} - \{\mathrm{E}[Y'_p] - \mathrm{E}[Y'_1]\} \\ &= \{\mathrm{E}[Y_p] - \mathrm{E}[Z_{max}]\} + \mathrm{E}[Z_{min}] \ \ge\ 0. \\ \text{Case (4)}: &\ \{\mathrm{E}[Y_p] - \mathrm{E}[Y_1]\} - \{\mathrm{E}[Y'_p] - \mathrm{E}[Y'_1]\} \\ &= \{\mathrm{E}[Y_p] - \mathrm{E}[Z_{max}]\} + \mathrm{E}[W_{min}] \ \ge\ 0. \end{aligned}$$

□

PROPOSITION 12. *The expected value of the average idle time (3) does not increase after a NR load balancing step, that is, $\mathrm{E}\left[Y'_p - \eta_{X'}\right] \le \mathrm{E}\left[Y_p - \eta_X\right]$.*

Proof: The decrease in the expected average idle

time is (since $\eta_{X'} = \eta_X$ by Lemma 1)

$$\mathrm{E}\left[Y_p - \eta_X\right] - \mathrm{E}\left[Y'_p - \eta_{X'}\right] = \mathrm{E}\left[Y_p\right] - \mathrm{E}\left[Y'_p\right] \ .$$

From the proof of Proposition 11,

$$Y'_p = \max\{Z_{max}, W_{max}\} \leq Y_p.$$

Therefore,

$$\mathrm{E}\left[Y_p\right] - \mathrm{E}\left[Y'_p\right] \geq 0.$$

□

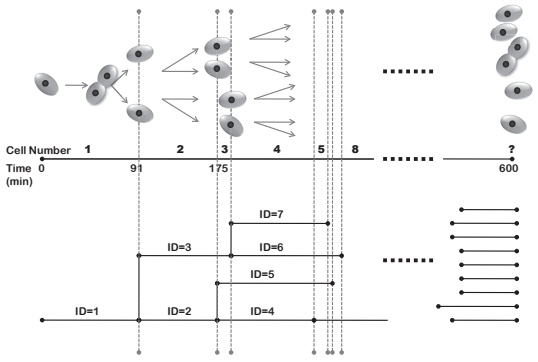


Fig. 4. Multistage cell cycle tracking diagram. ID is the cell identification tag. Cell modeling simulations should be executed beginning at each cell emergence time.

5 Theoretical and Experimental Results

This section provides theoretical and experimental load balancing results with the budding yeast cell cycle model. To evaluate the proposed load balancing algorithms, the ensemble of simulations is executed on Virginia Tech's System X supercomputer [32]. The supercomputer has 1,100 Apple PowerMac G5 nodes, with dual 2.3 GHz PowerPC 970FX processors and 4GB memory.

5.1 Cell Cycle Simulations

5.1.1 The Stochastic Simulation Algorithm (SSA)

Consider a biochemical system or pathway that involves N molecular species $S_1, \ldots, S_N$. $X_i(t)$ denotes the number of molecules of species S_i at time t. Stochastic simulations generate the evolution of the state vector $X(t) = (X_1(t), ..., X_N(t))$ given that the system was initially in the state vector $X(t_0)$. Suppose the system is composed of M reaction channels R_1, $\ldots$, R_M. In a constant volume Ω, assume that the system is well-stirred and in thermal equilibrium at some constant temperature. There are two important entities in reaction channel R_j: the state change vector $\nu_{\cdot j} = (\nu_{1j}, ..., \nu_{Nj})$, and the propensity function a_j. ν_{ij} is defined as the change in the S_i molecules' population caused by one R_j reaction. $a_j(x)dt$ gives the probability that one R_j reaction will occur in the next infinitesimal time interval $[t, t + dt)$.

The SSA simulates every reaction event [33]. $X(t) = x$, $p(\tau, j|x, t)d\tau$ is defined as the probability that the next reaction in the system will occur in the infinitesimal time interval $[t+\tau, t+\tau+d\tau)$, and will be an R_j reaction. By letting $a_0(x) \equiv \sum_{j=1}^{M} a_j(x)$, the equation

$$p(\tau, j|x, t) = a_j(x) \exp(-a_0(x)\tau)$$

can be obtained. A Monte Carlo method is used to generate τ and j. On each step of the SSA, random numbers r_1 and r_2 are generated from the uniform (0,1) distribution. From probability theory, the time for the next reaction to occur is given by $t + \tau$, where

$$\tau = (1/a_0(\mathbf{x})) \ln(1/r_1).$$

The next reaction index j is given by the smallest integer satisfying

$$\sum_{j'=1}^{j} a_{j'}(x) > r_2 a_0(x).$$

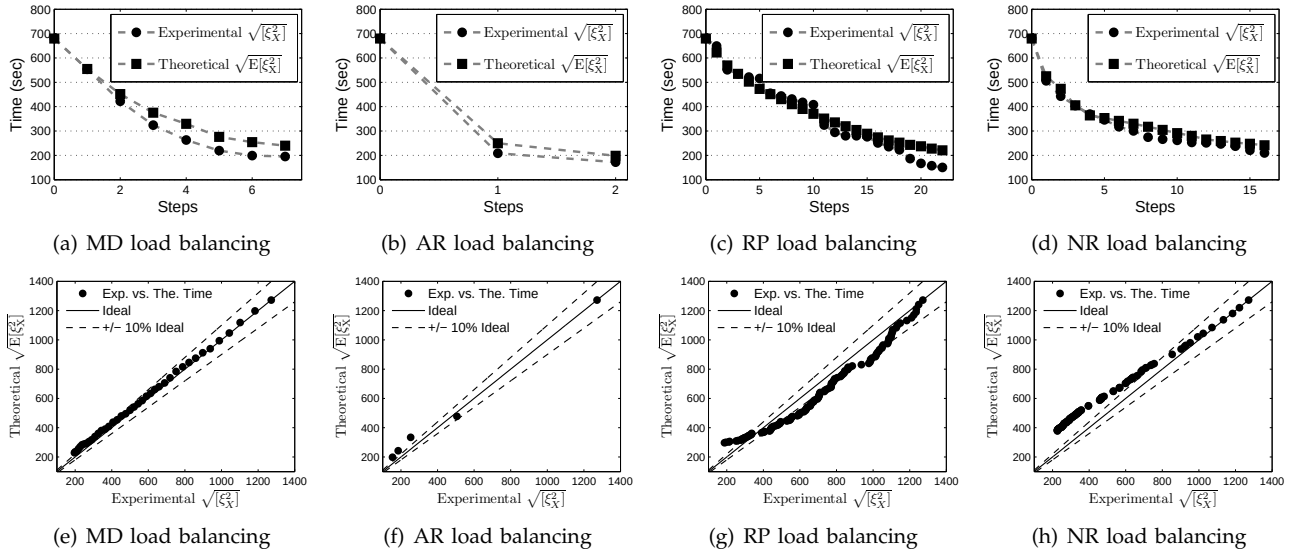
After τ and j are obtained, the system states are updated by $X(t+\tau) := x+\nu_j$, and the time is updated by $t := t+\tau$. This simulation proceeds iteratively until the time t reaches its termination value.

It is clear from the stochastic nature of the system that a different simulation of the same cell over the same interval (using a different seed for the pseudo-random number generator) will involve a different number of reactions, and therefore will require a different compute time.

5.1.2 The Budding Yeast Cell Cycle Model

The cycle of cell growth, DNA synthesis, mitosis, and cell division is the fundamental process by which cells grow, develop, and reproduce. The molecular machinery of eukaryotic cell cycle control is known in more detail for budding yeast, *Saccharomyces cerevisiae*, than for any other organism. Therefore, the unicellular budding yeast is an excellent organism for which to study cell cycle regulation.

We have implemented a stochastic model for the budding yeast cell cycle [34], [35] based on the original model of Chen et al. [36]. Gillespie's SSA [33] is executed on the cell cycle model. To accurately mimic the experimental protocol, we choose cells from a specific distribution of initial conditions, and simulate all of their progeny. Existing stochastic simulators based on the Gillespie's SSA treat one system with one initial molecular state vector. To simulate all of the progeny, whose initial states are different, multicycle cell lineage tracking is needed, as illustrated in Fig. 4. Biologists are interested in the number of cells in existence at a specific final time. The algorithm for the multistage cell cycle implementation is described in detail in [37].



(a) MD load balancing (b) AR load balancing (c) RP load balancing (d) NR load balancing

(e) MD load balancing (f) AR load balancing (g) RP load balancing (h) NR load balancing

Fig. 5. Numerical comparison of the experimental RAV to the theoretical root expected algebraic variance of compute times across the processors for the four load balancing algorithms. 1,000 runs with 25 processors for (a)–(d) and 10,000 runs with 100 processors for (e)–(h).

5.2 Numerical Evaluation of Static Distribution

To assess how well the theoretical estimates of load imbalance metrics agree with the simulation results, consider the case with $n = 1,000$ cell cycle simulations distributed evenly across $p = 25$ processors, which results in $R = 40$ tasks per processor. To evaluate probabilistic measures the expected maximum CPU time $\mathrm{E}[Y_p]$ and minimum CPU time $\mathrm{E}[Y_1]$ can be calculated in two ways: the integral method (14a)–(14b) and the approximation method (6a)–(6b). $\mathrm{E}[Y_p] = 20,973$ and $\mathrm{E}[Y_1] = 18,075$ calculated from the integral method are similar to the approximation method results of $\mathrm{E}[Y_p] = 20,965$ and $\mathrm{E}[Y_1] = 18,083$. Results from both methods match the experimental results in Table 2.

Probabilistic measures (1)–(3) of load imbalance are the root expected algebraic variance of times across the processors,

$$\sqrt{\mathrm{E}\left[\xi_X^2\right]} = \sqrt{\frac{p}{p-1} \cdot R \cdot \sigma_T^2} \approx 752.65 \text{ seconds},$$

the expected worst case load imbalance,

$$\mathrm{E}[Y_p] - \mathrm{E}[Y_1] \approx 2,898 \text{ seconds},$$

and the expected idle time per processor,

$$\mathrm{E}\left[Y_p - \eta_X\right] \approx 1,449 \text{ seconds}.$$

In the simulation experiment based on 1,000 simulations with fa static distribution over 25 processors, the root algebraic variance of CPU times is 679.83 seconds, the maximum load imbalance $Y_p - Y_1$ is $2,740.42$ seconds, and the average CPU idle time $(1/p)\sum_{i=1}^{p}(Y_p - X_i) = 1,270.75$ seconds. The theoretical probabilistic measures of load imbalance are consistent with the simulation experiment values.

5.3 Numerical Evaluation of Theoretical Analysis for the Dynamic Load Balancing Algorithms

In this section, the approximations employed in the theoretical analysis of the four different dynamic load balancing algorithms are compared to the experimental results numerically. Figures 5 (a)–(d) compare the theoretical root expected algebraic variance of compute times across the processors for each load balancing step to the experimental square root of the algebraic variance (RAV) with $n = 1,000$ tasks on $p = 25$ processors. To investigate in the case of many tasks on many processors, the theoretical and experimental results of $n = 10,000$ tasks on $p = 100$ processors are considered in Figures 5 (e)–(h).

The numerical reduction of the expected algebraic variance of the compute times across the processors before and after a load balancing step is quantified in Propositions 1, 4, 7, and 10 for each load balancing algorithm. In the MD analysis, Proposition 1 provides that the numerical root expected algebraic variance of the compute times across the processors after a load balancing step that is

$$\sqrt{\mathrm{E}[\xi_{X'}^2]} = \sqrt{\mathrm{E}[\xi_X^2] - \frac{R_p\left(R_p - 1\right)}{2\left(p-1\right)}\mu_T^2}.$$

In the AR analysis, Proposition 4 provides that

$$\sqrt{\mathrm{E}[\xi_{X'}^2]} = \sqrt{\mathrm{E}[\xi_X^2] - \left(\mathrm{V}(\widehat{R}) - \mathrm{V}(\widehat{R}')\right)\mu_T^2}$$

where

$$\mathrm{V}(\widehat{R}') = \frac{p\left(4b+1\right) - \left(2b+1\right)^2}{4\,p\left(p-1\right)}.$$

TABLE 1
Experimental and theoretical RAV (square root of the algebraic variance) of compute times across the processors for the four load balancing algorithms. Units are seconds.

	1,000 Runs (25 processors)				10,000 Runs (100 processors)			
Metrics	MD	AR	RP	NR	MD	AR	RP	NR
Experimental RAV of compute times	195.14	172.22	150.32	209.96	195.85	153.77	187.45	226.68
Theoretical $\sqrt{\xi_X^2}$ of compute times	239.98	198.32	220.53	241.37	229.01	198.24	297.26	378.27

In the RP analysis, Proposition 7 provides that

$$\sqrt{\mathrm{E}[\xi_{X'}^2]} = \sqrt{\mathrm{E}[\xi_X^2] - \frac{(\mathrm{M}(R))^2 - \mathrm{M}(R) + \mathrm{V}(R)}{2(p-1)}\mu_T^2}.$$

In the NR analysis, Proposition 10 provides that

$$\sqrt{\mathrm{E}[\xi_{X'}^2]} = \sqrt{\mathrm{E}[\xi_X^2] - \frac{k-1}{p-1}\left(\widetilde{\mathrm{V}}(\widehat{R}) - \widetilde{\mathrm{V}}(\widehat{R}')\right)\mu_T^2}$$

where

$$\widetilde{\mathrm{V}}(\widehat{R}') = \frac{k\,(4b+1) - (2b+1)^2}{4\,k\,(k-1)}.$$

Figure 5 shows that the variance decreases consistently on each iteration as predicted by the theory for all load balancing cases. Table 1 shows the final root expected algebraic variance of the compute times versus experimental root of the algebraic variance across the processors. As expected, the theoretical values are larger than experimental results since the theory provides upper bounds for the metric (1).

5.4 Load Balancing Results for Wild-Type Yeast

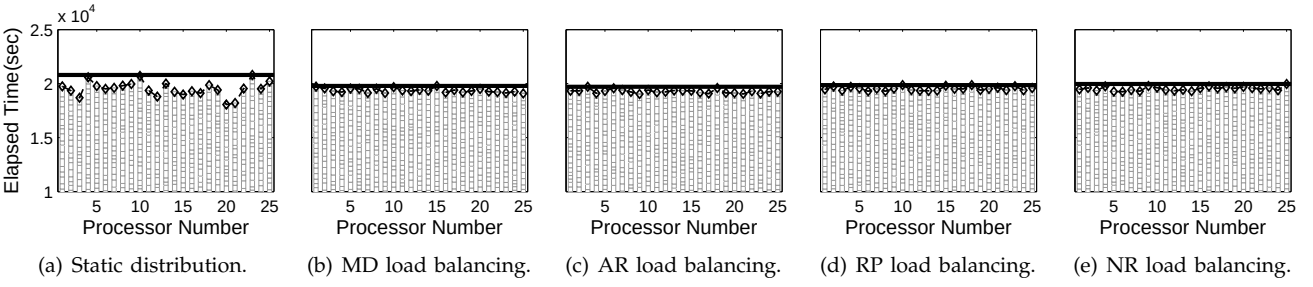
This section describes load balancing results for the wild-type budding yeast cell cycle model. Fig. 6 compares the processor CPU times and wall clock time using the no DLB, MD, AR, RP, and NR DLB algorithms. 1,000 simulations with 25 processors and 10,000 simulations with 100 processors are executed for this experiment. With the static distribution (no load balancing), the variance of the CPU times is not huge because wild-type cells divide in a relatively regular fashion. The simulation time is just affected by the stochastic nature of the SSA. Nevertheless, the four dynamic load balancing methods reduce the wall clock time compared to the static method; the differences are approximately 1,000 seconds (4.9% of static distribution wall clock time) for 1,000 runs with 25 processors, and 2,800 seconds (5.4% of static distribution wall clock time) for 10,000 runs with 100 processors.

Table 2 demonstrates the efficiency of the four dynamic load balancing algorithms clearly. The average idle CPU times (3) for the no-balancing simulation are 1271 seconds for 1,000 runs with 25 processors and 3170 seconds for 10,000 runs with 100 processors. Therefore, the average idle CPU time has increased a lot with the increasing number of jobs per processor. The average idle CPU times for the load balancing algorithms, however, increases little with the number of jobs per processor. For the MD load balancing simulation, the average idle times are 419 seconds for 1,000 runs with 25 processors and 511 seconds for 10,000 runs with 100 processors. For the AR load balancing simulation, the average idle times are 432 seconds for 1,000 runs with 25 processors and 374 seconds for 10,000 runs with 100 processors. For the RP load balancing simulation, the average idle times are 321 seconds for 1,000 runs with 25 processors and 421 seconds for 10,000 runs with 100 processors. For the NR load balancing simulation, the average idle times are 352 seconds for 1,000 runs with 25 processors and 536 seconds for 10,000 runs with 100 processors. Fig. 7 compares the average idle CPU times for the static and four DLB algorithms. For wild-type yeast simulations, the dynamic load balancing algorithms have eliminated approximately two thirds of the idle time for 25 processors (from 6.5% of the total CPU time down to 2% of the total CPU time), and roughly 85% for the 100 processor experiment (from 7% of the total CPU time down to 1% of the total CPU time).

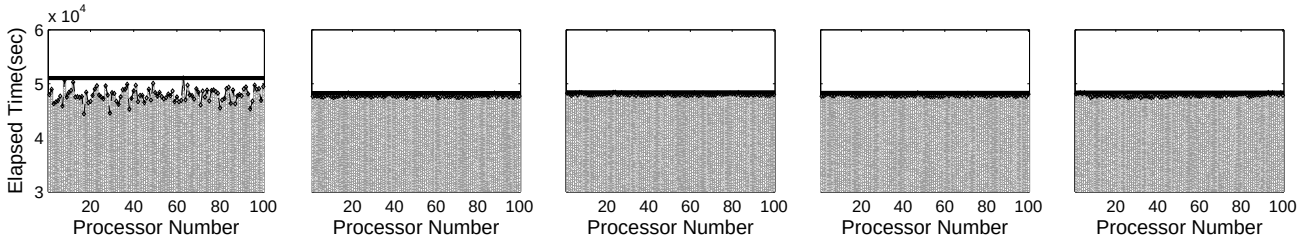
The communication time for the load balancing methods should be considered. The total communication times for the four dynamic load balancing algorithms are approximately 0.2 seconds for 1,000 runs with 25 processors and 1.0 second for 10,000 runs with 100 processors. Therefore, the total communication time for the load balancing is negligible compared to elapsed wall clock time. The centralized and decentralized DLB algorithms have similar performance for these simulations without considering scalability. Both of the load balancing strategies reduce system resource demands for the wild-type cell cycle simulation.

5.5 Load Balancing Results for Mutant Yeast

This section presents experimental results for a prototype budding yeast mutant cell cycle model. For the mutant strain considered, the initial cell might never divide at all or it might divide several times and then cease division [36]. Therefore, the CPU time to simulate such a mutant cell varies, even if the end time of the simulation is fixed. For these simulations, the four dynamic load balancing algorithms show huge advantages in CPU utilization.



(a) Static distribution. (b) MD load balancing. (c) AR load balancing. (d) RP load balancing. (e) NR load balancing.



(f) Static distribution. (g) MD load balancing. (h) AR load balancing. (i) RP load balancing. (j) NR load balancing.

Fig. 6. Elapsed compute times per processor (diamond marker) and wall clock time (solid line) for wild-type multistage cell cycle simulations. 1,000 runs with 25 processors for (a)–(e) and 10,000 runs with 100 processors for (f)–(j). Small grey rectangular height represents each job time for the processor.

TABLE 2
Average, maximum, minimum, RAV (square root of the algebraic variance) of compute times, maximum idle time, and average (percentage) idle time for wild-type cell simulations. The static and the four proposed load balancing approaches are compared by results from both a small and a large ensemble. Units are seconds.

	1,000 Runs (25 processors)					10,000 Runs (100 processors)				
Metrics	Static	MD	AR	RP	NR	Static	MD	AR	RP	NR
Avg compute time	19524	19362	19277	19515	19578	47880	47778	48039	47991	48020
Max compute time	20795	19781	19709	19836	19931	51050	48289	48413	48412	48556
Min compute time	18055	19084	19033	19254	19175	44431	47354	47802	47725	47643
RAV of compute times	680	195	172	150	210	1272	196	154	187	227
Max idle time	2740	697	676	582	756	6619	935	611	687	914
Avg idle time	1271	419	432	321	352	3170	511	374	421	536
Percentage idle time	6.5%	2.2%	2.2%	1.7%	1.8%	6.6%	1.1%	0.8%	0.9%	1.1%

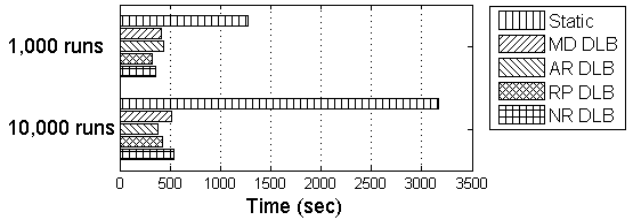


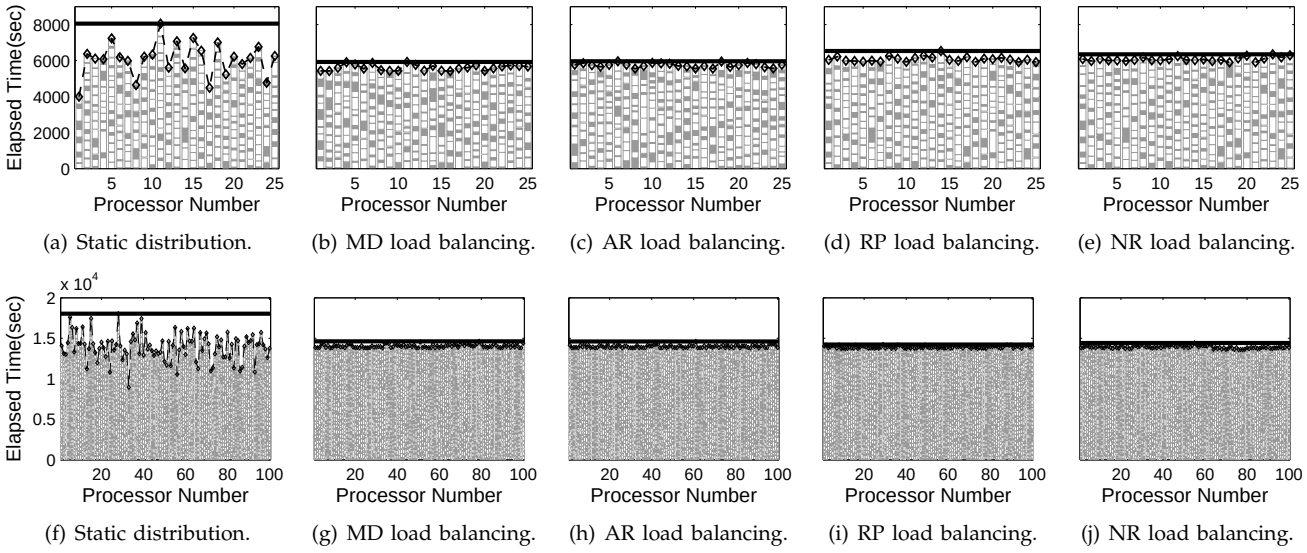
Fig. 7. The average idle CPU times comparison for the static distribution and the final step of the load balancing methods.

Figure 8 shows the overall wall clock times per processor. Figures 8 (a)–(e) show results for 1,000 runs with 25 processors and Figures 8 (f)–(j) show results for 10,000 runs with 100 processors. For the static load balancing case, the variance of compute times is huge because of the characteristics of mutant simulations. The DLB algorithms reduce the wall clock times by approximately 26% for 1,000 runs with 25 processors, and by approximately 21% for 10,000 runs with 100 processors. The four DLB algorithms lead to greater improvements for the mutant than for the wild-type simulation.

Table 3 also shows the improved efficiency of the four DLB algorithms compared to a static method. Statements similar to those for Table 2 can be made about Table 3, but the differences for mutant simulation are considerably more pronounced than for wild-type simulation. Average processor idle time was reduced by 85% or more for each dynamic algorithm and on each ensemble (from 30% of the total CPU time down to only 4% of the total CPU time).

6 Conclusions and Future Work

This paper introduces a new probabilistic framework to analyze the effectiveness of load balancing strategies in the context of large ensembles of stochastic



(a) Static distribution. (b) MD load balancing. (c) AR load balancing. (d) RP load balancing. (e) NR load balancing.

(f) Static distribution. (g) MD load balancing. (h) AR load balancing. (i) RP load balancing. (j) NR load balancing.

Fig. 8. Elapsed compute times per processor (diamond marker) and wall clock time (solid line) of prototype mutant multistage cell cycle simulations. 1,000 runs with 25 processors for (a)–(e) and 10,000 runs with 100 processors for (f)–(j). Small grey rectangular height represents each job time for the processor.

TABLE 3
Average, maximum, minimum, RAV (square root of the algebraic variance) of compute times, maximum idle time, and average (percentage) idle time for mutant cell simulations. The static and the four proposed load balancing approaches are compared by results from both a small and a large ensemble. Units are seconds.

	1,000 Runs (25 processors)					**10,000 Runs (100 processors)**				
Metrics	Static	MD	AR	RP	NR	Static	MD	AR	RP	NR
Avg compute time	6079	5612	5740	6090	6044	13921	14042	13990	13911	13927
Max compute time	8054	5922	5965	6387	6333	18038	14617	14606	14371	14466
Min compute time	3995	5417	5554	5921	5865	8950	13801	13815	13767	13545
RAV of compute times	943	165	118	125	150	1695	193	164	137	229
Max idle compute time	4059	505	411	466	468	9088	815	791	604	921
Avg idle time	1975	310	225	297	289	4117	575	616	460	539
Percentage idle time	32.5%	5.5%	3.9%	4.9%	4.8%	29.6%	4.1%	4.4%	3.3%	3.9%

simulations. Ensemble simulations are employed to estimate the statistics of possible future states of the system, and are widely used in important applications such as climate change and biological modeling. The present work is motivated by stochastic cell cycle modeling, but the proposed analysis framework can be directly applied to any ensemble simulation where many tasks are mapped onto each processor, and where the task compute times vary considerably.

The analysis assumes only that the compute times of individual tasks can be modeled as independent identically distributed random variables. This is a natural assumption for an ensemble computation, where the same model is run repeatedly with different initial conditions and parameter values. No assumption is made about the shape of the underlying probability density; therefore the analysis is widely applicable. The level of load imbalance, as given by well defined metrics, is also a random variable. The analysis focuses on determining the decrease in the expected value of load imbalance after each work redistribution step. The analysis is applied to the proposed four dynamic load balancing strategies. The analysis reveals that the expected level of load imbalance is monotonically decreased after one step of each of the algorithms.

Numerical results support the theoretical analysis. On an ensemble of budding yeast cell cycle simulations, compute times required to simulate each cell cycle progression using Gillespie's algorithm are inherently variable due to the stochastic nature of the model. Dynamic load balancing reduces the total compute (wall clock) times by about 5% for ensembles of wild type cells, and by about 25% for ensembles of mutant cells. Average processor idle time is reduced by 85% or more for ensembles of mutant cells, which have widely varying running times.

Future work will apply the theoretical analysis pro-

posed here to dynamic load balancing algorithms for a cloud environment. Scalability, not investigated here, will also be analyzed in the future. Since the centralized load balancing algorithms are not expected to scale well, the results of our analysis showing global improvements by the local load balancing algorithms in especially significant. Finally, a challenging problem is to analyze load balancing for large ensemble runs with different models, where the i.i.d. assumption does not hold.

ACKNOWLEDGMENTS

This work is supported in part by awards NIGMS /NIH 5 R01 GM078989, AFOSR FA9550–09–1–0153, NSF DMS–0540675, NSF CCF–0916493, and NSF OCI–0904397.

REFERENCES

[1] H. McAdams and A. Arkin, "Stochastic mechanisms in gene expression," *Proc. Natl. Acad. Sci.*, vol. 94, pp. 814–819, 1997.

[2] J. Murphy, D. Sexton, D. Barnett, G. Jones, M. Webb, M. Collins, and D. Stainforth, "Quantification of modelling uncertainties in a large ensemble of climate change simulations," *Nature*, vol. 430, pp. 768–772, 2004.

[3] V. Nefedova, R. Jacob, I. Foster, Z. Liu, Y. Liu, E. Deelman, G. Mehta, M.-H. Su, and K. Vahi, "Automating climate science: large ensemble simulations on the teragrid with the GriPhyN virtual data system," in *Proc. of the Second IEEE Int. Conf. on e-Science and Grid Computing (E-SCIENCE '06)*. Washington, DC, USA: IEEE Computer Society, 2006, pp. 32–37.

[4] W. Chu, L. Holloway, M.-T. Lan, and K. Efe, "Task allocation in distributed data processing," *Computer*, vol. 13, no. 11, pp. 57–69, 1980.

[5] M. Iqbal, J. Saltz, and S. Bokhari, "A comparative analysis of static and dynamic load balancing strategies," *ACM Performance Evaluation Revision*, vol. 11, no. 1, pp. 1040–1047, 1985.

[6] D. Bertsekas and J. Tsitsiklis, *Parallel and Distributed Computation: Numerical Methods*. Upper Saddle River, NJ, USA: Prentice-Hall, Inc., 1989.

[7] B. Lester, *The Art of Parallel Programming*. Upper Saddle River, NJ, USA: Prentice-Hall, Inc., 1993.

[8] J. Jacob and S.-Y. Lee, "Task spreading and shrinking on a network of workstations with various edge classes," in *Proc. 1996 Int'l Conf. Parallel Processing*, vol. 3, 1996, pp. 174–181.

[9] C. Polychronopoulos and D. Kuck, "Guided self-scheduling: A practical scheduling scheme for parallel supercomputers," *IEEE Trans. on Computers*, vol. 36, pp. 1425–1439, December 1987.

[10] L. Flynn and S. Hummel, "The mathematical foundations of the factoring scheduling method," IBM Research Report RC18462, Tech. Rep., Oct 1992.

[11] S. Hummel, E. Schonberg, and L. Flynn, "Factoring: a practical and robust method for scheduling parallel loops," *Comm. of the ACM*, vol. 35, no. 8, pp. 90–101, 1992.

[12] L. Rudolph, M. Slivkin-Allalouf, and E. Upfal, "A simple load balancing scheme for task allocation in parallel machines," in *Proc. of Sym. on Parallel Algorithms and Architectures*, ser. SPAA '91. New York, NY, USA: ACM, 1991, pp. 237–245.

[13] R. Karp and Y. Zhang, "Randomized parallel algorithms for backtrack search and branch-and-bound computation," *Journal of the ACM*, vol. 40, pp. 765–789, July 1993.

[14] R. Blumofe and C. Leiserson, "Scheduling multithreaded computations by work stealing," in *Proc. of Ann. Symp. on Foundations of Computer Science*, Nov 1994, pp. 356–368.

[15] A. Grama, G. Karypis, V. Kumar, and A. Gupta, *Introduction to Parallel Computing*, 2nd ed. Boston, MA, USA: Addison-Wesley, 2002.

[16] B. Wilkinson and M. Allen, *Parallel Programming: Techniques and Applications Using Networked Workstations and Parallel Computers*, 2nd ed. Upper Saddle River, NJ, USA: Prentice-Hall, Inc., 2004.

[17] E. Dijkstra and C. Scholten, "Termination detection for diffusing computations," *Information Processing Letters*, vol. 11, no. 1, pp. 1–4, 1980.

[18] N. Shavit and N. Francez, "A new approach to detection of locally indicative stability," in *Proceedings of the 13th International Colloquium on Automata, Languages and Programming, ICALP '86*. London, UK: Springer-Verlag, 1986, pp. 344–358. [Online]. Available: http://portal.acm.org/citation.cfm?id=646240.683532

[19] C. Z. Xu and F. C. M. Lau, "Analysis of the generalized dimension exchange method for dynamic load balancing," *Journal of Parallel and Distributed Computing*, vol. 16, no. 4, pp. 385–393, 1992.

[20] K. Mehrotra, S. Ranka, and J.-C. Wang, "A probabilistic analysis of a locality maintaining load balancing algorithm," in *Proc. 7th International Parallel Processing Symposium*. IEEE Computer Society Press, 1993, pp. 369–373.

[21] P. Sanders, "A detailed analysis of random polling dynamic load balancing," in *Proc. Int. Symposium on Parallel Architectures, Algorithms and Networks*, dec 1994, pp. 382–389.

[22] S. Hummel, J. Schmidt, R. Uma, and J. Wein, "Load-sharing in heterogeneous systems via weighted factoring," in *Proc. ACM symposium on Parallel Algorithms and Architectures*. New York, NY, USA: ACM, 1996, pp. 318–328.

[23] H. David and H. Nagaraja, *Order Statistics*, 2nd ed. Hoboken, NJ, USA: Wiley-Interscience, 2003.

[24] S. Tayal, "Tasks scheduling optimization for the cloud computing system," *Int. J. of Advanced Engineering Sciences and Technologies*, vol. 5, pp. 111–115, 2011.

[25] Apache Hadoop. [Online]. Available: {http://hadoop.apache.org/}

[26] C. Powley, C. Ferguson, and R. Korf, "Depth-first heuristic search on a SIMD machine," *Artif. Intell.*, vol. 60, no. 2, pp. 199–242, 1993.

[27] W. Hillis, *The Connection Machine*. Cambridge, MA, USA: MIT Press, 1986.

[28] G. Cybenko, "Dynamic load balancing for distributed memory multiprocessors," *J. Parallel Distrib. Comput.*, vol. 7, pp. 279–301, October 1989. [Online]. Available: http://dl.acm.org/citation.cfm?id=67279.67283

[29] J. Rice, *Mathematical Statistics and Data Analysis*, 3rd ed. Belmont, CA, USA: Duxbury Press, 2001.

[30] K. Trivedi, *Probability and Statistics with Reliability, Queueing, and Computer Science Applications*, 2nd ed. Hoboken, NJ, USA: Wiley-Interscience, 2001.

[31] C.-C. Chen and C. Tyler, "Accurate approximation to the extreme order statistics of gaussian samples," *Communications in Statistics - Simulation and Computation*, vol. 28, no. 1, pp. 177–188, 1999.

[32] System X Supercomputer. [Online]. Available: {http://www.arc.vt.edu/arc/SystemX/}

[33] D. Gillespie, "Exact stochastic simulation of coupled chemical reactions," *Journal of Physical Chemistry*, vol. 81, no. 25, pp. 2340–2361, 1977.

[34] P. Wang, R. Randhawa, C. Shaffer, Y. Cao, and W. Baumann, "Converting macromolecular regulatory models from deterministic to stochastic formulation," in *Proceedings of the 2008 Spring Simulation Multiconference (SpringSim'08), High Performance Computing Symposium (HPC-2008)*. San Diego, CA, USA: Society for Computer Simulation International, 2008, pp. 385–392.

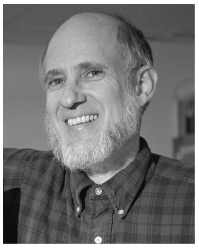
[35] T.-H. Ahn, L. Watson, Y. Cao, C. Shaffer, and W. Baumann, "Cell cycle modeling for budding yeast with stochastic simulation algorithms," *Computer Modeling Engrg. Sci.*, vol. 51, no. 1, pp. 27–52, 2009.

[36] K. Chen, L. Calzone, A. Csikasz-Nagy, F. Cross, B. Novak, and J. Tyson, "Integrative analysis of cell cycle control in budding yeast," *Mol. Biol. Cell*, vol. 15, no. 8, pp. 3841–3862, 2004.

[37] D. Ball, T.-H. Ahn, P. Wang, K. Chen, Y. Cao, J. Tyson, J. Peccoud, and W. Baumann, "Stochastic exit from mitosis in budding yeast: Model predictions and experimental observations," *Cell Cycle*, vol. 10, pp. 999–1099, March 2011.

Tae-Hyuk Ahn is a Ph.D. student in the Department of Computer Science at Virginia Tech. After he received a B.S. in Electrical Engineering from Yonsei University in S. Korea, he worked for Samsung SDS for 4 years. He received his M.S. in Electrical and Computer Engineering from Northwestern University. His current research interests are computational biology, numerical analysis, and parallel computing.

Adrian Sandu obtained the Diploma in Electrical Engineering – Control Systems from the Technical University Bucharest, Romania, M.S. in Computer Science and Ph.D. in Applied Mathematical and Computational Sciences from the University of Iowa. Between 1998–2003 he served as a faculty in the Department of Computer Science at Michigan Tech. In 2003 he joined Virginia Tech's Department of Computer Science. Sandu's research interests are in the area of computational science and engineering.



Layne T. Watson received the B.A. degree (magna cum laude) in psychology and mathematics from the University of Evansville, Indiana, in 1969, and the Ph.D. degree in mathematics from the University of Michigan, Ann Arbor, in 1974. He is a professor of computer science and mathematics at Virginia Tech. His research interests include fluid dynamics, solid mechanics, numerical analysis, optimization, parallel computation, mathematical software, image processing, and bioinformatics. He is a fellow of the IEEE, the National Institute of Aerospace, and the International Society of Intelligent Biological Medicine.

Clifford A. Shaffer received the PhD degree from the University of Maryland. He is a professor in the Department of Computer Science at Virginia Tech. His current research interests include problem-solving environments, bioinformatics, component architectures, visualization, algorithm design and analysis, and data structures. He is a senior member of the IEEE.

Yang Cao received his Ph.D. degree in computer science from the University of California, Santa Barbara in 2003. He is an Assistant Professor in the Computer Science Department at Virginia Tech. His research focuses on the development of multiscale, multiphysics stochastic modeling and simulation methods and tools that help biologists build, simulate and analyze complex biological systems. He has published around 40 refereed journal articles.

William T. Baumann received the B.S, M.S, and Ph.D. degrees in electrical engineering from Lehigh University, the Massachusetts Institute of Technology, and the Johns Hopkins University, respectively. He joined the Bradley Department of Electrical and Computer Engineering at Virginia Tech in 1985 where he is currently an associate professor. His research interests include active structural acoustic control, control of thermoacoustic instabilities, and, most recently, systems biology.