# Abstract

We wish to install a distributed programming environment based upon Hadoop including the new Apache Spark processing engine. This work will serve several purposes. First, we can teach students with hands-on experience of distributed computing. Second, we can support large datasets, and parallelization of suitable algorithms; this includes algorithms for computational medicine. We can provide more extensive support for our statistical calculations (which support biomarker discovery), and carry them out faster, in the distributed programming framework, taking advantage of multiple inexpensive machines. Biomarkers are helpful in medical diagnosis. Kits that test for biomarkers are a possible product suitable for manufacture.

Apache Spark libraries that include SQL, Dataframes, Machine Learning, Graph and Streaming capabilities will provide valuable tools for our research. It’s support of the Scala, Python and R programing languages will better support the algorithms we will be implementing.

# Narrative

## Significance

Non-invasive methods of medical diagnosis have steadily increased over the last 4 decades. The promise of making an accurate diagnosis without surgery and its associated risks, especially in early stages of the disease prior to any symptoms, drives researchers to discover new and less-invasive methods. Examples of this approach include using ultrasound [1] and breathalyzer diagnostics [2].

Incorporating data mining algorithms to large amounts of data can be used by researchers to find patterns that can lead to new non-invasive diagnostics. Using the Hadoop platform, an open source, programming framework that supports the processing and storage of extremely large data sets in a distributed computing environment, has made it possible to incorporate more data into the data mining of bioinformatic data and decrease the time needed to complete the analysis. Halevy and Norvig [19] have make a strong case that the inclusion of large amounts of data improve the quality of the model more effectively than potential improvements in the algorithm used to develop the model.

Instructing students in recent theory and techniques is an important role that we take on as educators. Companies looking for employees with skills in Big Data technologies exist across all industries ranging from business to health care. An article in *Science Magazine*, published June 2014, states that ‘Big data is everywhere, and its influence and practical omnipresence across multiple industries will just continue to grow. For life scientists with expertise and an interest in bioinformatics, computer science, statistics, and related skill sets, the job outlook couldn’t be rosier” [3a]. Across all industries, demand for new hires with Big Data skills has an upward trajectory. According to an article published in *Forbes* *Magazine* in June 2015, “Demand for Computer Analysts with big data expertise increased by 89.9% in the last twelve months” [4a].

Our research proposal has four goals:

* determine the best alternative for a reproducible, distributed processing research platform, examining both local and cloud choices;
* design and provide distributed processing infrastructure for our own research in computational medicine;
* conduct research on biomarkers that is intended to lead to manufacturable test kits, likely with consumables, analogous to home pregnancy tests, or blood sugar testing strips;
* provide distributed processing infrastructure to be used and maintained by the Computer Science department, and made available to the Biomolecular Sciences department for their use and teaching students about distributed algorithms.

2.1.1 A Reproducible, Distributed Processing Research Platform

Choosing a computer environment for scientific research in a small to medium sized university is often a matter of availability. Teaching universities do not have shared computer resources designated for research or the IT support capabilities that a research university would provide. Local computer resources can place restrictive limits on the amount of data and processing needs that can be used in research.

With the advent of inexpensive computers (RPi, Arduino) and cloud-computing services (AWS, Google, Azure), researchers have choices that allow them to build research platforms inexpensively and can help researchers overcome the prior mentioned local environment restrictions. In the case of cloud computing, the researchers are charged only for its use and the cloud provider is responsible for many management issues (hardware upgrades, OS software patches, etc.). Many universities have begun exploring the cloud as a collaborative research platform, often referred to as a science gateway [3] [4]. Cloud platforms have also been used to do distributed public health research [5]. Researchers have also begun to use the Raspberry Pi as a viable research environment. Although much of the research has focused on using the Raspberry Pi as a teaching tool, researchers have explored its use as a Hadoop environment [5][6] and it has been used to do biometric analysis for neonatal identification [7].

Our intent of our research is to determine which of these choices, Raspberry Pi or the cloud, will provide the best big data platform to develop a collaborative research environment that can be used for our biomarker research, as well as for future research. By providing a facility for a science gateway, and making it available to members of the Computer Science and Biomolecular Sciences departments, we hope to increase the visibility of CCSU’s CS department. Conceivably in the future we might extend the availability of this facility more broadly.

The designed platform must have the ability to capture runtime characteristics, including configuration and execution logs, that could be provided for reproducibility.

2.1.2 Use Hadoop Platform to Conduct Research on Cancer Biomarkers

We hope to use this capability to support our research in computational [medicine [AS13,](#_bookmark1) [SK99].](#_bookmark14) Our goal is to support existing projects at the larger scale available with distributed processing, including the search for biomarkers in the relatively restricted contexts of blood tests, urine tests and breath tests. We hope to develop opportunities for commercial activity in the development of these tests, which correspond to manufacturable test kits. Because of the anticipated support for commercial activity, we hope to develop external funding.

Hadoop has been an important tool in bioinformatics research [12] [13]. Other researchers have used cloud providers to develop platforms for doing proteomic analysis [4]. The field of Big Data, although nascent, is a fast-moving area. MapReduce, the original processing engine for Hadoop, has been superseded by a new processing engine, Apache Spark, which due to its more efficient use of memory, has delivered faster turnaround times. Researchers are beginning to apply this new technology to bioinformatic problems [14]. It is also driving the development of Bioinformatic frameworks in Spark to solve genomic processing problems [15]. We plan to use Apache Spark to develop algorithms that support relatively non-invasive diagnostics, including cancer diagnostics.

2.1.3 Cross Department Sharing and Education Benefits

This activity will develop infrastructure for distributed processing, that augments our department’s existing support for cloud computing. We have established coordination with the Biomolecular Sciences department (Professors Martin-Troy and Hoopengardner), regarding a planned graduate specialization in computational support for biomedicine. We hope that this facility will support cooperation between our faculty members. We hope to support existing projects at the larger scale available with distributed processing.

We will also be able to use this infrastructure to educate the students with hands-on experience on algorithms that exploit parallel processing in a distributed mode. Such algorithms include Hadoop’s Map Reduce applied to a gene analysis toolkit [[MHB+10,](#_bookmark10) [Tay10],](#_bookmark18) and work with FASTA and FASTQ files [[FPRCG17]](#_bookmark6) and others [[CGP+](#_bookmark3)16].

We would like to extend our research in the learning of students of computer science about mathematical proofs [[SM13,](#_bookmark15) [SM14,](#_bookmark16) [Smi16]](#_bookmark17) to mathematical proofs about software executing in distributed systems, as are given in Lynch’s Distributed Algorithms [[Lyn](#_bookmark9)96].

### 2.2 Outline of Related Research

2.2.1 Hadoop Platform

Hadoop and its original processing engine, MapReduce, have been very useful tools in bioinformatics [[Tay10,](#_bookmark18) [FPRCG17]](#_bookmark6) and computational medicine [[WLL+](#_bookmark19)11] research. MapReduce has been useful in finding biomarkers in support of survival analysis [Ro[d15].](#_bookmark12) Survival analysis and Hadoop has provided insights useful to both insurance and health care [[BGK+16,](#_bookmark2) [h](#_bookmark7)tt]. Researchers have used survival analysis in development of a test refining a diagnosis of myocardial infarction[APC[+](#_bookmark0)07]. Odom et al. [[KSS+15]](#_bookmark8) developed a breath test for malaria.

However, practitioners have bumped into performance thresholds using MapReduce for particular types of large workloads. These problems involve server resource allocation and overhead due to writing to local disk for intermediate datasets. The resource allocation issue has been documented in bioinformatics research by Dhorte [DSSS15]. Other open source teams have attacked the MapReduce limitations from a broad view. Zaharia [17] has developed a new Big Data processing engine, Apache Spark, that runs within the Hadoop framework and addresses the MapReduce performance issues. It also provides a higher-level programming abstraction which allows developers to build solutions easier with fewer components. Researchers are now looking to Spark as a potential solution to their toughest problems. Mushtaq [9] has developed a Spark framework for cost effective, fast and accurate DNA analysis. Their framework can spread the input data more uniformly across the computational nodes; it can be executed on less expensive nodes (i.e. 16GB of memory) and is 71% faster that previous solutions.

2.2.2 Hadoop and Raspberry PI

Although most of the research around the Raspberry Pi (RPi) has used it as a stand-alone education device, some researchers have begun to explore it as a cluster computing tool that can be used for scientific research. Fox [5] has configured RPIs into a Hadoop cluster and has used it as an inexpensive research platform for students. Lin [6] has used Hadoop, primarily its HDFS and HBASE components, on a Raspberry Pi to build a Web archiving and query tool. Finally, Sumathi [7] has implemented a neonatal identification system on a Raspberry Pi using OpenCV, an open source image processing engine, to compare characteristics of a newborn’s foot and palm print to an image stored in a database.

2.2.3 Research and The Cloud

There are many references in the literature that explore the use of cloud computing for various tasks. We want to present here a few that focus on its use as a research platform and in bioinformatics specifically.

Benchmarking studies provide a good indication of what to expect from a cloud vendor. He [18], noting that cloud computing could provide a more flexible platform for HPC science, completed performance benchmark tests on three cloud platforms. His work made the following recommendations: installing and running benchmarks as part of an implementation before performing research allows you to tune your cloud platform more effectively; and paying attention to your network configuration in the cloud is important to overcome significantly slower network performance that exists in the default network configurations of most cloud providers.

Kalyanam [3] described Purdue’s efforts to cloud-enable their geospatial science gateway. Purdue implemented general-purpose software building blocks (GABBs) that provide geospatial data management, analysis, visualization, and processing capabilities on the Amazon Web Services platform. They found that AWS provided an ideal test-bed for developing these types of packages; it democratized processing by providing computer resources to many collaborators that did not normally have the computer resources; and peripheral software products (OS, libraries) were easy to keep up to date. They used the AWS CloudFormation templates to define the required hardware and software components of their machines.

Schatz [20] presented a paper at the CHI XGen Congress in 2010 describing his efforts to move a genomic sequencing application, CloudBurst, to AWS and Hadoop MapReduce. The new software, christened CrossBow, successfully analyzed an entire human genome for less than $100 in approximately 4 hours. We anticipate that with today’s processors, costs, and Apache Spark it could be for less in a shorter timeframe.

## 2.3 Work Plan

The software infrastructure, a modification of Hadoop, has been developed by Roland DePratti. The plan is to identify machines onto which we can install this software, to make an operating facility. We plan to use machines obtained separately from the grant. T. Smith has some Raspberry Pi machines to offer, on a temporary to-be-returned basis, to the project. Hadoop has been shown by [[pih]](#_bookmark11) to be suitable for Raspberry Pi clusters. Raspberry Pis are small, which implies our need for space to be only a few square feet. Then we plan to install and verify the installation of the modified Hadoop. Then we plan to install software used by the application, including Python and R, which are generally useful packages. We plan to investigate a programmatic interface to Mathematica, as it is said to be installed on the Raspberry Pis. We would like to be able to interoperate Mathematica and R with the modified Hadoop. Then we plan to install software used by the application, a survival analysis package of R, which is more focused in purpose, though of interest to both insurance and medical applications. The biomarker software is in the process of being updated to use Linear Prefix Trees, which require less memory and less time compared to FPGrowth, itself an improvement over the Apriori implementation, this last being already available in R. We expect that the R environment in use in the new platform to be highly similar to the R environment already in use. This similarity should enable easy transitions from the R environments used by individual researchers as they transition work onto the proposed platform. A log of any adjustments will be kept, for use by others. To develop this transition procedure, we might consult with some of the existing users of R in the department of Mathematical Sciences. This will give us experience transitioning from both StatET and RStudio individual environments. Moreover, we expect to maintain a collection of examples of good programming practice, both in R and in parallel programming for our platform.Then we plan to load and execute our first application, which is expected to be the biomarker software, which uses Python and R. This software might be converted into strictly R, if that seems to be desirable. We plan to apply the biomarker software to larger datasets than those to which it has been applied so far; this will be facilitated by the modified Hadoop software. We plan to coordinate this facility’s capabilities with Biomolecular Sciences, to support any interest, they may have in a specialization of software engineering for computational medicine. We plan to coordinate this facility’s capabilities with Biomolecular Sciences, to support any computational facility, they might find useful.

### 3.2.1 Joint proposal individual contributions and level of participation

T. Smith has contributed, on a to-be-returned basis, the initial hardware.

T. Smith intends to devote 50% time in the summer, and over the break between fall and spring semesters, to this activity.

1. DePratti intends to contribute the modified Hadoop software, and to install it on any machines used in the platform.

## 3.3 Outcomes and Reporting

It is certainly our intention to submit the results of our biomarker research to a journal such as BMC Bioinformatics ([https://link.springer.com/journal/](https://link.springer.com/journal/12859) [12859](https://link.springer.com/journal/12859)). This research is related to our previous research [[AS13].](#_bookmark1)

We intend to submit the results of our research in approaches to teaching distributed programming to ICER and Koli Calling, which have accepted our work previously.

# CVs

## CV-TS

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    - 2009 - 2016 PhD student in Computer Science at University of Connecticut, Storrs
    - 2001 – 2010 subcontracted to Federal Aviation Administration (FAA)
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  2. **CV-SC**
  3. **CV-KM**

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## Optional Appendices

1. **proposal review criteria**

* coversheet abstract
* signoff statement
* proposal narrative

# Priorities

## Educational mission

* 1. **Visibility**
  2. **Research stature**