2018-2019 CSU-AAUP FACULTY RESEARCH GRANT

PROPOSAL COVER SHEET

Faculty Rank of Principal Contact:

Last Name: Smith

First Name: Therese

University**:** Central Connecticut State University

Department: Computer Science

Funding Request: $

Is this a Joint Proposal?  Yes  No

If Yes, please fill in information for co-proposers (add separate sheets as necessary):

Name\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ Rank\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ Department\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Name\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ Rank\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ Department\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Is this a Continuation Project?  Yes  No If Yes, you must complete Appendix A.2

E-mail of Principal Contact:       Phone Number of Principal Contact:

Campus Address­­­­­ of Principal Contact:

Please select one disciplinary group category in which this project best fits:

Fine Arts and Humanities Social Sciences, Business and Education

Life and Physical Sciences, Mathematics, Computer Science, Engineering and Technology

Please select one research focus area in which this project best fits:

Creation of new knowledge  Application of disciplinary/multidisciplinary knowledge, methodologies and/or insights  Production of creative works  Research in student learning

Project Title:

# 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.

IRB/IACUC Statement

(If "yes" to either question please see Section 5, p. 3 of the program guidelines)

YES NO

Does your research involve human beings as research subjects?

Does you research involve vertebrate animals?

Sign-Off Statement (To be signed individually by each faculty applicant. Please add separate sheets as needed)

*I hereby acknowledge my understanding that the lack of compliance with the proposal format and other requirements spelled out in the CSU - AAUP Faculty Research Grant Guidelines for the Spring 2018 Competition may result in the proposal being disqualified without review.*

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| Signature of Permanent, Full-Time Faculty |  | Date |

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# 

# 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 [3] 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” [4]. 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” [5].

Our research proposal has four goals:

* determine the best alternative for a reproducible, distributed processing research platform based in the cloud;
* 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 cloud-computing services (AWS, Google, IBM, Azure), researchers have choices that allow them to build research platforms inexpensively and can help researchers overcome the prior mentioned local environment restrictions. Using cloud computing, researchers are charged only for its use and the cloud provider is responsible for the 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 [6] [7]. Cloud platforms have also been used to do distributed public health research [8].

The intent of our research is to determine the best design of a 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 not only have the functionality needed to support biomarker research, but it must also support the ability to capture runtime characteristics, including configuration and execution logs, that would allow for the reproducibility of that research.

**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 [9,](#_bookmark1) 10] 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 [11] [12]. Other researchers have used cloud providers to develop platforms for doing proteomic analysis [7]. 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 [13]. It is also driving the development of Bioinformatic frameworks in Spark to solve genomic processing problems [14]. We plan to use Apache Spark to develop algorithms that support relatively non-invasive diagnostics, including cancer diagnostics.

**2.1.3 Biomarker Research**

\*\*\* Need this section filled in. \*\*\*\*

**2.1.4 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 begun conversations with the Biomolecular Sciences department 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 [[15,](#_bookmark10) [11],](#_bookmark18) and work with FASTA and FASTQ files [[16]](#_bookmark6) and others [17].

We would like to extend our research in the learning of students of computer science about mathematical proofs [[18,](#_bookmark15) [19,](#_bookmark16) [20]](#_bookmark17) to mathematical proofs about software executing in distributed systems, as are given in Lynch’s Distributed Algorithms [21].

### 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 [[11,](#_bookmark18) [16]](#_bookmark6) and computational medicine [22] research. MapReduce has been useful in finding biomarkers in support of survival analysis [[23].](#_bookmark12) Survival analysis and Hadoop has provided insights useful to both insurance and health care [24] [25]. Researchers have used survival analysis in development of a test refining a diagnosis of myocardial infarction [26]. Odom et al. [[27]](#_bookmark8) developed a breath test for malaria.

We use R in our single processor work, and there is an interface between Hadoop

and R [28], named RHIPE. We expect the combination of R-based survival

analysis and Hadoop to remain active, because it has been shown to be useful in marketing on the Internet [29].

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 [30]. Other open source teams have attacked the MapReduce limitations from a broad view. Zaharia [31] 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 [32] 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 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 [33], 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 [6] 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 [34] 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.

**2.2.3 Biomarker Related Research**

\*\*\* Need this section filed in \*\*\*.

## 2.3 Work Plan

## Research participants are Therese Smith (TS), Roland DePratti (RD), and ….

|  |  |  |
| --- | --- | --- |
| Task | Person | Completion |
| Complete Linear Prefix Tree Algorithm | TS |  |
| Identify Required Software Libraries | TS |  |
| Identify SparkR Requirements | RD |  |
| Research AWS Big Data Support | RD |  |
| Install Hadoop Platform and Configuration | RD |  |
| Review R Implmntn with Mathematics Dept | TS |  |
| Complete Platform Checkout with small tests | RD/TS |  |
| Capture/Move Large Data to Cluster | TS/RD |  |
| Complete Execution of Experimental Runs | TS/RD |  |
| Document Platform Configuration | RD |  |
| Document Experimental Findings | TS |  |
| Present Findings | TS/RD |  |

\*\* The following section is the original writeup that I translated to the table above. After confirmation, we can delete it. \*\*\*

The software infrastructure, a modification of Hadoop, has been developed by Roland DePratti. The plan is to identify a cloud platform hardware onto which we can install this software, to make an operating facility. 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 platform. 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 Proposed Budget

## \*\*\* we need to complete this section

2018-2019 CSU - AAUP Faculty Research Grant

|  |  |  |
| --- | --- | --- |
| Budget Item | Amount  (No Cents) | Brief Justification |
| Faculty Stipend |  |  |
| Support Services \* |  |  |
| Supplies and Equipment |  |  |
| Travel |  |  |
| Total |  | N/A |

\* For definition see Section 9.4 of the “Collective Bargaining Agreement between Connecticut State University, American Association of University Professors and Board of Regents for Connecticut State Colleges & Universities System, August 26, 2016 – August 26, 2021”, Section 9.4, pp. 56-57.

Note: This Budget Proposal Form enables you to succinctly describe the proposed expenditures, and their adequacy, appropriateness and importance. Please keep in mind that the extent to which a justification for proposed expenditures is provided is incorporated in the scoring used during proposal review. The “Amount” column delineates the requested amounts in whole dollar figures. In the “Brief Justification” column please provide a general for each cost, (e.g., name equipment purchased, provide approximate number of hours and hourly rate for student assistants). In the space below, please provide up to about 100 words of text with further details making a case for the proposed expenditures. In particular, justification for research-related travel is important. Proponents are reminded that each university receives a separate Special Funds travel allocation for this purpose.

## 4. Participant’s CVs

## 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 [[9].](#_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.

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## Optional Appendices

1. **proposal review criteria**

* coversheet abstract
* signoff statement
* proposal narrative

# Priorities

## Educational mission

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