

CSRA, Inc.

Lead Investigator: Bin Hu, Ph.D.

Current Team:

CSRA's Federal Health Program

*Supporting over 115 Projects with 1,600 People -
over 25 Years of support to Federal Health Program*

Unique Qualifications and Capabilities

CSRA is a premier Government services provider with broad expertise in human health and a 19 year old practice in bioinformatics, including extensive support of public health infectious disease diagnostics and surveillance. Our expertise and experience encompasses the full scope of analysis including laboratory method development and execution; high-throughput data analysis and HPC; and scientific data management and application development. Our portfolio of current clients include NIH, CDC, FDA, EPA, and the VA. One of our NIH projects, BRICS, won the 2017 Judges' Choice award for the *Bio-IT World Best Practices* competition; we routinely publish with our clients.

Our capabilities include:

1. Pathogen detection using genomic, phenotypic, biochemical, or mass spectrometry data using MicrobeNet (<http://microbenet.cdc.gov>);
2. Automated bioinformatics for rapid discovery and surveillance of viral and bacterial pathogens;
3. Automated typing of pathogens using genomic information.
4. Experience in agent-based modeling of complex biological systems.
5. Proven record of delivering cross-functional teams composed of both experienced bioinformatics scientists and top-tier software developers;
6. Development of advanced, cloud-based platforms for bioinformatics.
7. Next Generation Sequence data management and analysis.
8. Genotyping and SNP data analysis
9. Development, deployment, and operations of scientific HPC.
10. Reach-back to CSRA's large staff in the Defense and Intelligence sectors.

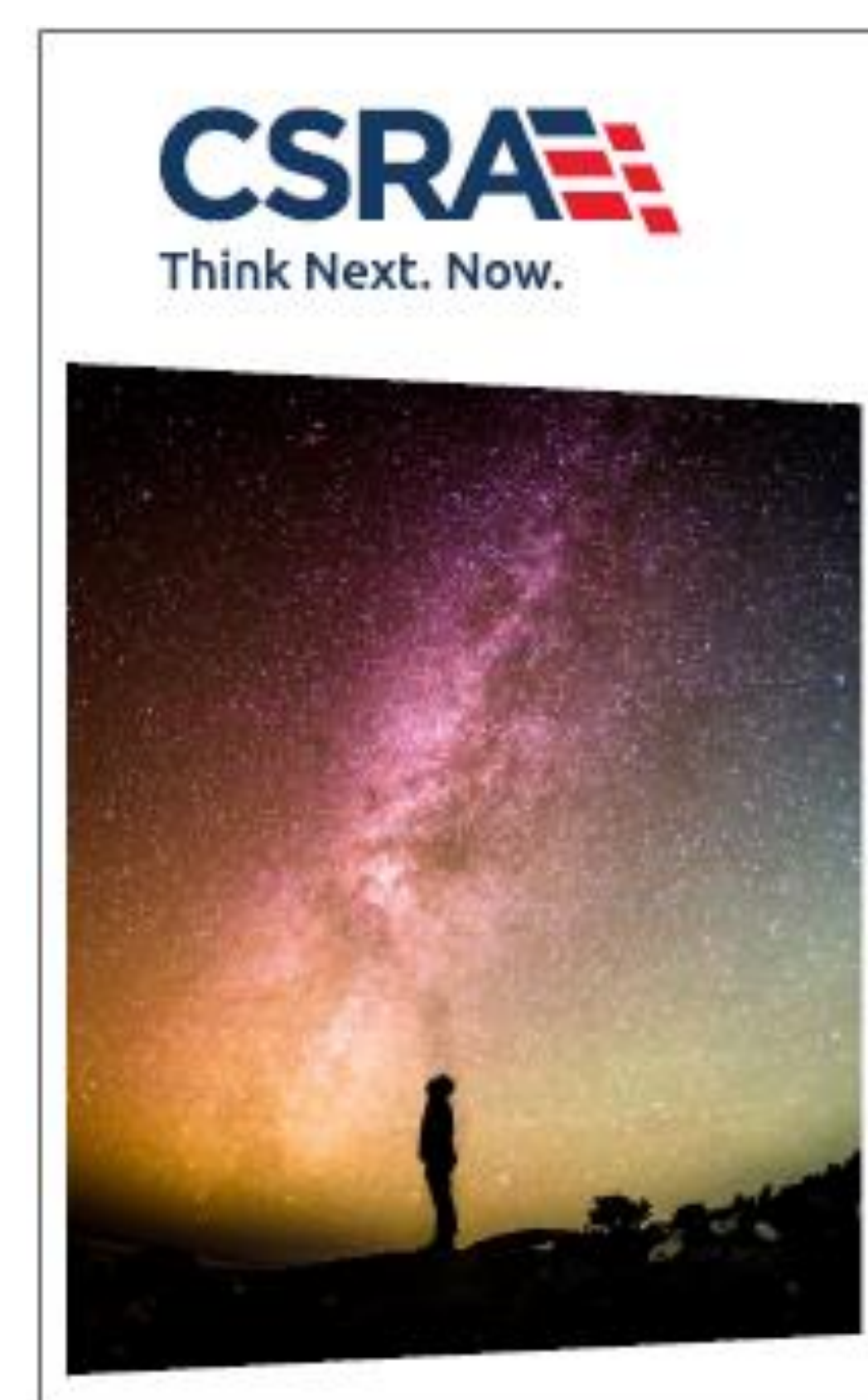
CSRA Seeks Partners/Opportunities in the following areas:

- 1) Pathogenicity;
- 2) Pathogen immunology;
- 3) Pathogen evolution;
- 4) Synthetic biology and genome editing;
- 5) Artificial intelligence and machine learning

Research Areas of Interest

CSRA is interested in novel, high throughput bioinformatics approaches for detection, identification, and classification of naturally evolved and/or human-engineered pathogens. This includes:

- 1) Software platforms that allow rapid pathogen identification, including antimicrobial resistance information, using multi-omics data;
- 2) Metagenomics evaluation of environmental samples to detect pathogens using NGS and other methods;
- 3) Methods for identifying trace molecules associated with artificial genome editing methods;
- 4) *In silico* pathogenicity and virulence evaluation using nucleotide sequence and other data;
- 5) Methods for integrating multi-omics data for pathogen detection;
- 6) Methods for encrypting information using genomes;
- 7) Using mixed computational environments for processing sensitive data;
- 8) Identification of signature sequences from major pathogen labs across the world.
- 9) Methods and platforms to promote wider applicability of genomic signature identification methods for multiple species.



Point of Contact

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