

A collaborative and reproducible approach to large-scale bioinformatics analysis

WHY PARTNER WITH EMMES' BIOINFORMATICS TEAM?

1 What we offer

Start-to-end scalable, reproducible bioinformatics analysis solutions and software development services for bioinformatics workflows.

2 How we work

Collaboration is integral to our success. You'll see this in the way that we listen and offer solutions that are tailored to your project.

3 The result

We provide high quality analysis datasets, comprehensive summary reports, and publication-ready figures and tables.

CLINICAL TRIAL BIOINFORMATICS SERVICES

Our best practice bioinformatics solutions cover:

- Transcriptomics analysis (RNA-Seq, microarrays, and ribosomal profiling)
- Proteomics analysis (LC-MS/MS, iTRAQ, 2D-DIGE, and protein microarrays)
- Metabolomics and lipidomics analysis (LC-MS)
- Metagenomics analysis (WGS and 16S)
- Variant calling (WGS and WES)

We customize analytical modules to your project needs, such as:

- Data normalization, missing value imputation, and batch correction
- Data reduction techniques for visualizing trends in high-dimensional data
- Prediction of treatment, disease, or other outcome-predictive markers
- Identification of functional modules and multi-omics data integration
- Pathway enrichment analysis and color-coded pathway maps

We use state-of-the-art information technologies, including:

- In-house and open-source software to facilitate start-to-end reproducibility
- Cloud computing for reliable data storage and on-demand data analysis
- Virtual machine image technology to maintain software snapshots

WHAT SETS EMMES APART?

- ✓ 40 years of public health experience (we have completed over 2,000 clinical trials conducted in 30,000 sites)
- ✓ Multidisciplinary bioinformatics team that values collaboration, quality, and reproducibility
- ✓ Use of state-of-the-art statistical methodology and information technologies

**Automated processes
to ensure
reproducibility of
your results**

TECHNOLOGY HIGHLIGHT

Our RSEQREP (RNA-Seq Reports) software exemplifies our approach to facilitate start-to-end transcriptomics analysis to characterize gene expression changes in human cells following treatment. Our publication features results for a published RNA-Seq study to characterize transcriptomics changes following influenza vaccination.

Jensen TL, Frasketi M, Conway K, Villarroel L, Hill H, Krampis K, Goll JB. RSEQREP: RNA-Seq Reports, an open-source cloud-enabled framework for reproducible RNA-Seq data processing, analysis, and result reporting. *F1000Research*. 2017 Dec 21;6.

**Analytical solutions
customized for your
clinical trial**

CLINICAL TRIAL ANALYSIS HIGHLIGHT

Our team's bioinformatics analysis capabilities are illustrated by a recent flu vaccine trial. The goal was to better understand how the AS03 vaccine adjuvant enhances human immune responses to the vaccine on the molecular level by measuring changes in thousands of white blood cell molecules simultaneously over time. We used scalable cloud resources for analyzing two terabytes of raw data generated by transcriptomics (RNA-Seq) and proteomics (iTRAQ) technologies. Together these analyses provided evidence that AS03 administered with H5N1 avian flu vaccine stimulated subsets of white blood cells to increase expression of genes and proteins that improve uptake and processing of antigens.

Galassie AC, Goll JB, Samir P, Jensen TL, Hoek KL, Howard LM, Allos TM, Niu X, Gordy LE, Creech C, Hill H. Proteomics show antigen presentation processes in human immune cells after AS03-H5N1 vaccination. *Proteomics*. 2017 Jun 17.

Howard LM, Hoek KL, Goll JB, Samir P, Galassie A, Allos TM, Niu X, Gordy LE, Creech CB, Prasad N, Jensen TL. Cell-based systems biology analysis of human AS03-adjuvanted H5N1 avian influenza vaccine responses: a phase I randomized controlled trial. *PLoS one*. 2017 Jan 18;12(1):e0167488.

Emmes at a Glance

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We collaborate with our clients to produce valued, trusted scientific research. Our team members at Emmes are passionate about making a difference in the quality of human health, and we have supported more than a thousand studies across a diverse range of diseases since our formation in 1977. Our research is contributing to a healthier world.