

Mark Ziemann PhD

2023-05-10

 @mdziemmann

 0000-0002-7688-6974

 <https://github.com/markziemmann>

Breadth of expertise in bioinformatics analyses & specific strengths

Capabilities:

- Unix shell
- R
- Big data
- HPC/Cloud
- Containers
- “Soft” skills

1. Collaborative analyses

NGS analysis¹
Epigenomics &
Transcriptomics²

**Integrative
multi-omics³**

Pathway analysis⁴
Phylogenetics &
molecular evolution⁵

Diabetes⁶

Epilepsy⁷

Perioperative care⁸

Cardiovascular
disease⁹

Plant/microbial
genomics¹⁰

2. Bioinformatics infrastructure

Mass RNA-seq
reprocessing¹¹

Bioconductor
multi-contrast
enrichment package¹²

Galaxy tool factory¹³

3. Research methodology and rigour

Enrichment analysis¹⁴

Software/pipeline
evaluations¹⁵

Spreadsheets¹⁶

Bibliography

1. Pirola L, Balcerczyk A, Tothill RW, et al. Genome-wide analysis distinguishes hyperglycemia regulated epigenetic signatures of primary vascular cells. *Genome Res* 2011; 21: 1601–1615.
2. Kobow K, Kaspi A, Harikrishnan KN, et al. Deep sequencing reveals increased DNA methylation in chronic rat epilepsy. *Acta Neuropathol* 2013; 126: 741–756.
3. Sim CB, Ziemann M, Kaspi A, et al. Dynamic changes in the cardiac methylome during postnatal development. *FASEB J* 2015; 29: 1329–1343.
4. Felisbino MB, Ziemann M, Khurana I, et al. Valproic acid influences the expression of genes implicated with hyperglycaemia-induced complement and coagulation pathways. *Sci Rep* 2021; 11: 2163.
5. Ziemann M, Bhawe M, Zachgo S. Origin and diversification of land plant CC-type glutaredoxins. *Genome Biol Evol* 2009; 1: 265–277.
6. Khurana I, Kaipananickal H, Maxwell S, et al. Reduced methylation correlates with diabetic nephropathy risk in type 1 diabetes. *J Clin Invest*; 133. 2023. DOI: 10.1172/JCI160959.
7. Kobow K, Ziemann M, Kaipananickal H, et al. Genomic DNA methylation distinguishes subtypes of human focal cortical dysplasia. *Epilepsia* 2019; 60: 1091–1103.
8. Bain CR, Ziemann M, Kaspi A, et al. DNA methylation patterns from peripheral blood separate coronary artery disease patients with and without heart failure. *ESC Heart Fail* 2020; 7: 2468–2478.
9. Marques FZ, Nelson E, Chu P-Y, et al. High-fiber diet and acetate supplementation change the gut Microbiota and prevent the development of hypertension and heart failure in hypertensive mice. *Circulation* 2017; 135: 964–977.
10. Nejat N, Cahill DM, Vadamalai G, et al. Transcriptomics-based analysis using RNA-Seq of the coconut (*Cocos nucifera*) leaf in response to yellow decline phytoplasma infection. *Mol Genet Genomics* 2015; 290: 1899–1910.
11. Ziemann M, Kaspi A, El-Osta A. Digital expression explorer 2: a repository of uniformly processed RNA sequencing data. *Gigascience*; 8. 2019. DOI: 10.1093/gigascience/giz022.
12. Kaspi A, Ziemann M. Mitch: Multi-contrast pathway enrichment for multi-omics and single-cell profiling data. *BMC Genomics* 2020; 21: 447.
13. Lazarus R, Kaspi A, Ziemann M, et al. Creating reusable tools from scripts: the Galaxy Tool Factory. *Bioinformatics* 2012; 28: 3139–3140.
14. Wijesooriya K, Jadaan SA, Perera KL, et al. Urgent need for consistent standards in functional enrichment analysis. *PLoS Comput Biol* 2022; 18: e1009935.
15. Ziemann M, Kaspi A, El-Osta A. Evaluation of microRNA alignment techniques. *RNA* 2016; 22: 1120–1138.
16. Ziemann M, Eren Y, El-Osta A. Gene name errors are widespread in the scientific literature. *Genome Biol*; 17. 2016. DOI: 10.1186/s13059-016-1044-7.

Specific strengths

- Depth of knowledge in omics
- Ability to pick up new things
- Teaching & training
- Patience & persistence

Methylomic and transcriptomic characterization of postoperative systemic inflammatory dysregulation

Chris R. Bain^{1,2,3}, Paul S. Myles^{2,3}, Rachael Taylor¹, Hugh Trahair¹, Yin Peng Lee⁴, Larry Croft⁴, Philip J. Peyton⁵, Thomas Painter⁶, Matthew T.V. Chan⁷, Sophie Wallace^{2,3}, Tomás Corcoran^{8,9}, Andrew D. Shaw^{10,11}, Eldho Paul¹², Mark Ziemann^{4,13}, Kiyomet Bozaoglu^{1,14}

Show more

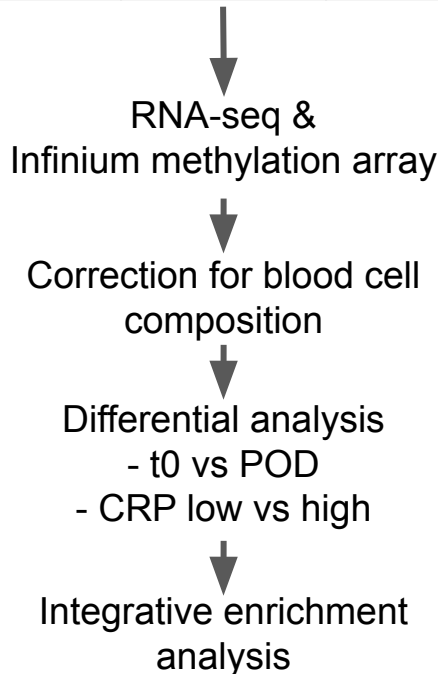
+ Add to Mendeley Share Cite

<https://doi.org/10.1016/j.trsl.2022.04.004>

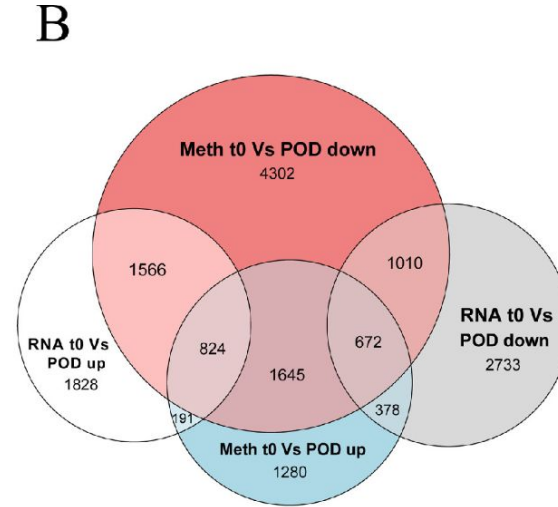
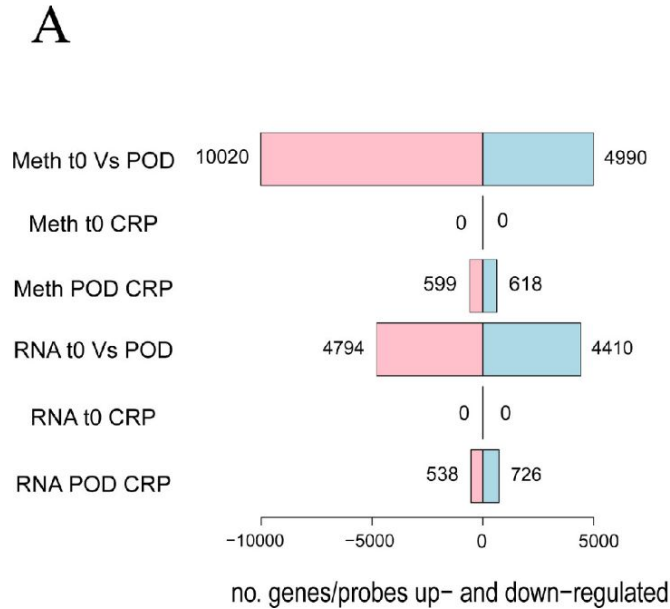
Get rights and content

In this study, we define and validate a state of postoperative systemic inflammatory dysregulation (PSID) based on postoperative phenotypic extremes of plasma C-reactive protein concentration following major abdominal surgery. PSID manifested clinically with significantly higher rates of sepsis, complications, longer hospital stays and poorer short, and long-term outcomes. We hypothesized that PSID will be associated with, and potentially predicted by, altered patterns of genome-wide peripheral blood mononuclear cell differential DNA methylation and gene expression. We identified altered DNA methylation and differential gene expression in specific immune and metabolic pathways during PSID. Our findings suggest that dysregulation results in, or from, dramatic changes in differential DNA methylation and highlights potential targets for early detection and treatment. The combination of altered DNA methylation and gene expression suggests that dysregulation is mediated at multiple levels within specific gene sets and hence, nonspecific anti-inflammatory treatments such as corticosteroids alone are unlikely to represent an effective therapeutic strategy.

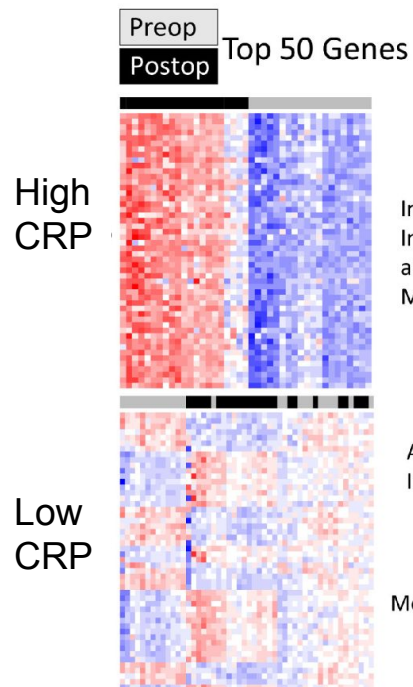
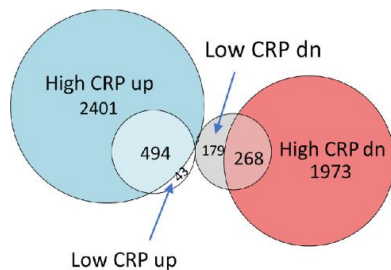
	Baseline (t0)	Post-op (POD)
Low CRP	25	25
High CRP	21	21



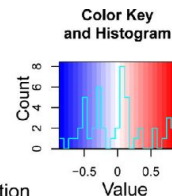
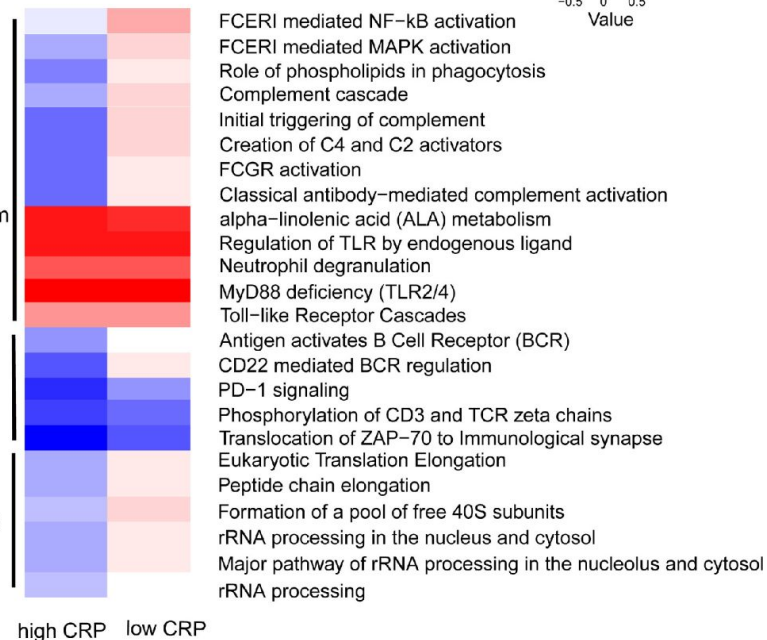
Expression and methylation differences observed during abdominal surgery



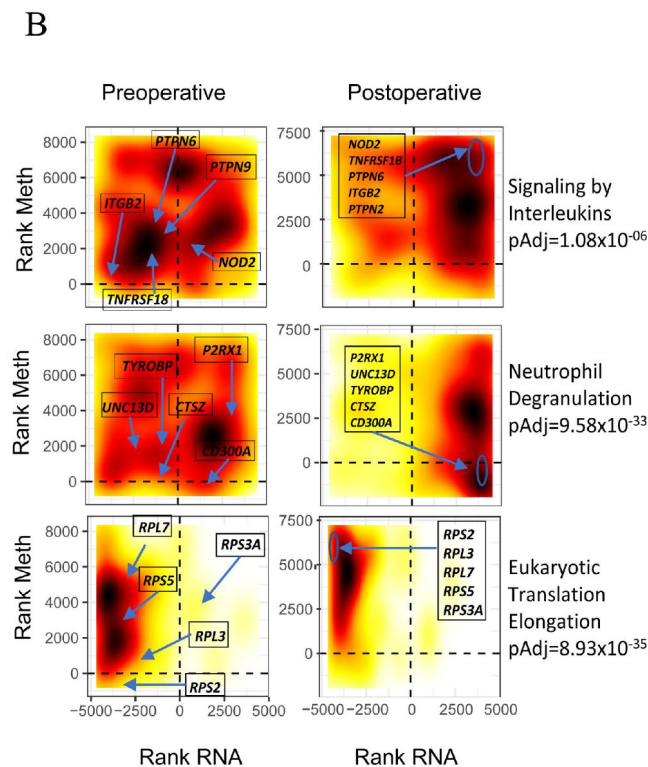
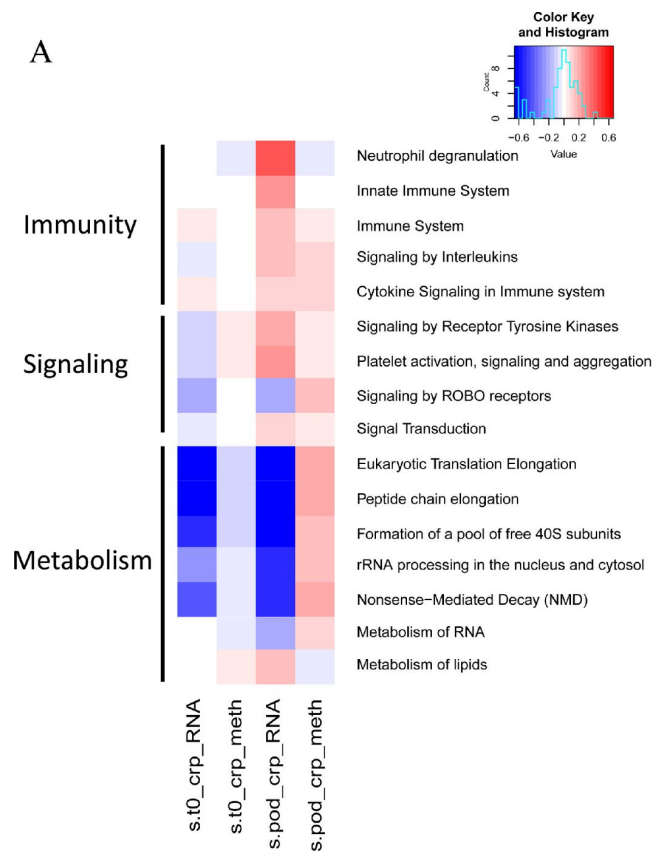
Transcriptome analysis - t0 vs POD



C



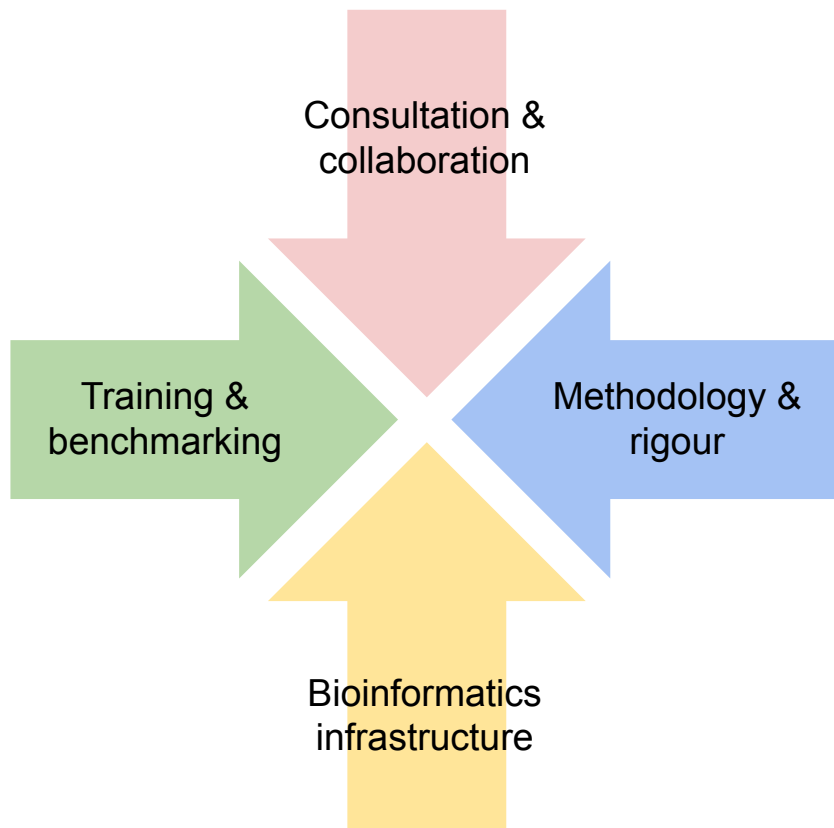
Integrated multi-omics enrichment analysis - CRP low vs high



Outcome and impact

- Confirmed and further resolved genes regulated by major surgery
- First comprehensive analysis of perioperative DNA methylation
- First formal description of PSID, with corresponding genes and pathways
- New directions for drug development and patient management

Building a community of practice in bioinformatics



Key priorities

- Consult, scope needs and identify strengths & weaknesses
- Collaboration, service, dissemination
- Enable existing staff & students
 - eResearch training
 - Regular user group sessions
 - Troubleshooting slack group
 - Setting up common protocols & infrastructure
- Tap into existing networks and resources, eg: ABACBS, Australian BioCommons
- Recruit into specialist growth interest areas, eg: ML, single cell. Recognise diverse backgrounds and skill sets

Thanks for your attention

Copy of slides for future reference:



 @mdziemmann

 0000-0002-7688-6974

 <https://github.com/markziemmann>