

# Stanford

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## Aaron Newman

Assistant Professor of Biomedical Data Science

Department of Biomedical Data Science

### CONTACT INFORMATION

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### Bio

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### ACADEMIC APPOINTMENTS

- Assistant Professor, Department of Biomedical Data Science
- Member, Bio-X
- Member, Institute for Stem Cell Biology and Regenerative Medicine
- Member, Stanford Cancer Institute

### HONORS AND AWARDS

- Interdisciplinary Initiatives Seed Grants Program Award, Stanford Bio-X (2018)
- Stem Cell Research Award, Stinehart/Reed Foundation (2017)
- K99/R00 Pathway to Independence Award, NIH/NCI (2015 - Pres)
- Visionary Postdoctoral Fellowship, Dept. of Defense (2012 - 2015)
- NIH T32 Cancer Biology Training Grant, Stanford University (2012)
- Siebel Fellow, The Siebel Stem Cell Institute (Stanford/UC Berkeley) (2011-2015)
- Graduate Dissertation Fellowship Award, UCSB (2009)

### BOARDS, ADVISORY COMMITTEES, PROFESSIONAL ORGANIZATIONS

- Member, International Society for Computational Biology (ISCB) (2008 - present)
- Associate Member, American Association for Cancer Research (AACR) (2012 - present)

### PROFESSIONAL EDUCATION

- PhD, University of California, Santa Barbara , Biomolecular Science and Engineering Program (2010)

### LINKS

- Newman Lab: <http://newmanlab.stanford.edu>

## Research & Scholarship

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### CURRENT RESEARCH AND SCHOLARLY INTERESTS

Our group combines computational and experimental techniques to study the cellular organization of complex tissues, with a focus on determining the phenotypic diversity and clinical significance of tumor cell subsets. Although our research cuts across disciplinary boundaries, we specialize in the development of robust computational strategies to address key questions in the cancer genomics field, with an emphasis on clinical translation of our findings into novel biomarkers and individualized therapies.

As a member of the Department of Biomedical Data Science and the Institute for Stem Cell Biology and Regenerative Medicine, and as an affiliate of graduate programs in Biomedical Informatics, Cancer Biology, and Immunology, we are also interested in the development of impactful biomedical data science tools in areas beyond our immediate research focus, including developmental biology, regenerative medicine, and systems immunology.

## Teaching

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### STANFORD ADVISEES

#### Postdoctoral Faculty Sponsor

Farshad Farshidfar, Milad Rafiee Vahid

#### Postdoctoral Research Mentor

Farshad Farshidfar, Chloe Steen

### GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biomedical Informatics (Phd Program)
- Cancer Biology (Phd Program)
- Immunology (Phd Program)
- Stem Cell Biology and Regenerative Medicine (Phd Program)

## Publications

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### PUBLICATIONS

- **Determining cell type abundance and expression from bulk tissues with digital cytometry.** *Nature biotechnology*  
Newman, A. M., Steen, C. B., Liu, C. L., Gentles, A. J., Chaudhuri, A. A., Scherer, F., Khodadoust, M. S., Esfahani, M. S., Luca, B. A., Steiner, D., Diehn, M., Alizadeh, A. A.  
2019
- **Integrated digital error suppression for improved detection of circulating tumor DNA** *NATURE BIOTECHNOLOGY*  
Newman, A. M., Lovejoy, A. F., Klass, D. M., Kurtz, D. M., Chabon, J. J., Scherer, F., Stehr, H., Liu, C., Bratman, S. V., Say, C., Zhou, L., Carter, J. N., West, et al  
2016
- **Robust enumeration of cell subsets from tissue expression profiles** *NATURE METHODS*  
Newman, A. M., Liu, C., Green, M. R., Gentles, A. J., Feng, W., Xu, Y., Hoang, C. D., Diehn, M., Alizadeh, A. A.  
2015
- **The prognostic landscape of genes and infiltrating immune cells across human cancers** *NATURE MEDICINE*  
Gentles, A. J., Newman, A. M. (co-first author), Liu, C., Bratman, S. V., Feng, W., Nair, V. S., Xu, Y., Khuong, A., Hoang, C. D., Diehn, M., West, R. B., Plevritis, S. K., Alizadeh, et al  
2015
- **An ultrasensitive method for quantitating circulating tumor DNA with broad patient coverage** *NATURE MEDICINE*

- Newman, A. M., Bratman, S. V., To, J., Wynne, J. F., Eclov, N. C., Modlin, L. A., Liu, C. L., Neal, J. W., Wakelee, H. A., Merritt, R. E., Shrager, J. B., Loo, B. W., Alizadeh, et al  
2014; 20 (5): 552-558
- **Identification of a colonial chordate histocompatibility gene** *SCIENCE*  
Voskoboinik, A., Newman, A. M. (co-first author), Corey, D. M., Sahoo, D., Pushkarev, D., et al  
2013; 341 (6144): 384-387
  - **Lab-Specific Gene Expression Signatures in Pluripotent Stem Cells** *CELL STEM CELL*  
Newman, A. M., Cooper, J. B.  
2010; 7 (2): 258-262
  - **Dynamic Risk Profiling Using Serial Tumor Biomarkers for Personalized Outcome Prediction.** *Cell*  
Kurtz, D. M., Esfahani, M. S., Scherer, F., Soo, J., Jin, M. C., Liu, C. L., Newman, A. M., Duhresen, U., Huttmann, A., Casasnovas, O., Westin, J. R., Ritgen, M., Bottcher, et al  
2019
  - **A functional subset of CD8+ T cells during chronic exhaustion is defined by SIRPalpha expression.** *Nature communications*  
Myers, L. M., Tal, M. C., Torrez Dulgeroff, L. B., Carmody, A. B., Messer, R. J., Gulati, G., Yiu, Y. Y., Staron, M. M., Angel, C. L., Sinha, R., Markovic, M., Pham, E. A., Fram, et al  
2019; 10 (1): 794
  - **Reply to J. Wang et al.** *Journal of clinical oncology : official journal of the American Society of Clinical Oncology*  
Kurtz, D. M., Scherer, F., Jin, M. C., Soo, J., Craig, A. F., Esfahani, M. S., Chabon, J. J., Stehr, H., Liu, C. L., Tibshirani, R., Maeda, L. S., Gupta, N. K., Khodadoust, et al  
2019: JCO1801907
  - **Computational approaches for characterizing the tumor immune microenvironment.** *Immunology*  
Liu, C. C., Steen, C. B., Newman, A. M.  
2019
  - **Method of Isolating and Transplanting the Hematopoietic Stem Cell with Its Microenvironment Which Improves Functional Hematopoietic Engraftment**  
Borrelli, M. R., Lopez, M., Gulati, G., Murphy, M. P., Sinha, R., Longaker, M. T., Weissman, I. L., Newman, A. M., Chan, C. K., Sokol, J.  
ELSEVIER SCIENCE INC.2018: E224
  - **Circulating tumor DNA (ctDNA) in B-cell lymphoma**  
Scherer, F., Kurtz, D. M., Newman, A. M., Stehr, H., Craig, A. M., Esfahani, M. S., Lovejoy, A. F., Chabon, J. J., Klass, D. M., Green, M. R., Liu, C. L., Zhou, L., Glover, et al  
WILEY.2018: 16-17
  - **Circulating Tumor DNA Measurements As Early Outcome Predictors in Diffuse Large B-Cell Lymphoma.** *Journal of clinical oncology : official journal of the American Society of Clinical Oncology*  
Kurtz, D. M., Scherer, F., Jin, M. C., Soo, J., Craig, A. F., Esfahani, M. S., Chabon, J. J., Stehr, H., Liu, C. L., Tibshirani, R., Maeda, L. S., Gupta, N. K., Khodadoust, et al  
2018: JCO2018785246
  - **Circulating Tumor DNA Quantitation for Early Response Assessment of Immune Checkpoint Inhibitors for Metastatic Non-Small Cell Lung Cancer**  
Chaudhuri, A. A., Nabet, B. Y., Merriott, D. J., Jin, M., Chen, E. L., Chabon, J. J., Newman, A. M., Stehr, H., Say, C., Carter, J. N., Walters, S., Becker, H., Das, et al  
ELSEVIER SCIENCE INC.2018: E1-E2
  - **Complex mammalian-like haematopoietic system found in a colonial chordate.** *Nature*  
Rosental, B., Kowarsky, M., Seita, J., Corey, D. M., Ishizuka, K. J., Palmeri, K. J., Chen, S. Y., Sinha, R., Okamoto, J., Mantalas, G., Manni, L., Raveh, T., Clarke, et al  
2018
  - **Circulating tumor DNA levels correlate with response to treatment in LMS patients**  
Przybyl, J., Chabon, J. J., Spans, L., Ganjoo, K., Vennam, S., Newman, A. M., Forgo, E., Varma, S., Zhu, S., Debiec-Rychter, M., Alizadeh, A., Diehn, M., van de Rijn, et al  
AMER ASSOC CANCER RESEARCH.2018: 38-39

- **Combination approach for detecting different types of alterations in circulating tumor DNA in leiomyosarcoma.** *Clinical cancer research : an official journal of the American Association for Cancer Research*  
Przybyl, J., Chabon, J. J., Spans, L., Ganjoo, K., Vennam, S., Newman, A. M., Forgó, E., Varma, S., Zhu, S., Debiec-Rychter, M., Alizadeh, A. A., Diehn, M., van de Rijn, et al  
2018
- **Genomic feature selection by coverage design optimization** *Journal of Applied Statistics*  
Reid, S., Newman, A. M., Diehn, M., Alizadeh, A. A., Tibshirani, R.  
2018
- **Early B cell changes predict autoimmunity following combination immune checkpoint blockade.** *The Journal of clinical investigation*  
Das, R., Bar, N., Ferreira, M., Newman, A. M., Zhang, L., Bailur, J. K., Bacchiocchi, A., Kluger, H., Wei, W., Halaban, R., Sznol, M., Dhodapkar, M. V., Dhodapkar, et al  
2018
- **Profiling Tumor Infiltrating Immune Cells with CIBERSORT.** *Methods in molecular biology (Clifton, N.J.)*  
Chen, B., Khodadoust, M. S., Liu, C. L., Newman, A. M., Alizadeh, A. A.  
2018; 1711: 243–59
- **Macrophage infiltration and genetic landscape of undifferentiated uterine sarcomas.** *JCI insight*  
Przybyl, J., Kowalewska, M., Quattrone, A., Dewaele, B., Vanspauwen, V., Varma, S., Vennam, S., Newman, A. M., Swierniak, M., Bakula-Zalewska, E., Siedlecki, J. A., Bidzinski, M., Cools, et al  
2017; 2 (11)
- **Antigen presentation profiling reveals recognition of lymphoma immunoglobulin neoantigens** *NATURE*  
Khodadoust, M. S., Olsson, N., Wagar, L. E., Haabeth, O. A., Chen, B., Swaminathan, K., Rawson, K., Liu, C. L., Steiner, D., Lund, P., Rao, S., Zhang, L., Marceau, et al  
2017; 543 (7647): 723-?
- **Data normalization considerations for digital tumor dissection.** *Genome biology*  
Newman, A. M., Gentles, A. J., Liu, C. L., Diehn, M., Alizadeh, A. A.  
2017; 18 (1): 128
- **Targeted chromatin ligation, a robust epigenetic profiling technique for small cell numbers.** *Nucleic acids research*  
Zarnegar, M. A., Reinitz, F., Newman, A. M., Clarke, M. F.  
2017; 45 (17): e153
- **Early detection of molecular residual disease in localized lung cancer by circulating tumor DNA profiling.** *Cancer discovery*  
Chaudhuri, A. A., Chabon, J. J., Lovejoy, A. F., Newman, A. M., Stehr, H., Azad, T. D., Khodadoust, M. S., Esfahani, M. S., Liu, C. L., Zhou, L., Scherer, F., Kurtz, D. M., Say, et al  
2017
- **Distinct biological subtypes and patterns of genome evolution in lymphoma revealed by circulating tumor DNA** *SCIENCE TRANSLATIONAL MEDICINE*  
Scherer, F., Kurtz, D. M., Newman, A. M., Stehr, H., Craig, A. F., Esfahani, M. S., Lovejoy, A. F., Chabon, J. J., Klass, D. M., Liu, C. L., Zhou, L., Glover, C., Visser, et al  
2016; 8 (364)
- **Role of KEAP1/NRF2 and TP53 Mutations in Lung Squamous Cell Carcinoma Development and Radiation Resistance.** *Cancer discovery*  
Jeong, Y., Hoang, N. T., Lovejoy, A., Stehr, H., Newman, A. M., Gentles, A. J., Kong, W., Truong, D., Martin, S., Chaudhuri, A., Heiser, D., Zhou, L., Say, et al  
2016
- **High-throughput genomic profiling of tumor-infiltrating leukocytes.** *Current opinion in immunology*  
Newman, A. M., Alizadeh, A. A.  
2016; 41: 77-84
- **Circulating tumour DNA profiling reveals heterogeneity of EGFR inhibitor resistance mechanisms in lung cancer patients** *NATURE COMMUNICATIONS*  
Chabon, J. J., Simmons, A. D., Lovejoy, A. F., Esfahani, M. S., Newman, A. M., Haringsma, H. J., Kurtz, D. M., Stehr, H., Scherer, F., Karlovich, C. A., Harding, T. C., Durkin, K. A., Otterson, et al  
2016; 7

- **Identification of tumorigenic cells and therapeutic targets in pancreatic neuroendocrine tumors** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Krampitz, G. W., George, B. M., Willingham, S. B., Volkmer, J., Weiskopf, K., Jahchan, N., Newman, A. M., Sahoo, D., Zemek, A. J., Yanovsky, R. L., Nguyen, J. K., Schnorr, P. J., Mazur, et al  
2016; 113 (16): 4464-4469
- **Skin fibrosis. Identification and isolation of a dermal lineage with intrinsic fibrogenic potential.** *Science*  
Rinkevich, Y., Walmsley, G. G., Hu, M. S., Maan, Z. N., Newman, A. M., Drukker, M., Januszkyk, M., Krampitz, G. W., Gurtner, G. C., Lorenz, H. P., Weissman, I. L., Longaker, M. T.  
2015; 348 (6232)
- **Potential clinical utility of ultrasensitive circulating tumor DNA detection with CAPP-Seq.** *Expert review of molecular diagnostics*  
Bratman, S. V., Newman, A. M., Alizadeh, A. A., Diehn, M.  
2015: 1–5
- **Large-Scale and Comprehensive Immune Profiling and Functional Analysis of Normal Human Aging.** *PloS one*  
Whiting, C. C., Siebert, J., Newman, A. M., Du, H., Alizadeh, A. A., Goronzy, J., Weyand, C. M., Krishnan, E., Fathman, C. G., Maecker, H. T.  
2015; 10 (7)
- **In Vivo clonal analysis reveals lineage-restricted progenitor characteristics in Mammalian kidney development, maintenance, and regeneration.** *Cell reports*  
Rinkevich, Y., Montoro, D. T., Contreras-Trujillo, H., Harari-Steinberg, O., Newman, A. M., Tsai, J. M., Lim, X., Van-Amerongen, R., Bowman, A., Januszkyk, M., Pleniceanu, O., Nusse, R., Longaker, et al  
2014; 7 (4): 1270-1283
- **Efficient Selection of Biomining DNA Aptamers Using Deep Sequencing and Population Clustering** *ACS Nano*  
Bawazer, L. A., Newman, A. M. (co-first author) , Gu, Q., Ibish, A., Arcila, M., Cooper, J. B., Meldrum, F., Morse, D. E.  
2014; 8 (1): 387-395
- **FACTERA: a practical method for the discovery of genomic rearrangements at breakpoint resolution** *BIOINFORMATICS*  
Newman, A. M., Bratman, S. V., Stehr, H., Lee, L. J., Liu, C., Diehn, M., Alizadeh, A. A.  
2014
- **Identifying Stem Cell Gene Expression Patterns and Phenotypic Networks with AutoSOME.** *Methods in molecular biology (Clifton, N.J.)*  
Newman, A. M., Cooper, J. B.  
2014; 1150: 115-130
- **The genome sequence of the colonial chordate, Botryllus schlosseri.** *eLife*  
Voskoboinik, A., Neff, N. F., Sahoo, D., Newman, A. M., Pushkarev, D., Koh, W., Passarelli, B., Fan, H. C., Mantalas, G. L., Palmeri, K. J., Ishizuka, K. J., Gissi, C., Griggio, et al  
2013; 2
- **Systems-level analysis of age-related macular degeneration reveals global biomarkers and phenotype-specific functional networks** *GENOME MEDICINE*  
Newman, A. M., Gallo, N. B., Hancox, L. S., Miller, N. J., Radeke, C. M., Maloney, M. A., Cooper, J. B., Hageman, G. S., Anderson, D. H., Johnson, L. V., Radeke, M. J.  
2012; 4
- **A proteomic approach for the identification of novel lysine methyltransferase substrates** *EPIGENETICS & CHROMATIN*  
Levy, D., Liu, C. L., Yang, Z., Newman, A. M., Alizadeh, A. A., Utz, P. J., Gozani, O.  
2011; 4
- **Global Analysis of Proline-Rich Tandem Repeat Proteins Reveals Broad Phylogenetic Diversity in Plant Secretomes** *PLOS ONE*  
Newman, A. M., Cooper, J. B.  
2011; 6 (8)
- **clusterMaker: a multi-algorithm clustering plugin for Cytoscape** *BMC BIOINFORMATICS*  
Morris, J. H., Apeltsin, L., Newman, A. M. (co-first author) , Baumbach, J., Wittkop, T., Su, G., Bader, G. D., Ferrin, T. E.  
2011; 12: 436
- **AutoSOME: a clustering method for identifying gene expression modules without prior knowledge of cluster number** *BMC BIOINFORMATICS*  
Newman, A. M., Cooper, J. B.

2010; 11

- **XSTREAM: A practical algorithm for identification and architecture modeling of tandem repeats in protein sequences** *BMC BIOINFORMATICS*  
Newman, A. M., Cooper, J. B.  
2007; 8