

Stanford



Jose Seoane Fernandez

Instructor, Stanford Cancer Institute

Bio

BIO

Throughout my doctoral training, I focused on methods development and application for bioinformatics and machine learning approaches. During my postdoctoral training I contributed to the development of machine learning based approaches and applied them to cardiovascular and cancer genetic data. My current interest are in the development of methods to investigate how different layers of (epi)genomic data can be integrated in order to establish a holistic view of the molecular mechanisms underlying cancer initiation, progression and drug resistance.

ACADEMIC APPOINTMENTS

- Instructor, Stanford Cancer Institute

HONORS AND AWARDS

- Susan G. Komen Postdoctoral Fellowship, The Susan G. Komen Breast Cancer Foundation (June 2016)

PROFESSIONAL EDUCATION

- PhD, University of A Coruna , Computer Science (2012)

Publications

PUBLICATIONS

- **Metabolic Profiling Reveals a Dependency of Human Metastatic Breast Cancer on Mitochondrial Serine and One-Carbon Unit Metabolism.** *Molecular cancer research : MCR*
Li, A. M., Ducker, G. S., Li, Y., Seoane, J. A., Xiao, Y., Melemenidis, S., Zhou, Y., Liu, L., Vanharanta, S., Graves, E. E., Rankin, E. B., Curtis, C., Massague, et al
2020
- **Chromatin state as a mechanism of anthracycline response in breast cancer**
Seoane, J. A., Kirkland, J. G., Caswell-Jin, J. L., Crabtree, G. R., Curtis, C.
AMER ASSOC CANCER RESEARCH.2019
- **Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen** *NATURE COMMUNICATIONS*
Menden, M. P., Wang, D., Mason, M. J., Szalai, B., Bulusu, K. C., Guan, Y., Yu, T., Kang, J., Jeon, M., Wolfinger, R., Nguyen, T., Zaslavskiy, M., Jang, et al
2019; 10: 2674
- **Quantitative evidence for early metastatic seeding in colorectal cancer.** *Nature genetics*
Hu, Z., Ding, J., Ma, Z., Sun, R., Seoane, J. A., Scott Shaffer, J., Suarez, C. J., Berghoff, A. S., Cremolini, C., Falcone, A., Loupakis, F., Birner, P., Preusser, et al
2019
- **Dynamics of breast-cancer relapse reveal late-recurring ER-positive genomic subgroups.** *Nature*
Rueda, O. M., Sammut, S., Seoane, J. A., Chin, S., Caswell-Jin, J. L., Callari, M., Batra, R., Pereira, B., Bruna, A., Ali, H. R., Provenzano, E., Liu, B., Parisien, et al

2019

- **Chromatin regulators mediate anthracycline sensitivity in breast cancer.** *Nature medicine*

Seoane, J. A., Kirkland, J. G., Caswell-Jin, J. L., Crabtree, G. R., Curtis, C.

2019

- **Assessment of ERBB2/HER2 Status in HER2-Equivocal Breast Cancers by FISH and 2013/2014 ASCO-CAP Guidelines.** *JAMA oncology*

Press, M. F., Seoane, J. A., Curtis, C., Quinaux, E., Guzman, R., Sauter, G., Eiermann, W., Mackey, J. R., Robert, N., Pienkowski, T., Crown, J., Martin, M., Valero, et al

2018

- **The DLK1-DIO3 imprinted region regulates long-term proliferation in normal and malignant breast epithelium**

Zabala, M., Lobo, N. A., Seoane, J. A., Stelzer, Y., Luong, A. V., Isobe, T., Zarnegar, M. A., Watanabe, N., Antonana, S., Lam, J., Qian, D., Sikandar, S. S., Kuo, et al

AMER ASSOC CANCER RESEARCH.2018: 95

- **Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas** *CANCER CELL*

Liu, Y., Sethi, N. S., Hinoue, T., Schneider, B. G., Cherniack, A. D., Sanchez-Vega, F., Seoane, J. A., Farshidfar, F., Bowlby, R., Islam, M., Kim, J., Chatila, W., Akbani, et al

2018; 33 (4): 721-+

- **Mapping the in vivo fitness landscape of lung adenocarcinoma tumor suppression in mice** *NATURE GENETICS*

Rogers, Z. N., McFarland, C. D., Winters, I. P., Seoane, J. A., Brady, J. J., Yoon, S., Curtis, C., Petrov, D. A., Winslow, M. M.

2018; 50 (4): 483-+

- **Identification and validation of a novel drug target in an organoid model of esophageal cancer.**

Shukla, N., Salahudeen, A., de la O, S., Hart, D., Taylor, G., Zhu, J., Yuki, K., Seoane, J., Ma, Z., Ding, J., Han, K., Morgens, D., Bassik, et al

AMER SOC CLINICAL ONCOLOGY.2018

- **The chromatin accessibility landscape of primary human cancers.** *Science (New York, N.Y.)*

Corces, M. R., Granja, J. M., Shams, S., Louie, B. H., Seoane, J. A., Zhou, W., Silva, T. C., Groeneveld, C., Wong, C. K., Cho, S. W., Satpathy, A. T., Mumbach, M. R., Hoadley, et al

2018; 362 (6413)

- **Genome co-amplification upregulates a mitotic gene network activity that predicts outcome and response to mitotic protein inhibitors in breast cancer (vol 18, pg 70, 2016)** *BREAST CANCER RESEARCH*

Hu, Z., Mao, J., Curtis, C., Huang, G., Gu, S., Heiser, L., Lenburg, M. E., Korkola, J. E., Bayani, N., Samarajiwa, S., Seoane, J. A., Dane, M. A., Esch, et al

2017; 19: 17

- **Integrated genomic characterization of oesophageal carcinoma** *NATURE*

Kim, J., Bowlby, R., Mungall, A. J., Robertson, A. G., Odze, R. D., Cherniack, A. D., Shih, J., Pedamallu, C. S., Cibulskis, C., Dunford, A., Meier, S. R., Kim, J., Raphael, et al

2017; 541 (7636): 169-?

- **A p53 Super-tumor Suppressor Reveals a Tumor Suppressive p53-Ptpn14-Yap Axis in Pancreatic Cancer.** *Cancer cell*

Mello, S. S., Valente, L. J., Raj, N., Seoane, J. A., Flowers, B. M., McClendon, J., Bieging-Rolett, K. T., Lee, J., Ivanochko, D., Kozak, M. M., Chang, D. T., Longacre, T. A., Koong, et al

2017; 32 (4): 460-73.e6

- **Genome co-amplification upregulates a mitotic gene network activity that predicts outcome and response to mitotic protein inhibitors in breast cancer** *BREAST CANCER RESEARCH*

Hu, Z., Mao, J., Curtis, C., Huang, G., Gu, S., Heiser, L., Lenburg, M. E., Korkola, J. E., Bayani, N., Samarajiwa, S., Seoane, J. A., Dane, M. A., Esch, et al

2016; 18

- **Texture analysis in gel electrophoresis images using an integrative kernel-based approach** *SCIENTIFIC REPORTS*

Fernandez-Lozano, C., Seoane, J. A., Gestal, M., Gaunt, T. R., Dorado, J., Pazos, A., Campbell, C.

2016; 6

- **RRegrs: an R package for computer-aided model selection with multiple regression models** *JOURNAL OF CHEMINFORMATICS*

Tsiliki, G., Munteanu, C. R., Seoane, J. A., Fernandez-Lozano, C., Sarimveis, H., Willighagen, E. L.

2015; 7: 46

- **Texture classification using feature selection and kernel-based techniques** *SOFT COMPUTING*
Fernandez-Lozano, C., Seoane, J. A., Gestal, M., Gaunt, T. R., Dorado, J., Campbell, C.
2015; 19 (9): 2469-2480
- **Canonical Correlation Analysis for Gene-Based Pleiotropy Discovery** *PLOS COMPUTATIONAL BIOLOGY*
Seoane, J. A., Campbell, C., Day, I. M., Casas, J. P., Gaunt, T. R.
2014; 10 (10): e1003876
- **A pathway-based data integration framework for prediction of disease progression** *BIOINFORMATICS*
Seoane, J. A., Day, I. M., Gaunt, T. R., Campbell, C.
2014; 30 (6): 838-45
- **Breast density classification to reduce false positives in CAde systems** *COMPUTER METHODS AND PROGRAMS IN BIOMEDICINE*
Vallez, N., Bueno, G., Deniz, O., Dorado, J., Antonio Seoane, J., Pazos, A., Pastor, C.
2014; 113 (2): 569-84
- **An artificial neural network improves the non-invasive diagnosis of significant fibrosis in HIV/HCV coinfected patients** *JOURNAL OF INFECTION*
Resino, S., Antonio Seoane, J., Maria Bellon, J., Dorado, J., Martin-Sanchez, F., Alvarez, E., Cosin, J., Carlos Lopez, J., Lopez, G., Miralles, P., Berenguer, J.
2011; 62 (1): 77-86