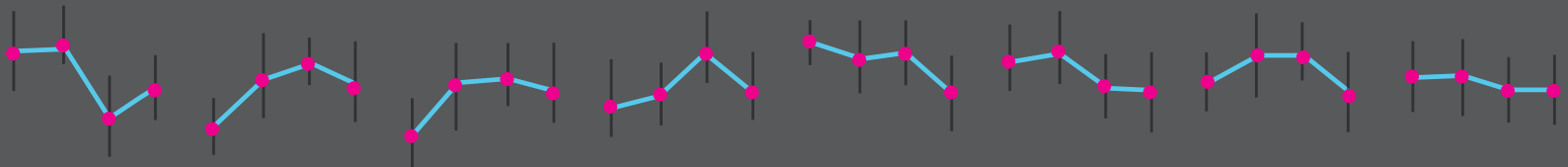


A DAY OF

CREATING EFFECTIVE VISUAL EXPLANATIONS OF CONCEPTS AND DATA IN BIOINFORMATICS

Martin Krzywinski / BC Cancer Genome Sciences Center, Vancouver, Canada

Martin works in bioinformatics, data visualization, science communication and the interface of science and art. He applies design, both data and artistic, to assist discovery, explanation and engagement with scientific data and concepts. His is the creator of Circos and hive plots and his information graphics have appeared in the New York Times, Wired, Scientific American and covers of numerous books and scientific journals such as Nature and Genome Research. He is a co-author of the Nature Methods Points of View and Points of Significance columns.



WEBINAR

Monday, 3 February 2020

12.00–13.00 AEDT

11.00–12.00 AEST 9.00–10.00 AWST

THE ESSENCE OF DATA VISUALIZATION IN BIOINFORMATICS

Explain, do not merely show.

Progress in science requires effective communication—do not leave your audience confused, bored, or uninspired. Using critique by redesign and drawing from published examples in bioinformatics and molecular biology, I will show you how small changes to critical elements can turn a muddled figure into one that is clear and concise. You will learn how to discover, evaluate and create structure in visual explanations by paying attention to the building blocks: salience, continuity, color, type, order, Gestalt and layout. The presentation does not assume familiarity with specific software or specialized bioinformatics knowledge.

REGISTER

www.biocommons.org.au/events/krzywinski

WORKSHOP

Monday, 3 February 2020

14.00–17.00 AEDT

13.00–16.00 AEST 11.00–14.00 AWST

USING CIRCOS IN GALAXY AUSTRALIA

Learn to use Circos through the popular and convenient Galaxy interface.

An introduction to Circos, its applications and use within the Galaxy Australia. This interactive workshop will show you how to select, filter and visualize heterogenous data and create Circos diagrams with line plots, histograms, heatmaps, links and chords using the Galaxy Australia frontend. I will cover practical scenarios such as drawing genome annotations, mutations, alignments and variants. You will also learn how Circos works under the hood to help you add customizations to its configuration and extend use cases explored in the workshop.

REGISTER

www.biocommons.org.au/events/circos2020

The webinar and workshop are independent events. To participate in both, you must register for each separately.