Martin Krzywinski
martink@bcgsc.ca
http://mkweb.bcgsc.ca

Genome Sciences Centre
British Columbia Cancer Agency
100-570 West 7th Avenue
Vancouver, BC, V5Z 4S6, Canada
1.604.877.6000 *x* 673262

Education

1996-1998	M.Sc. (Physics)
1990-1996	B.Sc. (Hon) (Physics-Math)
	B.Sc (Biochemistry)

Employment

2004–	Staff Scientist	
	Canada's Michael Smith Genome Sciences Center	
2002–2004	Bioinformatics Leader	
	Canada's Michael Smith Genome Sciences Center	
1999–2002	System Administrator	
	Canada's Michael Smith Genome Sciences Center	

Research experience

genome and data visualization; physical map analysis; numerical simulation and modelling; network application development; bioinformatics infrastructure design and management

Impact

	all	since 2018
citations	31,001	16,298
h-index	56	45
i10-index	92	76

updated 29 Aug 2023

Publications—Refereed papers

Hallam, S., Kieft, B., Finke, N., McLaughlin, R., Nallan, A., Krzywinski, M. & Crowe, S. Genome-resolved correlation mapping links microbial community structure to metabolic interactions driving methane production from wastewater. *Nat Commun* (2023) (accepted).

Reisle, C., Williamson, L.M., Pleasance, E., Davies, A., Pellegrini, B., Bleile, D.W., Mungall, K.L, Chuah, E., Jones, M.R., Ma, Y., Lewis, E., Beckie, I., Pham, D., Matiello Pletz, R., Muhammdzadeh, A., Pierce, B.M., Li, J., Stevenson, R., Wong, H., Bailey, L., Reisle, A., Douglas, M., Bonakdar, M., Nelson, J.M.T., Grisdale, C.J., **Krzywinski, M.**, Fisic, A., Mitchell, T., Renouf, D.J., Yip, S., Laskin, J., Marra, M.A., Jones, S.J.M. A platform for oncogenomic reporting and interpretation. *Nat Commun* **13,** 756 (2022).

Traving, S.J., Kellogg, C.T.E., Ross, T., McLaughlin, R., Kieft, B., Ho, G.Y., Peña, A., **Krzywinski, M.**, Robert, M. & Hallam, S.J. Prokaryotic responses to a warm temperature anomaly in northeast subarctic Pacific waters. *Communications Biology* **4**: 1217 (2021).

Krzywinski, M. Capturing the data moment: Effective public health communication in a pandemic UBC Medical Journal (2021) **12**:6–10.

Perez, S., Hahn, A., **Krzywinski, M.** & Hallam, S. Hive Panel Explorer: an interactive visualization tool to explore topological and data association patterns in large networks. Bioinformatics (2021) 20;37(3):436-437.

Krzywinski, M. Enhancing research communication through information design and visual storytelling: Reflections on 10 years of APSS proceedings figures. (2018) *Proceedings of the Australian Poultry Science Symposium* **29:**135–144.

Albuquerque, M.A., Grande, B.M., Ritch, E.J., Pararajalingam, P., Jessa, S., **Krzywinski, M.**, Grewal, J.K., Shah, S.P., Boutros, P.C. and Morin, R.D., (2017) Enhancing knowledge discovery from cancer genomics data with Galaxy. *Giga Science*, *6*(5), pp. 1–13.

Lever, J., Gakkhar, S., Gottlieb, M., Rashnavadi, T., Lin, S., Siu, C., Smith, M., Jones, M., **Krzywinski, M.**, Jones, S. (2017) A collaborative filtering based approach to biomedical knowledge discovery. *Bioinformatics*, **34**:652–659.

Krzywinski, M., Nip, K.M., Birol, I. & Marra, M. (2017) Differential Hive Plots—Seeing Networks Change. Leonardo Special Section: Arts, Humanities and Complex Networks 2015. *Leonardo*, **50**:504 doi:10.1162/LEON_a_01278

Krzywinski, M. & Hirst, M. (2016) SnapShot: Epigenomic Assays. *Cell* **167**:1430.e1.

Xylinas, E., Hassler, M.R., Zhuang, D., **Krzywinski, M.** *et al.* (2016) An epigenomic approach to improving response to neoadjuvant cisplatin chemotherapy in bladder cancer. *Biomolecules* **6**:37.

Krzywinski, M. (2016) Visualizing Clonal Evolution in Cancer. *Molecular Cell* **62**:652–656.

Hoskins, R.A., Carlson, J.W., Wan, K.H., Park, S., Mendez, I., Galle, S.E., Booth, B.W., Pfeiffer, B.D., George, R.A., Svirskas, R., **Krzywinski, M.** et al. (2015) The release 6 reference sequence of the *Drosophila melanogaster* genome. *Genome Research* **25**:445-458.

Lim EL, Trinh DL, Scott DW, Chu A, **Krzywinski M.** *et al.* (2015) Comprehensive miRNA sequence analysis reveals survival differences in diffuse large B-cell lymphoma patients. *Genome Biology* **16**:18.

Ray, W.C., Rumpf, R.W., Sullivan, B., Callahan, N., Magliery, T., Machiraju, R., Wong, B., **Krzywinski, M. &** Bartlett, C.W. Understanding the sequence requirements of protein families: insights from the BioVis 2013 contests. (2014) *BMC Proceedings of the 3rd Annual Symposium on Biological Data Visualization* **8**:Supplement 2:S1 doi: 10.1186/1753-6561-8-S2-S1

de Martino, M., Zhuang, D., Klatte, T., Rieken, M., Rouprêt, M., Xylinas, E., Clozel, T., **Krzywinski, M.** *et al.* (2014) Impact of ERBB2 mutations on in vitro sensitivity of bladder cancer to lapatinib. *Cancer Biology & Therapy* **15**:1239-47.

Pugh TJ, Morozova O, Attiyeh EF, Asgharzadeh S, Wei JS, Auclair D, Carter SL, Cibulskis K, Hanna M, Kiezun A, Kim J, Lawrence MS, Lichenstein L, McKenna A, Pedamallu CS, Ramos AH, Shefler E, Sivachenko A, Sougnez C, Stewart C, Ally A, Birol I, Chiu R, Corbett RD, Hirst M, Jackman SD, Kamoh B, Khodabakshi AH, **Krzywinski M**, *et al.* (2013) The genetic landscape of high-risk neuroblastoma. *Nature Genet* **45**:279-284.

Castellarin M, Warren RL, Freeman JD, Dreolini L, **Krzywinski M**, *et al.* Fusobacterium nucleatum infection is prevalent in human colorectal carcinoma. *Genome Res* 2012, 22:299-306.

Astanehe A, Finkbeiner MR, **Krzywinski M**, *et al.* Mknk1 is a yb-1 target gene responsible for imparting trastuzumab resistance and can be blocked by rsk inhibition. *Oncogene* 2012.

Zhang X, Robertson G, **Krzywinski M**, *et al.* Pics: Probabilistic inference for chip-seq. *Biometrics* 2011, 67:151-163.

Morin RD, Mendez-Lago M, Mungall AJ, Goya R, Mungall KL, Corbett RD, Johnson NA, Severson TM, Chiu R, Field M, Jackman S, **Krzywinski M**, *et al.* Frequent mutation of histone-modifying genes in non-hodgkin lymphoma. *Nature* 2011 476:298-303.

Krzywinski M, *et al.* Hive plots—rational approach to visualizing networks. *Briefings in Bioinformatics* 2011 doi: 10.1093/bib/bbr069

D'Souza CA, Kronstad JW, Taylor G, Warren R, Yuen M, Hu G, Jung WH, Sham A, Kidd SE, Tangen K, Lee N, Zeilmaker T, Sawkins J, McVicker G, Shah S, Gnerre S, Griggs A, Zeng Q, Bartlett K, Li W, Wang X, Heitman J, Stajich JE, Fraser JA, Meyer W, Carter D, Schein J, **Krzywinski M**, *et al.* Genome variation in cryptococcus gattii, an emerging pathogen of immunocompetent hosts. *mBio* 2011 2:e00342-00310.

Castellarin M, Warren RL, Freeman JD, Dreolini L, **Krzywinski M**, *et al.* Fusobacterium nucleatum infection is prevalent in human colorectal carcinoma. *Genome Research* 2011 doi:10.1101/gr.126516.111

Mandakova T, Joly S, **Krzywinski M**, *et al.* Fast diploidization in close mesopolyploid relatives of Arabidopsis. *Plant Cell* 2010 22:2277-90.

Costello JF, **Krzywinski M**, Marra MA. A first look at entire human methylomes. *Nature Biotechnology* 2009 27:1130-2.

Pugh TJ, Keyes M, Barclay L, Delaney A, **Krzywinski M,** *et al.* Sequence variant discovery in DNA repair genes from radiosensitive and radiotolerant prostate brachytherapy patients. *Clinical Cancer Research* 2009 15:5008-16.

Krzywinski M *et al.* Circos: an Information Aesthetic for Comparative Genomics. *Genome Res*earch 2009 19:1639-1645.

Meyer C, Kowarz E, Hofmann J, Renneville A, Zuna J, Trka J, Ben Abdelali R, Macintyre E, De Braekeleer E, De Braekeleer M, Delabesse E, de Oliveira MP, Cavé H, Clappier E, van Dongen JJ, Balgobind BV, van den Heuvel-Eibrink MM, Beverloo HB, Panzer-Grümayer R, Teigler-Schlegel A, Harbott J, Kjeldsen E, Schnittger S, Koehl U, Gruhn B, Heidenreich O, Chan LC, Yip SF, **Krzywinski M**, Eckert C, Möricke A, Schrappe M, Alonso CN, Schäfer BW, Krauter J, Lee DA, Zur Stadt U, Te Kronnie G, Sutton R, Izraeli S, Trakhtenbrot L, Lo Nigro L, Tsaur G, Fechina L, Szczepanski T, Strehl S, Ilencikova D, Molkentin M, Burmeister T, Dingermann T, Klingebiel T, Marschalek R. New insights to the MLL recombinome of acute leukemias. Leukemia. 2009 Aug;23(8):1490-9. doi: 10.1038/leu.2009.33. Epub 2009 Mar 5.

Robertson AG, Bilenky M, Tam A, Zhao Y, Zeng T, Thiessen N, Cezard T, Fejes AP, Wederell ED, Cullum R, Euskirchen G, **Krzywinski M**, Birol I, Snyder M, Hoodless PA, Hirst M, Marra MA, Jones SJ. Genome-wide relationship between histone H3 lysine 4 mono- and tri-methylation and transcription factor binding. *Genome Research* 2008 18:1906-17.

Morin R, Bainbridge M, Fejes A, Hirst M, **Krzywinski M**, Pugh T, McDonald H, Varhol R, Jones S, Marra M. Profiling the HeLa S3 transcriptome using randomly primed cDNA and massively parallel short-read sequencing. *Biotechniques* 2008 45:81-94.

Krzywinski M, Bosdet I, Mathewson C, Wye N, Brebner J, Chiu R, Corbett R, Field M, Lee D, Pugh T, Volik S, Siddiqui A, Jones S, Schein J, Collins C, Marra M. A BAC clone fingerprinting approach to the detection of human genome rearrangements. *Genome Biology* 2007 8:R224.

Kelleher C, Shin H, Bosdet I, Fjell C, Chiu R, **Krzywinski M** *et al.* A physical map of the highly heterozygous Pupulus genome: integration with the genome sequence and genetic map. *Plant J* 2007 Jun;50(6):1063-78. Epub 2007 May 3.

Warren R, Varabei D, Platt D, Huang X, Messina D, Yang S, Kronstad J, **Krzywinski M** *et al.* Physical map-assisted whole-genome shotgun sequence assemblies. *Genome Research.* 2006 June;16:768-775.

Friedman JM, Baross A, Delaney AD, Ally A, Arbour L, Asano J, Bailey DK, Barber S, Birch P, Brown-John M, Cao M, Chan S, Charest DL, Farnoud N, Fernandes N, Flibotte S, Go A, Gibson WT, Holt RA, Jones SJM, Kennedy GC, **Krzywinski M** *et al.* Oligonucleotide Microarray Analysis of Genomic Imbalance in Children with Mental Retardation. *Am. J. Hum Genet.* 2006 Sep;79(3):500-13. Epub 2006 Jul 25.

Ng SHS, Artieri CG, Bosdet IE, Chiu R, Danzmann RG, Davidson WS, Ferguson MM, Fjell CD, Hoyheim B, Jones SJM, de Jong PD, Koop BF, **Krzywinski MI** *et al.* A physical map of the genome of Atlantic salmon, *Salmo salar. Genomics.* 2005 Oct;86(4):396-404.

Loftus BJ, Fung E, Roncaglia P, Rowley D, Amadeo P, Bruno D, Vamathevan J, Miranda M, Anderson IJ, Fraser JA, Allen JE, Bosdet IE, Brent MR, Chiu R, Doering TL, Donlin MJ, D'Souza CA, Fox DS, Grinberg V, Fu J, Fukushima M, Haas BJ, Huang JC, Janbon G, Jones SJ, Koo HL, **Krzywinski M** *et al.* The genome of the basidiomycetous yeast and human pathogen Cryptococcus neoformans. Science. 2005 Feb 25;307(5713):1321-4.

Wallis JW, Aerts J, Groenen MA, Crooijmans RP, Layman D, Graves TA, Scheer DE, Kremitzki C, Fedele MJ, Mudd NK, Cardenas M, Higginbotham J, Carter J, McGrane R, Gaige T, Mead K, Walker J, Albracht D, Davito J, Yang SP, Leong S, Chinwalla A, Sekhon M, Wylie K, Dodgson J, Romanov MN, Cheng H, de Jong PJ, Osoegawa K, Nefedov M, Zhang H, McPherson JD, **Krzywinski M**, Schein J, Hillier L, Mardis ER, Wilson RK, Warren WC. A physical map of the chicken genome. *Nature.* 2004 Dec 9;432(7018):761-4.

Gerhard DS, Wagner L, Feingold EA, Shenmen CM, Grouse LH, Schuler G, Klein SL, Old S, Rasooly R, Good P, Guyer M, Peck AM, Derge JG, Lipman D, Collins FS, Jang W, Sherry S, Feolo M, Misquitta L, Lee E, Rotmistrovsky K, Greenhut SF, Schaefer CF, Buetow K, Bonner TI, Haussler D, Kent J, Kiekhaus M, Furey T, Brent M, Prange C, Schreiber K, Shapiro N, Bhat NK, Hopkins RF, Hsie F, Driscoll T, Soares MB, Casavant TL, Scheetz TE, Brown-stein MJ, Usdin TB, Toshiyuki S, Carninci P, Piao Y, Dudekula DB, Ko MS, Kawakami K, Suzuki Y, Sugano S, Gruber CE, Smith MR, Simmons B, Moore T, Waterman R, Johnson SL, Ruan Y, Wei CL, Mathavan S, Gunaratne PH, Wu J, Garcia AM, Hulyk SW, Fuh E, Yuan Y, Sneed A, Kowis C, Hodgson A, Muzny DM, McPherson J, Gibbs RA, Fahey J, Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M, Madari A, Young AC, Wetherby KD, Granite SJ, Kwong PN, Brinkley CP, Pearson RL, Bouffard GG, Blakesly RW, Green ED, Dickson MC, Rodriguez AC, Grimwood J, Schmutz J, Myers RM, Butterfield YS, Griffith M, Griffith OL, **Krzywinski M** *et al.*; MGC Project Team. The status, quality and expansion of the NIH full-length cDNA project: the Mammalian Gene Collection (MGC). *Genome Research* 2004 Oct;14(10B):2121-7.

Krzywinski M. *et al.* A set of BAC clones spanning the human genome. *Nucleic Acids Res.* 2004 Jul 9;32(12):3651-60. Print 2004.

Flibotte S, Chiu R, Fjell C, **Krzywinski M**, Schein JE, Shin H, Marra MA. *Automated ordering of fingerprinted clones. Bioinformatics.* 2004 May 22;20(8):1264-71. Epub 2004 Feb 10.

Krzywinski M *et al.* Integrated and sequence-ordered BAC- and YAC-based physical maps for the rat genome. *Genome Research* 2004 Apr;14(4):766-79.

Gibbs RA, Weinstock GM, Metzker ML, Muzny DM, Sodergren EJ, Scherer S, Scott G, Steffen D, Worley KC, Burch PE, Okwuonu G, Hines S, Lewis L, DeRamo C, Delgado O, Dugan-Rocha S, Miner G, Morgan M, Hawes A, Gill R, Celera, Holt RA, Adams MD, Amanatides PG, Baden-Tillson H, Barnstead M, Chin S, Evans CA, Ferriera S, Fosler C, Glodek A, Gu Z, Jennings D, Kraft CL, Nguyen T, Pfannkoch CM, Sitter C, Sutton GG, Venter JC, Woodage T, Smith D, Lee HM, Gustafson E, Cahill P, Kana A, Doucette-Stamm L, Weinstock K, Fechtel K, Weiss RB, Dunn DM, Green ED, Blakesley RW, Bouffard GG, De Jong PJ, Osoegawa K, Zhu B, Marra M, Schein J, Bosdet I, Fjell C, Jones S, **Krzywinski M** *et al.*; Rat Genome Sequencing Project Consortium. Genome sequence of the Brown Norway rat yields insights into mammalian evolution. *Nature.* 2004 Apr 1;428(6982):493-521.

Fuhrmann DR, **Krzywinski MI** *et al.* Software for automated analysis of DNA fingerprinting gels. *Genome Research* 2003 May;13(5):940-953.

Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD, Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T, Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL, Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P, Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH, Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW, Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J, Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW, Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J, Schmutz J, Myers RM, Butterfield YS, **Krzywinski MI**, Skalska U, Smailus DE, Schnerch A, Schein JE, Jones SJ, Marra MA. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences. *Proc Natl Acad Sci USA.* 2002 Dec 24;99(26):16899-903. Epub 2002 Dec 11.

Vatcher G, Smailus D, **Krzywinski M**, Guin R, Stott J, Tsai M, Chan S, Pandoh P, Yang G, Asano J, Olson T, Prabhu AL, Coope R, Marziali A, Schein J, Jones S, Marra M. Resuspension of DNA sequencing reaction products in agarose increases sequence quality on an automated sequencer. *Biotechniques.* 2002 Sep;33(3):532-4, 536, 538-9.

Gregory SG, Sekhon M, Schein J, Zhao S, Osoegawa K, Scott CE, Evans RS, Burridge PW, Cox TV, Fox CA, Hutton RD, Mullenger IR, Phillips KJ, Smith J, Stalker J, Threadgold GJ, Birney E, Wylie K, Chinwalla A, Wallis J, Hillier L, Carter J, Gaige T, Jaeger S, Kremitzki C, Layman D, Maas J, McGrane R, Mead K, Walker R, Jones S, Smith M, Asano J, Bosdet I, Chan S, Chittaranjan S, Chiu R, Fjell C, Fuhrmann D, Girn N, Gray C, Guin R, Hsiao L, **Krzywinski M**, Kutsche R, Lee SS, Mathewson C, McLeavy C, Messervier S, Ness S, Pandoh P, Prabhu AL, Saeedi P, Smailus D, Spence L, Stott J, Taylor S, Terpstra W, Tsai M, Vardy J, Wye N, Yang G, Shatsman S, Ayodeji B, Geer K, Tsegaye G, Shvartsbeyn A, Gebregeorgis E, Krol M, Russell D, Overton L, Malek JA, Holmes M, Heaney M, Shetty J, Feldblyum T, Nierman WC, Catanese JJ, Hubbard T, Waterston RH, Rogers J, de Jong PJ, Fraser CM, Marra M, McPherson JD, Bentley DR. A physical map of the mouse genome. *Nature.* 2002 Aug 15;418(6899):743-50.

Butterfield YS, Marra MA, Asano JK, Chan SY, Guin R, **Krzywinski MI**, Lee SS, MacDonald KW, Mathewson CA, Olson TE, Pandoh PK, Prabhu AL, Schnerch A, Skalska U, Smailus DE, Stott JM, Tsai MI, Yang GS, Zuyderduyn SD, Schein JE, Jones SJ. An efficient strategy for large-scale high-

throughput transposon-mediated sequencing of cDNA clones. *Nucleic Acids Res*. 2002 Jun 1;30(11):2460-8.

Ness SR, Terpstra W, **Krzywinski M**, Marra MA, Jones SJ. Assembly of fingerprint contigs: parallelized FPC. *Bioinformatics*. 2002 Mar;18(3):484-5.

Sossi V, Holden JE, Chan G, **Krzywinski M**, Stoessl AJ, Ruth TJ. Analysis of four dopaminergic tracers kinetics using two different tissue input function methods. *J Cereb Blood Flow Metab*. 2000 Apr;20(4):653-60.

Sossi V, **Krzywinski MI**, Cohen P, Mankoff DA, DeRosario J, Ruth TJ. Effect of count rate on contrast in the ADAC MCD camera. *IEEE Trans Nucl Sci*. 1999;46:1907-1911.

Krzywinski M, Sossi V, et al. Comparison of FORE, OSEM and SAGE algorithms to 3DRP in 3D PET using phantom and human subject data. *IEEE Transactions on Nuclear Science*. 1999;46:1114-1120.

Sossi V, **Krzywinski M**, *et al*. Performance of the ADAC MCD dual head coincidence camera. *Journal of Nuclear Medicine*. 1998;39: 173.

Hubert SJ, **Krzywinski M**, *et al*. Reptation dynamics with random local interactions. *Macromolecules*. 1998;31:181-192.

LeBlanc MAR, Cameron DSM, **Krzywinski M,** LeBlanc D. Magnetic relaxation on bridges between the envelopes of major hysteresis loops of type II superconductors. *Superconductor Science & Technology*. 1997;10:625-639.

LeBlanc MA, Wang SX, LeBlanc D, **Krzywinski M** and Meng J. Investigation of the dB/dH effect using trapped flux in type-II superconductors. *Phys Rev B Condens Matter*. 1995 Nov 1;52(17):12895-12910.

Scaiano JC, Barra M, **Krzywinski M**, Hancock T, Calabrese G, Sinta R. Photoreaction of Vicinal Dibromides with Alcohols - Chain-Amplified Generation of Hydrogen Bromide. *Chemistry of Materials*. 1995; 7: 936-940.

Krzywinski MI, Armitage J, Oakham G. Fast Simulation of the ALTAS End Cap and Forward Hadronic Calorimeters using Parametric Method, *ATLAS Internal Calorimeter Note ATL-LARG-95-028*. 1995.

Armitage J, **MI Krzywinski**, G Oakham. Optimization of Shaping in the ATLAS End-cap and Forward Hadronic Calorimeters, *ATLAS Internal Calorimeter Note ATL-LARG-95-027*. 1995.

Scaiano, JC, M Barra, **M Krzywinski**, R Sinta and G Calabrese. Laser Flash-Photolysis Determination of Absolute Rate Constants for Reactions of Bromine Atoms in Solution. *Journal of the American Chemical Society*. (1993) 115:8340-8344.

Publications—Columns

Derry, A., **Krzywinski, M.** & Altman, N. (2023) Points of significance: Convolutional neural networks. Nature Methods 20

Derry, A., **Krzywinski, M.** & Altman, N. (2023) Points of significance: Neural network primer. Nature Methods 20:165–167.

Dey, T., Lipsitz, S.R., Cooper, Z., Trinh, Q., **Krzywinski, M.** & Altman, N. (2022) Points of significance: Regression modelling of time-to-event data with censoring. Nature Methods 19:1513–1515.

Dey, T., Lipsitz, S.R., Cooper, Z., Trinh, Q., **Krzywinski, M.** & Altman, N. (2022) Points of significance: Survival analysis — time-to-event data and censoring. Nature Methods 19:906–908.

Megahed, F.M, Chen, Y-J., Megahed, A., Ong, Y., Altman, N. & **Krzywinski, M.** (2021) Points of significance: The class imbalance problem. *Nature Methods* **18**:1270–1272.

Altman, N. & **Krzywinski, M**. (2021) Points of significance: Graphical assessment of tests and classifiers. *Nature Methods* **18**:840–842.

Altman, N. & **Krzywinski, M**. (2021) Points of significance: Testing for rare conditions. *Nature Methods* **18**:224–225.

Voelkl, B., Würbel, H., **Krzywinski, M.** & Altman, N. (2021) Points of significance: The standardization fallacy. *Nature Methods* **18**:5–7.

Bjørnstad, O.N., Shea, K., **Krzywinski, M.** & Altman, N. (2020) Points of significance: Uncertainty and the management of epidemics. *Nature Methods* **17**:867–868.

Bjørnstad, O.N., Shea, K., **Krzywinski, M.** & Altman, N. (2020) Points of significance: The SEIRS model for infectious disease dynamics. *Nature Methods* **17**:557–558.

Bjørnstad, O.N., Shea, K., **Krzywinski, M.** & Altman, N. (2020) Points of significance: Modeling infectious epidemics. *Nature Methods* **17**:455–456.

Grewal, J., **Krzywinski, M.** & Altman, N. (2020) Points of significance: Markov models — training and evaluation of hidden Markov models. *Nature Methods* **17**:121–122.

Grewal, J., **Krzywinski, M.** & Altman, N. (2019) Points of significance: Hidden Markov models. *Nature Methods* **16**:795–796.

Grewal, J., **Krzywinski, M.** & Altman, N. (2019) Points of significance: Markov models: Markov Chains. *Nature Methods* **16**:663–664.

Das, K., **Krzywinski, M.** & Altman, N. (2019) Points of significance: Quantile regression. *Nature Methods* **16**:451–452.

Greco, L., Luta, G., **Krzywinski**, **M.** & Altman, N. (2019) Points of significance: Analyzing outliers: Robust methods to the rescue. *Nature Methods* **16**:275–276.

Smucker, B., **Krzywinski, M.** & Altman, N. (2019) Points of significance: Two-level factorial experiments *Nature Methods* **16**:211–212.

Altman, N. & **Krzywinski, M.** (2018) Points of significance: Predicting with confidence and tolerance *Nature Methods* **15**:843–844.

Smucker, B., **Krzywinski, M.** & Altman N. (2018) Points of significance: Optimal experimental design. *Nature Methods* **15**:559–560.

Altman, N. & **Krzywinski, M.** (2018) Points of significance: Curse(s) of dimensionality. *Nature Methods*. **15**:299–400.

Bzdok, D., **Krzywinski, M.** & Altman, N. (2018) Points of significance: Statistics vs machine learning. *Nature Methods* **15**:233–234.

Bzdok, D., **Krzywinski, M.** & Altman, N. (2018) Points of significance: Machine learning: supervised methods. *Nature Methods* **15**:5–6.

Bzdok, D., **Krzywinski, M.** & Altman, N. (2017) Points of significance: Machine learning: a primer. *Nature Methods* **14**:1119–1120.

Altman, N. & **Krzywinski, M.** (2017) Points of significance: Ensemble methods: Bagging and random forests. *Nature Methods* **14**:933–934.

Krzywinski, M. & Altman, N. (2017) Points of significance: Classification and decision trees. *Nature Methods* **14**:757–758.

Lever, J., **Krzywinski, M.** & Altman, N. (2017) Points of significance: Principal component analysis. *Nature Methods* **14**:641–642.

Altman, N. & **Krzywinski, M.** (2017) Points of significance: Clustering. *Nature Methods* **14**:545–546.

Altman, N. & **Krzywinski, M**. (2017) Points of Significance: Tabular data. *Nature Methods* **14**:329–330.

Altman, N. & **Krzywinski, M**. (2017) Points of Significance: Interpreting *P* values. *Nature Methods* **14**:213–214.

Altman, N. & **Krzywinski, M.** (2017) Points of significance: *P* values and the search for significance. *Nature Methods* **14**:3–4.

Lever, J., **Krzywinski, M.** & Altman, N. (2016) Points of significance: Regularization. *Nature Methods* **13**:803–804.

Lever, J., **Krzywinski, M.** & Altman, N. (2016) Points of significance: Model selection and overfitting. *Nature Methods* **13**:703–704.

Krzywinski, M. (2016) Points of View: Intuitive design. *Nature Methods* **13**:895.

Krzywinski M. (2016) Points of View: Binning high-resolution data *Nature Methods* **13**:463.

Lever, J., **Krzywinski, M.** & Altman, N. (2016) Points of significance: Classifier Evaluation. *Nature Methods* **13**:603–604.

Lever, J., **Krzywinski, M.** & Altman, N. (2016) Points of significance: Logistic regression. *Nature Methods* **13**:541–542.

Altman, N. & **Krzywinski, M.** (2016) Points of significance: Regression diagnostics. *Nature Methods* **13**:385–386.

Altman, N. & Krzywinski, M. (2016) Points of significance: Analyzing outliers: Influential or nuisance. *Nature Methods* **13**:281–282.

Hunnicutt, B.J. & **Krzywinski, M.** (2016) Points of View: Neural circuit diagrams *Nature Methods* **13**:189.

Hunnicutt, B.J. & **Krzywinski, M.** (2016) Points of View: Pathways *Nature Methods* **13**:5.

Krzywinski, M. & Altman, N. (2015) Points of significance: Multiple linear regression. *Nature Methods* **12**:1103–1104.

Altman, N. & **Krzywinski, M.** (2015) Points of significance: Simple linear regression. *Nature Methods* **12**:999–1000.

Altman, N. & **Krzywinski, M.** (2015) Points of significance: Association, correlation and causation. *Nature Methods* **12**:899–900.

Puga, J.L, **Krzywinski, M.** & Altman, N. (2015) Points of significance: Bayesian networks. *Nature Methods* **12**:799–800.

McInerny, G. & **Krzywinski, M.** (2015) Points of View: Untangling Complex Plots. *Nature Methods* **12**:591**.**

Kulesa, A., **Krzywinski, M.**, Blainey, P. & Altman, N (2015) Points of Significance: Sampling distributions and the bootstrap. *Nature Methods* **12**:477–478.

Puga, J.L, **Krzywinski, M.** & Altman, N. (2015) Points of Significance: Bayesian Statistics *Nature Methods* **12**:277–278.

Puga, J.L, **Krzywinski, M**. & Altman, N. (2015) Points of Significance: Bayes' Theorem *Nature Methods* **12**:277–278.

Altman, N. & **Krzywinski, M.** (2015) Points of Significance: Split Plot Design. *Nature Methods* **12**:165–166.

Altman, N. & **Krzywinski, M.** (2015) Points of Significance: Sources of Variation. *Nature Methods* **12**:5–6.

Krzywinski, M., Altman, N. & Blainey, P. (2014) Points of Significance: Two factor designs. *Nature Methods* **11**:1187-1188.

Krzywinski, M., Altman, N. & Blainey, P. (2014) Points of Significance: Nested designs. *Nature Methods* **11**:977-978.

Blainey, P., **Krzywinski, M.** & Altman, N. (2014) Points of Significance: Replication. *Nature Methods* **11**:879-880.

Krzywinski, M. & Altman, N. (2014) Points of Significance: Analysis of Variance and Blocking. *Nature Methods* 11:699-670.

Krzywinski, M. & Altman, N. (2014) Points of Significance: Designing Comparative Experiments. *Nature Methods* 11:597-598.

Krzywinski, M. & Altman, N. (2014) Points of Significance: Non-parametric tests. *Nature Methods* 11:467-468.

Krzywinski, M. & Altman, N. (2014) Points of Significance: Comparing Samples — Part 2 — Multiple testing. *Nature Methods* 11:355-356.

Krzywinski, M. & Altman, N. (2014) Points of Significance: Comparing samples — Part 1 — t-tests. *Nature Methods* 11:215-216.

Krzywinski, M. & Altman, N. (2014) Points of Significance: Visualizing samples with box plots. *Nature Methods* 11:119-120.

Krzywinski, M. & Altman, N. (2013) Points of Significance: Power and sample size. *Nature Methods* 10:1139-1140.

Krzywinski, M. & Altman, N. (2013) Points of Significance: Significance, P values and t-tests. *Nature Methods* 10:1041-1042.

Krzywinski, M. & Altman, N. (2013) Points of Significance: Error bars. *Nature Methods* 10:921-922.

Krzywinski, M. & Altman, N. (2013) Points of Significance: Importance of being uncertain. *Nature Methods* 10:809-810.

Krzywinski, M. & Cairo, A. (2013) Points of View: Storytelling. *Nature Methods* 10:687-687.

Krzywinski, M. & Savig, E. (2013) Points of View: Multidimensional Data. *Nature Methods* 10:595-595.

Krzywinski, M. & Wong, B. (2013) Points of View: Plotting symbols. *Nature Methods* 10:451.

Krzywinski, M. (2013) Points of View: Elements of visual style. *Nature Methods* 10:371.

Krzywinski, M. (2013) Points of View: Labels and callouts. *Nature Methods* 10:275.

Krzywinski, M. (2013) Points of View: Axes, ticks and grids. *Nature Methods* 10:183.

Altschul S, Demchak B, Durbin R, Gentleman R, **Krzywinski M.** *et al.* (2013) The anatomy of successful computational biology software. *Nat Biotechnol* 31: 894-897.

Publications—Book Chapters

Krzywinski, M. Scientific data visualization: Aesthetic for diagrammatic clarity. Chapter 3 in *Scientific Data Visualization: Aesthetic for Diagrammatic Clarity. More Than Pretty Pictures* (2017) Edited by Rikke Schmidt Kjærgaard & Lotte Philipsen. Routledge, NY.

Honaas, L, Altman, N, **Krzywinski M.** Study design for sequencing studies. *Methods in Statistical Genomics*. 1st ed Springer. (2016) Methods Mol Biol. 1418:39-66.

Chun HJE, Khattra J, **Krzywinski M**, Aparicio SA, Marra MA (Dellaire GD, Berman JN, Arceci RJ. editors). Cancer Genomics. 1st ed. Elsevier; 2013.

Krzywinski M, Corum J, Patterson K. Chapter 1: Visualization Principles for Scientific Communication. Visualizing Biological Data – A Practical Guide. Editors: Seán I. O'Donoghue & James B. Procter. Cambridge University Press. *In production*.

Schein JE, **Krzywinski M**. Part 2: Genomics. 2.2 Mapping. Fingerprint mapping. Encyclopedia of Genetics, Genomics, Proteomics and Bioinformatics. Editors: Lynn Jorde, Peter Little, Mike Dunn, Shankar Subramaniam.

Sossi V, Holden JE, Chan G, **Krzywinski M**, Stoessl AJ, Ruth TJ. Measuring the BP of four dopaminergic tracers utilizing a tissue input function. Physiological Imaging of the Brain with PET. Editors Gjedde, Hansen, Moos-Knudsen. 2001;131-137.

Publications—Magazines

Krzywinski M, Schemaball: A New Spin on Database Visualization. *SysAdmin Magazine.* 2004; 13(8): 23-28.

Krzywinski M, Clusterpunch: Distributed Cluster Resource Monitoring. *SysAdmin Magazine.* 2003; 12(7): 24-29.

Krzywinski M, Butterfield YS. Sequencing the SARS Virus. *Linux Journal.* 2003; (115): 44-54.

Krzywinski M, Port Knocking: Look Ma – No ports! *Linux Journal, web edition* 2003; (http://www.linuxjournal.com/article.php?sid=6811)

Krzywinski M. Port Knocking: Network Authentication Across Closed Ports. *SysAdmin Magazine.* 2003; 12(6): 12-17.

Krzywinski M. Picking Cluster Parts: Cluster Construction at the Genome Sequence Centre. *login: The Magazine of USENIX and SAGE*, 2001; 26:36-44.

Invited Presentations & Lectures

Showing data and explaining science visually: the rules, the guidelines and the warnings. POET Congress, Calgary, Canada. 12–13 October 2023.

Effective poster design: legible, clear, concise and compelling. BCCHRI, Vancouver, Canada. 5 July 2023.

Essence of data visualization and design in science: what makes a good figure? Department of Pathology, Boston Children's Hospital, Boston, USA. 15 June 2023.

Visualization workshop. Boehringer Ingelheim Fonds Communicating Science Workshop, Schloss Lautrach, Germany. 5–10 May 2023.

Essence of data visualization and design in science: what makes a good figure? Max Planck Institute, Munich, Germany. 4 May 2023.

Engage my brain, not my eye – the non-negotiables in visual communication of data and concepts. UBC Pharmaceutical Sciences, University of British Columbia, Vancouver, Canada. 28 April 2023.

Essence of data visualization and design in science: what makes a good figure? International Congress on Academic Medicine (ICAM), Quebec City, Canada. 13 April 2023.

Engage my brain, not my eye – the non-negotiables in visual communication of data and concepts. KT Connects Webinar, Michael Smith Health Research BC, Vancouver, Canada. 31 March 2023.

Essence of data visualization and design in science: what makes a good figure? CHEM/CHBE, University of British Columbia, Vancouver, Canada. 16 & 23 March 2023.

Graphical abstracts: designing for small spaces. BMEG518. University of British Columbia, Vancouver, Canada. 27 February 2023.

What makes a good figure? MEDS3001 Masterclass. University of Sydney, Sydney, Australia. 27 February 2023.

Design of effective scientific figures. Human Proteome Organization webinar. 31 January 2023.

Art is Science in Love. Vrije Universiteit, Amsterdam, Netherlands. 19 December 2022.

Explain visually, explain well: what makes a good figure? Genetics Department, UMCG, Groningen, Netherlands. 8 December 2022.

Visualization workshop. Boehringer Ingelheim Fonds Communicating Science Workshop, Schloss Lautrach, Germany. 2–5 December 2022.

Genomes: sets of sets of sets. Set Visualization and Uncertainty. Schloss Dagstuhl - Leibniz-Zentrum fur Informatik GmbH. 13–18 November, 2022.

Effectively communicating research through visuals. Science Communication, UBC Pharmaceutical Studies, BC Children's Hospital. 10 November 2022.

Visualization workshop. Boehringer Ingelheim Fonds Communicating Science Workshop, CSHL, USA, 30 October – 2 November 2022.

Communicating with Data. Canadian National Proteomics Network. 31 August 2022.

A pandemic of bad charts. BioVis Meetup. 24 May 2022.

Telling stories with data. MEDS3001 Masterclass – Visualizing Data. University of Sydney, Australia. 14 April 2022.

Art is Science in Love. Network Institute, Vrije Universiteit Amsterdam – Nieuw Universiteitsgebouw, Amsterdam, Netherlands. 14 April 2022.

Visualization workshop. Boehringer Ingelheim Fonds Communicating Science Workshop, Schloss Lautrach, Germany. 27–28 March 2022.

Eye for design, mind for data: in search of balance. Visualization masterclass. VIZBI 2022. 14 March 2022.

How to tell a story to the eye — design of data graphics. MEDS1001 Masterclass — Visualizing Data, University of Sydney, Australia. 10 March 2022

Turning Tables into Graphics: What's the story and where are the outliers? MICB425 Lecture. UBC. 9 March 2022.

Graphical abstract — designing for small spaces. Practical tips and redesign examples for creating scientific graphical abstracts. BMEG518 lecture. UBC. 1 March 2022.

How to tell a story to the eye — design of data graphics. Science communication workshop, East of Scotland Doctoral Training Partnership (EASTBIo), Rules of Life. 25 February 2022.

Data visualisation principles and resources. SOMS4101 Honours Module on Data Analysis and Visualization, School of Medical Sciences, Faculty of Medicine and Health, University of Sydney, Australia. 24 February 2022.

Adobe Illustrator for scientist and practical data visualization workshop. Rock lab, Rockefeller University, New York, USA. 3 Feburary 2022.

How to tell a story to the eye — design of data graphics. SeRC course on Visual Storytelling, Linköping University, Sweden. 14 January 2022.

Science — Clearly. CSCI-CITAC General Meeting, University of Toronto. 15 November 2021.

Visualization of Biological Data - From Analysis to Communication. Schloss Dagstuhl - Leibniz-Zentrum fur Informatik GmbH. 3–8 October, 2021.

Science, art and pandemics. Medical Science Interdisciplinary Project, MEDS3888, University of Sydney, Australia. 20 September 2021.

Science Polish Perspectives Meetup USA 2021. Panel discussion: where art meets science. 16 September, 2021.

Scientific Communication Workshop. Stewart Blusson Quantum Matter Institute, UBC. August 2021.

Effective poster design: legible, clear, concise and compelling. BCCHRI Seminar Series. Vancouver. July 2021.

BioMedVis Spring School on Biomedical Visualization. Europe. May 2021.

Visual design principles for scientific data, graphical abstracts and posters. 2021 Dermatology Skin Research Trainee Workshops, UBC. April 2021.

Design and delivery of effective visual conference presentations. 2021 ARCC pre-conference workshop. Canadian Center for Applied Research in Cancer Control. Vancouver. April 2021.

Design guidelines for posters and graphical abstracts. BCCHRI Seminar Series. Vancouver. March 2021.

Turning tables into graphics. MICB425. UBC, Vancouver. March 2021.

Graphical abstract – designing for small spaces. BMEG 518. UBC, Vancouver. March 2021.

Zoombean: Biosciences Education Australia Network Forum. Sydney, Australia. December 2020.

Rats tasting tea: some statistical issues in preclinical studies. With Naomi Altman. Preclinical Imaging and Testing Facility, MIT, USA. November 2020.

Scientific communication workshop: Till & McCulloch Meetings. October 2020.

Science communication: How to share science effectively and creatively. Epigene2SYS CNRS GDRi. October 2020.

Science, clearly: design, data and stories. Albert Einstein College of Medicine. New York, USA. September 2020.

Effective poster design: legible, clear, concise and compelling. BCCHRI Seminar, Vancouver. July 2020

Lecture. MICB425. Turning Tables into Graphics. UBC. March 2020

Invited talk. Putting the form in formalizing. Shonan Meeting 167, Tokyo, Japan.

Visualization workshop. The essence of data visualization in bioinformatics. Charles Perkins Centre, University of Sydney, Sydney, Australia. February 2020.

Invited talk. Cancer, Pi, Infinity. Charles Perkins Centre, University of Sydney, Australia. February 2020.

Invited talk. Fitting Big Science on a Small Page: Compact visual explanations of complicated things Lorne Proteomics Symposium, Lorne, Australia. February 2020.

Visualization workshop. The essence of data visualization in bioinformatics. International House, University of Melbourne, Melbourne, Australia. February 2020.

Visualization workshop. The essence of data visualization in bioinformatics. Peter Doherty Instituite for Infection and Immunity. University of Melbourne, Melbourne, Australia. February 2020.

Visualization workshop. Using Circos in Galaxy Australia. Australian BioCommons, University of Melbourne, Melbourne, Australia. February 2020.

Visualization workshop. The essence of data visualization in bioinformatics. Australian BioCommons, University of Melbourne, Melbourne, Australia. February 2020.

Invited talk. Genomes, cancer, infinity. Department of Molecular Biology and Genetics, Bogazici University, Istanbul, Turkey. December 2019.

Invited talk. Art is science in love. Science: Polish Perspectives (SPP). Cambridge, UK. November 2019.

Invited talk. Set visualization in genomics. SetVA at IEEE VIS 2019. Vancouver, Canada. October 2019.

Invited talk. Little table, what do you have to say of visualization? BioVis at IEEE 2019. Vancouver, Canada. October 2019.

Visualization workshop. Effective visual scientific communication. Exposome cluster, Michael Smith Laboratories, UBC. October 2019.

Visualization workshop. Effective visual scientific communication. Hirst Lab. Michael Smith Laboratories, UBC. October 2019.

Visualization workshop. Boehringer Ingelheim Fonds Communicating Science Workshop, Cold Spring Harbor, NY, September 2019

Visualization workshop, Kobor Lab, BC Children's Hospital Research Institute, Vancouver, July 2019

Visualization workshop. Bioinformatics and Genome Analysis Course. Trento, Italy. June 2019.

Visualization workshop (2 part). Stewart Blusson Quantum Matter Institute, UBC, May & June 2019

Visualization workshop. Boehringer Ingelheim Fonds. Mainz, Germany. May 2018.

Keynote. MBB Graduate Colloquium 2019 (20th anniversary), SFU, April 2019.

Invited talk. Bio-IT World Conference & Expo, Boston, USA, April 2019.

Invited talk. Integrative Omics, 14th Annual New Mexico BioInformatics, Science and Technology (NMBIST) Symposium, Santa Fe, March 2019.

Lecture. MBB462. SFU. January 2019.

Lecture. MICB 425, UBC, February 2019

Visualization workshop. Faculty of Land and Food Systems, UBC, January 2019

Visualization workshop. Scientific Storytelling, Canadian Stem Cell Network, November 2018

Bioinformatics and Genome Analysis Course. Institut Pasteur de Tunis. Tunis, Tunisia. October 2018.

Visual Design Principles for Scientific Data workshop. Brain and Mind Symposium. Helsinki, Finland. 20–21 September 2018.

Invited talk. Microsoft, Vancouver. 1 August 2018.

Keynote, BioVis2018, ISMB, Chicago, USA. 9 July 2018.

Visualization workshop. Trainee Symposium, BC Children's Hospital Research Institute, Van Dusen Gardens, Vancouver. 20 June 2018.

Visualization workshop. Boehringer Ingelheim Fonds. Mainz, Germany. 3–8 June 2018.

Public lecture: Bridging Science, Art and Design. Sydney Vivid Festival. Museum of Contemporary Art, Sydney, Australia. 1 June 2018.

Data Visualization Masterclass, Sydney Vivid Festival. UTS, Sydney, Australia. 31 May 2018.

Visualization Workshop, SFU Omics, Simon Fraser University, Vancouver, 16 March 2018.

Visualization of Biological Data—Crossroads. Schloss Dagstuhl - Leibniz-Zentrum für Informatik GmbH, Saarbrucken, Germany. 15–20 April 2018.

Public lecture: Art is Science in Love, Charles Perkins Center, University of Sydney, Australia. 14 February 2018.

Visualization lecture: Information design is data choreography for the page. Westmead Institute for Medical Research, Sydney, Australia. 9 February 2018.

Visualization Workshop: Communicating science visually: Design of scientific concept and data figures. The Australian Poultry Science Symposium (APSS). Sydney, Australia. 8 February 2018.

Invited talk: Enhancing research communication through information design and visual storytelling: Reflections on 10 years of APSS proceedings figures. The Australian Poultry Science Symposium (APSS). Sydney, Australia. 4–7 February 2018.

Public lecture: Art is Science in Love, Curiosity Collider, Vancouver. 31 January 2018.

Visualization workshop. 4th Canadian Conference on Epigenetics: Mechanisms of Disease. Whistler, Canada. 26–29 November 2017.

Visualization workshop. Boehringer Ingelheim Fonds. Mainz, Germany. 19–24 November 2017.

Visualization workshop. iNANO Autumn School. Himmerland, Denmark. 6–8 October 2017.

Visualization workshop. Spetses Summer School. Spetsai, Greece. 24 September–1 October 2017.

Scalable Set Visualization. Schloss Dagstuhl - Leibniz-Zentrum für Informatik GmbH, Saarbrucken, Germany. 13–18 August 2017.

Bioinformatics and Genome Analysis Course. Centre for Research & Technology – Hellas. Thessalonica, Greece. June 5–17 2017.

Visualization workshop. UBC & CIHR Skin Research Day. 16 Mar 2017.

Visualization workshop. Boehringer Ingelheim Fonds. Banbury Center, Cold Spring Harbor Labs. Feb 25 – Mar 1, 2017.

Improving Your Visual Science Communication: Plots & Figures. Westgrid Workshop. 8 February 2017.

Essentials of Data Visualization: Thinking about drawing data and communicating science. MBB462. Simon Fraser University. 24 Jan 2017.

Keynote. UCD Computational and Molecular Biology Symposium, Dublin, Ireland. 2 December 2016.

Visualization lecture. VizUM, University of Miami, Florida. 10 November 2016.

Visualization lecture. Central European Institute of Technology, Brno, Czech Republic. 4 October 2016.

Thinking Scientifically. SCIE 113. University of British Columbia. 22 September 2016.

Visualization workshop and lectures. University of Sydney, Australia. 23–31 August 2016.

Visualization lecture. University of Ankara, Turkey. 12 August 2016.

Seeing Networks Change. CANHEIT-HPCS2016 Conference: Shaping the Digital Landscape, Edmonton, 22 JUNE 2016.

Sense and Sensibility—Visual Design Principles for Scientific Data. CANHEIT-HPCS2016 Conference: Shaping the Digital Landscape, Edmonton, 21 June 2016.

The Quality of Quantity. University of Washington Free Public Lecture. University of Washington, Seattle. 21 April 2016.

Data Science Seminar—Seeing networks change. University of Washington, Seattle. 20 April 2016.

Creating better scientific figures. Western Washington University, Bellingham. 7 April 2016.

Fraser lecture series: The Big Data Revolution in Human and Environmental Health. Mt Baker Theater, Western Washington University, Bellingham. 6 April 2016.

B.I.G. Retreat 2016: Art and Science of Data Visualization Workshop. UBC. 11 March 2016.

Visual design principles for scientific data. Ecoscope seminar. UBC. 7 March 2016.

Bioinformatics and Genome Analysis Course. Izmir International Biomedicine and Genome Institute, Izmir, Turkey. May 2–14, 2016.

Thinking Scientifically. SCIE 113. University of British Columbia. 21 January 2016.

Visual Design Principles for Scientific Data workshop. Brain and Mind Symposium. Långvik Congress Center, Kirkkonummi, Finland. 17–18 September 2015.

Visual Design Principles for Scientific Data workshop. Bactory Summer School—Skills Beyond Science. Copenhagen, Denmark. 17–19 August 2015.

Seeing Networks Change (keynote). Arts, Humanities, and Complex Networks. 6th Leonardo satellite symposium. NetSci2015. Zaragoza, Spain. 2 June 2015.

Visual Design Principles for Scientific Data workshop. PhD programme retreat, Vienna Biocenter. Vienna, Austria. 28–30 May 2015.

Visual Design Principles for Scientific Data. Research Institute for Molecular Pathology. Vienna, Austria. 27 May 2015.

Visual Design Principles for Scientific Data workshop. Aarhus Institute of Advanced Studies, Aarhus, Denmark. 13 April 2015.

More Than Pretty Pictures—The Aesthetics of Scientific and Artistic Data Representation (keynote). Aarhus Institute of Advanced Studies, Aarhus, Denmark. 13–16 April 2015.

Visual Design Principles for Scientific Data (keynote). BiVi annual meeting. Edinburgh, Scotland. 16–17 December 2014.

AGTA Australasian Genomic Technologies Association Conference. Melbourne, Australia. October 2014.

Visual Design Principles for Scientific Data workshop. VLSCI. Melbourne, Australia. 14 October 2014.

Visual Design Principles for Scientific Data. Walter & Eliza Hall Research Institute. Melbourne, Australia. 13 October 2014.

Visual Design Principles for Scientific Data. Peter MacCallum Cancer Center. Melbourne, Australia. 13 October 2014.

Sense and Sensibility. Illumina webinar. Melbourne, Australia. 13 October 2014.

Seeing Networks Change. Australian Bioinformatics Conference (ABiC). Melbourne, Australia. 11–12 October 2014.

Communicating Science to Scientists. Melbourne Brain Center. Melbourne, Australia. 10 October 2014.

Visual Design Principles for Scientific Data. Post-graduate master class. VLSCI. Melbourne, Australia. 10 October 2014.

What Does Art Have To Do With Science. ICT for Life Sciences Forum. Public lecture. University of Melbourne Law School. Melbourne, Australia. 9 October 2014.

EMBO Global Exchange Lecture Course on High-throughput/NGS applied to infectious diseases. Institut Pasteur de Tunis. Tunis, Tunisia. September 2014.

WEST Water and Environment Student Talks. Vancouver, British Columbia. June 2014.

Bioinformatics and Comparative Genome Analysis. Pasteur Institute, Athens, Greece. May 2014.

Health Data Linkage Conference. Vancouver, British Columbia. April 2014.

Hereditary Cancer Program Rounds, BCCA, Vancouver, British Columbia. April 2014.

Collaborative Universities Biomedical Education Network Annual Conference. Canberra, Australia. December 2013.

Wired Health Data|Life Conference. New York City, New York. September 2013.

ICOP International Congress of Prositology. Vancouver, British Columbia. August 2013.

Bioinformatics Training Program and the Integrated Oncology Program Retreat. Vancouver, British Columbia. April 2013.

VizBi (keynote), Cambridge, Massachusetts. March 2013.

University of Virginia Biotechnology Training Program Symposium. Charlottesville, Virginia. Nov 2013.

Bloomberg Design Conference. San Francisco, California. Jan 2013.

ICDM International Conference on Data Mining (keynote). Brussels 2012.

Schloss Dagstuhl Seminar on Biological Data Visualization. Saarbrucken, Germany. Sept 2012.

Bioinformatics and Comparative Genome Analysis Course. Pasteur Institute, Naples, Italy. May 2012. Visualizing Genomes with Circos.

Visualization Principles. Visualizing Biological Data (Vizbi) 2012. Heidelberg, Germany. Mar 2012.

Behind Every Great Visualization is a Design Principle. Bioinformatics & Computational Biology Seminar Series, Iowa State University. Ames, Iowa. Feb 2012.

Bioinformatics and Comparative Genome Analysis Course. Pasteur Institute, Paris, France. June 2011. Visualizing Genomes with Circos.

Designing Effective Visualization in the Biological Sciences & Circos and Hive Plots: Challenging visualization paradigms in genomics and network analysis. PSA Annual Meeting 2011 Genomics Workshop. University of Washington. July 2011.

Bioinformatics and Comparative Genome Analysis Course. Pasteur Institute, Paris, France. July 2010. Visualizing Genomes with Circos.

Media—Covers, Interviews and Articles

Cell Genomics. January 2023. "Parent-of-origin chromosomes" cover.

Science Advances. January 2023. "Universal sequencing read interpreter" cover.

Annals of Oncology. September 2022. "Cancer treatment options" cover.

Nature Biotechnology. April 2022 "Phylogenetic tree" cover.

Cancer cell. April 2022 "Kaleidoscopic heterogeneity" cover.

Nature. 17 March 2022 "Gene Genie" cover.

PNAS. 25 January 2022 "Earth BioGenome Project" cover.

Science. 24 September 2021 "Human Genome Research Ultramarathon" cover.

Nature Genetics. August 2020 cover.

Splurge on a Better Keyboard, It's Worth It, Bloomberg Quint interview. May 2020.

Nature Cancer, April 2020 cover.

Enfield, N. Our job as scientists is to find the truth. But we must also be storytellers. Guardian, 19 July 2018. https://www.theguardian.com/commentisfree/2018/jul/20/our-job-as-scientists-is-to-find-the-truth-but-we-must-also-be-storytellers

Molecular Case Studies, cover, April 2018.

Nature 10, cover, 18 December 2017.

Human versus Machine, Nature Graphics, December 2018. http://naturegraphics.tumblr.com/

In silico flurries: Computing a world of snow. Scientific American SA Visual. 23 December 2017. https://blogs.scientificamerican.com/sa-visual/in-silico-flurries/

Pi in the Sky: elegant new visualization maps the digits of pi as a star catalogue. *Scientific American SA Visual*. 14 March 2017. https://blogs.scientificamerican.com/sa-visual/pi-in-the-sky/

Chatzigeorgiou, K. (Jan–Feb 2017). Designing π. *Pr1me Magazine*. Aristotle University of Thessaloniki. http://the-prime-magazine.math.auth.gr/data/documents/teukhos-3.pdf

Thatra, N. On the origins of scientists. *The Ubbyssey*. November (2016).

Webb, S. The Art of Big Data. *BioTechniques* (2016) 61:107–112

Accelerator. Magazine of the Multiple Myeloma Research Foundation. Summer 2016

Marx, V. Data Visualization: Ambiguity as a Fellow Traveler. *Nature Methods* (2013) 10:613–615.

UCSF Magazine. Fall 2013.

Nature Reviews Cancer Calendar. 2013.

Trends in Genetics. October 2012.

PNAS 109(18). May 2012.

EMBO Journal. 28(9) May 2009.

iGenetics: A Molecular Approach. 3rd ed. 2009

Media—Illustrations

Moskowitz, C. 3,117,275,501 bases, 0 gaps. Graphic Science, *Scientific American*, August 2022.

Anatomy of the SARS-Cov-2 virus. American Scientist. March/April 2022.

Wadman, M. Critics decry access, transparency issues with key trove of coronavirus sequences. *Science*, 10 Mar 2021, My COVID genome poster from the deadly genome series appears in a Science news article about issues with open access to SARS-CoV-2 genome data. https://www.sciencemag.org/news/2021/03/critics-decry-access-transparency-issues-key-trove-coronavirus-sequences

van Noorden, R. Scientist call for fully open sharing of coronavirus genome data. *Nature*, 3 Feb 2021. My COVID genome poster from the deadly genome series used in article. https://www.nature.com/articles/d41586-021-00305-7

Fischetti, M. How COVID-19 Spread Like Wildfire. Graphic Science, *Scientific American*, June 2020.

Fischetti, M. Take your medicine ... now. Graphic Science, *Scientific American*, January 2019.

Decoding hemophilia. Illustration. *Hemaware*. Fall 2018.

Johnson, H.L. The Whole Earth Catalogue. *Sactown*. June/July 2018, p. 89.

Fischetti, M. Mental Illness Overlap. Graphic Science, *Scientific American*. July 2018.

Genes that make us sick. Illustration in The Objects that Power the Global Economy. Quartz publishing. http://mkweb.bcgsc.ca/genes.that.make.us.sick/

Fischetti, M. The Bacteria Game. Graphic Science, *Scientific American*. December 2015.

Maron, D.F., A Road Map to the "Volume Control" of Genes. Graphic Science, *Scientific American*. June 2015.

Wong, K., Tiny Genetic Differences between Humans and Other Primates Pervade the Genome. Graphic Science, *Scientific American*. September 2014. (bronze medal, Malofiej 23).

Kolata, G. Cancers Share Gene Patterns, Studies Affirm. *New York Times* 1 May 2013.

Kolata, G. A New Treatment's Tantalizing Promise Brings Heartbreaking Ups and Downs. *New York Times* 8 July 2012.

Gorman, J. Ome—the Sound of the Scientific Universe Expanding. *New York Times* 3 May 2012

Aigner W, Miksch S, Schumann H et al. (2011) Visualization of Time-Oriented Data Springer-Verlag New York Inc.

Haynes H. Getting Lost. *Wired* 2010

Keim B. Beyond the Genome. *Wired* 2009

Zimmer C. Now: The Rest of the Genome. *New York Times* 10 November 2008

Constantine, D. Close-Ups of the Genome, Species by Species by Species. *New York Times* 23 January 2007

Public Art and Science Projects

Repeated Sequence. A modular synthesizer experience. 14 March 2023.
http://mkweb.bcgsc.ca/pi/piday2023/

Ascent. Music video with Max Cooper. October 2022. http://mkweb.bcgsc.ca/max-cooper-ascent

Understanding the genome. MIT Museum Gene Cultures exhibit. From October 2022
http://mkweb.bcgsc.ca/mit-museum-genome-exhibit

Three One Four: A number of notes. 14 March 2022. http://mkweb.bcgsc.ca/pi/piday2022/

Unspoken Words. Max Cooper. Track 4: Ascent. March 2022. https://maxcooper.net/unspoken-words

Ascent: Max Cooper Live at the Acropolis Odeon of Herodes Atticus, Athens, Greece. July 2021.

Ascent: Max Cooper Live at Grand Central Hall, Liverpool, July 2021.

Transcendence: Transcendence: a tactile audio-visual installation in collaboration with Max Cooper, Salvador Breed, and AND&. April 2021

Gene Machines. Music album for GSC 20th anniversary, with Jordan Sauer.
https://qrates.com/projects/20554

Clothing and promotional material design. GSC 20th anniversary. November 2019.
http://mkweb.bcgsc.ca/20th/

Yearning for the Infinite. Animation. Max Cooper, London, September 2019.

DNA on 10th. Wayfinding signs on 10th/Oak for Health Care Corridor. June 2019.
http://mkweb.bcgsc.ca/dnaon10th/

Difference of One. BG Genomics Art exhibit. AGBT 2017. http://mkweb.bcgsc.ca/agbt2017/

Smithsonian Genome Zone. Washington, DC. Summer 2014.

Beautiful Science. British Library. Feb–May 2014.

Rudnik, J., **Krzywinski, M**, de la Cruz, A. Interactive art piece and film short of the data and lives behind BRCA mutations. June 2013. https://www.youtube.com/watch?v=CDZy3z0d6XE.

Max Planck Science Gallery. Science Tunnel. 2012.

Max Planck Gallery Science Express. 2009.