

Martin Krzywinski

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

1.604.877.6000 x 673262

<http://mkweb.bcgsc.ca>

martink@bcgsc.ca

martin.krzywinski@gmail.com

@MKrzywinski

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 2012
citations	11,456	6,532
<i>h</i> -index	32	25
<i>i10</i> -index	48	38

updated 26 Jan 2017

Publications—Refereed papers

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

Lever, J., Gakkhar, S., Gottlieb, M., Rashnavadi, T., Lin, S., Siu, C., Smith, M., Jones, M., **Krzywinski, M.**, Jones, S. A collaborative filtering based approach to biomedical knowledge discovery. (submitted).

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.

Krzywinski, M., Nip, K.M., Birol, I. & Marra, M. (2016) Differential Hive Plots—Seeing Networks Change. Leonardo Special Section: Arts, Humanities and Complex Networks 2015. doi:10.1162/LEON_a_01278

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. (In preparation).

Nip, K.M., **Krzywinski, M.** & Birol, I. jhive: an interactive software to visualize and compare network graphs with hive plots. (In preparation).

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., Klatter, 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, Lichtenstein 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. Pica: 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.* Circo: an Information Aesthetic for Comparative Genomics. *Genome Research* 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, Molkenkin 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 trimethylation 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, Gage 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, Kiekhuis 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, Brownstein 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, Kettelman 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 ATLAS 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

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.

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

Hunnicut 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. More Than Pretty Pictures. 2016. Edited by Rikke Schmidt Kjærgaard & Lotte Philipsen. Routledge, NY. *In production.*

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—Preprints

Marco A Albuquerque, Bruno M Grande, Elie Ritch, Selin Jessa, **Martin I Krzywinski**, Jasleen Grewal, Sohrab Shah, Paul Boutros, Ryan Morin (2016) Enhancing Knowledge Discovery from Cancer Genomics Data with Galaxy. *bioRxiv* 089631; doi: <https://doi.org/10.1101/089631>

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

Bioinformatics and Genome Analysis Course. Centre for Research & Technology – Hellas. Thessalonica, Greece. June 5–17, 2016.

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

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

Principles of Data Visualization. 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. Saarbrücken, 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

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

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

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

Difference of One. AGBT 2017.

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=CDZy3zod6XE>.

Max Planck Science Gallery. Science Tunnel. 2012.

Max Planck Gallery Science Express. 2009.