

Educational Background and Training

- Ph.D. 2004–2008 **Bioinformatics**, Dept. Electrical Engineering, Katholieke Universiteit Leuven, Leuven, Belgium
Title: A Bayesian network integration framework for modeling biomedical data
Advisor: Prof. Bart De Moor
- M.S. 2003–2004 **Artificial Intelligence**, Katholieke Universiteit Leuven, Leuven, Belgium
- M.S. 2001–2003 **Electrical Engineering**, Katholieke Hogeschool Sint-Lieven, Ghent, Belgium
- B.S. 1999–2001 **Electrical Engineering**, Katholieke Hogeschool Sint-Lieven, Ghent, Belgium

Professional Appointments

- Assistant Professor, Medicine, Stanford University 08/01/2013–
My lab focuses on Biomedical Data Fusion by developing machine learning methods to integrate multi-omics, pathological and medical image data primarily in cancer research. 11/16/2012–
- Research Associate, Plevritis Lab, Radiology, Stanford University 07/31/2013
Developing mathematical methods for multi-scale data integration.
Advisor: Dr. Sylvia Plevritis, Dept. Radiology
- Post-doc, Plevritis Lab, Radiology, Stanford University 01/01/2010–
Investigating mathematical methods to integrate molecular biology and medical imaging data in lung and brain cancer. 11/15/2012
Advisor: Dr. Sylvia Plevritis, Dept. Radiology
- Post-doc, Bioinformatics@Sista/ESAT, Katholieke Universiteit Leuven, Leuven, Belgium. 01/01/2009–
Integration of data of cancer patients using advanced machine learning methods including Bayesian modeling and kernel methods. 12/31/2009
Advisor: Prof. Bart De Moor

Honors and Awards

- SNO/EANO Award from the European Association of Neuro-Oncology Meeting 2014
- Post-doctoral researcher of the Fund for scientific research Flanders (FWO-Vlaanderen). 2009–2012
- Honorary Fulbright Scholar of the Commission for Educational Exchange between the United States of America, Belgium and Luxembourg 2009–2010
- Fellow of the Belgian American Educational Foundation (BAEF)
- Henri Benedictus Fellow of the King Baudouin Foundation 2009–2010
- Ph.D. grant of the agency for Innovation by Science and Technology in Flanders (IWT-Vlaanderen) 2004–2008

Scholarly Publications

Peer-reviewed journal articles: Original research

Lab members and PI in bold.

- Last author starting 2014.
 1. Iv M, **Zhou M**, Shpanskaya K, Perreault S, **Wang Z**, Tranvinh E, Lanzman B, Vajapeyam S, Vitanza NA, Fisher P, Cho YJ, Cheshier SH, Ramaswamy V, Taylor M, Grant GA, Poussaint TY, **Gevaert O***, Yeom KW*. Magnetic Resonance Imaging-based Radiomic Signature of Distinct Molecular Subtypes of Medulloblastoma. *AJNR* 2018, In Press.
 2. **Cedoz PL, Prunello M, Brennan K, Gevaert O**. MethylMix 2.0: an R package for identifying DNA methylation genes. *Bioinformatics* 2018, In Press.
 3. Bulens P, Couwenberg A, Haustermans K, Debucquoy A, Vandecaveye V, Philippen M, Zhou M, **Gevaert O***, Intven M*. Development and validation of an MRI-based model to predict response to chemoradiotherapy for rectal cancer. *Radiother Oncol.* 2018 Jan 30. pii: S0167-8140(18)30025-2. doi: 10.1016/j.radonc.2018.01.008. PubMed PMID: 29395287. *Co-senior authors
 4. **Champion M, Brennan K**, Croonenborghs T, Gentles AJ, Pochet N, **Gevaert O**. Module analysis captures pancancer genetic and epigenetic deregulated cancer driver genes for smoking and antiviral response. *EBioMedicine.* 2018 Jan;27:156-166. doi: 10.1016/j.ebiom.2017.11.028. Epub 2017 Dec 1.
 5. **Brennan K**, Shin JH, Tay JT, **Prunello M**, Gentles AJ, Sunwoo JB, **Gevaert O**. NSD1 inactivation defines an immune cold, DNA hypomethylated subtype in squamous cell carcinoma, *Scientific Reports*, 2017 Dec 6;7(1):17064. doi: 10.1038/s41598-017-17298-x.
 6. **Bakr S**, Echegaray S, Shah R, Kamay A, Louie J, Napel S, Kothary N, **Gevaert O**. Non-invasive radiomics signature based on quantitative analysis of computed tomography images for prediction of microvascular invasion in hepatocellular carcinoma: A Pilot Study. *Journal of Medical Imaging*, 2017 Oct;4(4):041303. doi: 10.1117/1.JMI.4.4.041303.
 7. **Zhou M**, Scott J, Chaudhury B, Hall L, Goldgof D, Yeom KW, Iv M, Ou Y, Kalpathy-Cramer J, Napel S, Gillies R, **Gevaert O***, Gatenby R*. Radiomics in Brain Tumor: Image Assessment, Quantitative Feature Descriptors, and Machine-Learning Approaches. *AJNR Am J Neuroradiol.* 2018 Feb;39(2):208-216. doi: 10.3174/ajnr.A5391. Epub 2017 Oct 5. Review. * Co-corresponding senior authors.
 8. **Zhou M**, Leung A, Echegaray S, Gentles A, Shrager JB, Jensen KC, Berry GJ, Plevritis SK, Rubin D, Napel S, **Gevaert O**. Radiogenomics mapping of non-small cell lung cancer identifies prognostic relationships between semantic image features and metagenes captured using RNA sequencing. *Radiology.* 2018 Jan;286(1):307-315. doi: 10.1148/radiol.2017161845. Epub 2017 Jul 20.
 9. Wang S, **Zhou M**, Liu Z, Liu Z, Gu D, Zang Y, Dong D, **Gevaert O***, Tian J*. Central focused convolutional neural networks: Developing a data-driven model for lung nodule segmentation. *Med Image Anal.* 2017 Aug;40:172-183. doi: 10.1016/j.media.2017.06.014. Epub 2017 Jun 30. PubMed PMID: 28688283. *Co-corresponding authors
 10. Joye I, Debucquoy A, Deroose CM, Vandecaveye V, Cutsem EV, Wolthuis A, D'Hoore A, Sagaert X, Zhou M, **Gevaert O***, Haustermans K*. Quantitative imaging outperforms molecular markers when predicting response to chemoradiotherapy for rectal cancer. *Radiother Oncol.* 2017 Jul;124(1):104-109. doi: 10.1016/j.radonc.2017.06.013. Epub 2017 Jun 21. PubMed PMID: 28647399. *Co-corresponding authors
 11. **Brennan K, Koenig JL**, Gentles A, Sunwoo JB, **Gevaert O**. Identification of an atypical etiological head and neck squamous carcinoma subtype featuring the CpG island methylator phenotype. *EBioMedicine*, 2017 Mar;17:223-236. doi: 10.1016/j.ebiom.2017.02.025. Epub 2017 Mar 1.
 12. **Panahiazar M**, Dumontier M, **Gevaert O**. Predicting biomedical metadata in CEDAR: A study of Gene Expression Omnibus (GEO). *J Biomed Inform.* 2017 Aug;72:132-139. doi: 10.1016/j.jbi.2017.06.017. Epub 2017 Jun 16. PubMed PMID: 28625880.

13. **Cheerla N, Gevaert O.** MicroRNA based Pan-Cancer Diagnosis and Treatment Recommendation. *BMC Bioinformatics*. 2017 Jan 13;18(1):32. doi: 10.1186/s12859-016-1421-y. PubMed PMID: 28086747.
 14. **Brennan K,** Holsinger C., Dosiou C., Sunwoo J., Akatsu H., Haile R., **Gevaert O.** Development of prognostic signatures for intermediate-risk papillary thyroid cancer. *BMC Cancer*. 2016; 16: 736.
 15. Posch L., **Panahiazar M,** Dumontier M, **Gevaert O.** Predicting structured metadata from unstructured metadata. *Database*, 2016, baw080.
 16. **Planey RK, Gevaert O.** CoINcIDE: A framework for discovery of patient subtypes across multiple datasets. *Genome Med*. 2016 Mar 9;8(1):27. doi:10.1186/s13073-016-0281-4. PubMed PMID: 26961683; PubMed Central PMCID: PMC4784276.
 17. **Sweeney TE,** Chen AC, **Gevaert O.** Combined Mapping of Multiple clUsteriNg ALgorithms (COMMUNAL): A Robust Method for Selection of Cluster Number, *K. Sci Rep*. 2015 Nov 19;5:16971. doi: 10.1038/srep16971. PMID: 26581809; PMCID: PMC4652212.
 18. **Itakura H,** Achrol A, Mitchell AL, Loya JJ, Liu T, Westbroek EM, Feroze AH, Rodriguez S, Echegaray S, Azad TD, Yeom KW, Napel S, Rubin DL, Chang SD, Harsh GR IV, **Gevaert O.** Magnetic resonance image features identify glioblastoma phenotypic subtypes with distinct molecular pathway activities. *Science Translational Medicine*, 2015 Sep 2;7(303):303ra138. PMID: 26333934; PubMed Central PMCID: PMC4666025.
 19. **Gevaert O.** MethylMix: an R package for identifying DNA methylation-driven genes. *Bioinformatics*. 2015, 31(11):1839-41. PMCID: PMC4443673
 20. Manolakas A., **Ochoa I,** Venkat K., Goldsmith A., **Gevaert O.** CaMoDi: a new method for cancer module discovery. *BMC Genomics* 2014, 15(Suppl 10):S8.
- First author
 21. **Gevaert O,** Echegaray S, Khuong A, Hoang CD, Shrager JB, Jensen KC, Berry GJ, Guo HH, Lau C, Plevritis SK, Rubin DL, Napel S, Leung AN. Predictive radiogenomics modeling of EGFR mutation status in lung cancer. *Scientific Reports* 2017 Jan 31;7:41674. doi: 10.1038/srep41674. PubMed PMID: 28139704; PubMed Central PMCID: PMC5282551.
 22. **Gevaert O,** Tibshirani R, Plevritis S. Pancancer analysis of DNA methylation-driven genes using MethylMix. *Genome Biol*. 2015 Jan 29;16(1):17. PMCID: PMC4365533
 23. **Gevaert O,** Mitchell L, Achrol A, Xu J, Echegaray S, Steinberg G, Cheshier S, Napel S, Zaharchuk G, Plevritis S. Exploratory radiogenomics analysis of glioblastoma using quantitative image features. *Radiology* 2014, 273(1):168-74. PMID: 24827998; PMCID: PMC4263772.
 24. **Gevaert O,** Villalobos V, Sikic B, Plevritis S Identification of ovarian cancer driver genes by using module network integration of multi-omics data. *Interface focus*, 2013, 3 20130013.
 25. Nair VS*, **Gevaert O***, Davidzon G, Graves E, Napel S, Hoang CD, Quon A, Rubin D, Plevritis S. Unique 18F-FDG PET tumor uptake imaging features predict poor outcome and are associated with major oncogenomic dysregulation in resected non-small cell lung cancer. *Equally contributing authors. *Cancer Research* 2012, Aug 1;72(15):3725-34.
 26. **Gevaert O,** Xu J, Hoang C, Leung A, Xu Y, Quon A, Rubin D, Napel S, Plevritis S. Non-small cell lung cancer: identifying prognostic imaging biomarkers by leveraging public gene expression microarray data—methods and preliminary results. *Radiology*, 2012, Aug;264(2):387-96.
 27. Leunen K.*, **Gevaert O.***, Daemen A., Vanspauwen V., Michils G., De Moor B., Moerman P., Vergote I. and Legius E. Recurrent copy number alterations in BRCA1-mutated ovarian tumors alter biological pathways., *equally contributing first authors. *Human Mutation*, 30:1693–1702, 2009,
 28. **Gevaert O,** Daemen A., De Moor B., Libbrecht L. A Taxonomy of epithelial human cancer and their metastases. *BMC Medical Genomics*, 2009 2:69
 29. **Gevaert O,** De Moor B. Prediction of cancer outcome using DNA microarray technology: past, present and future, *Expert Opinion in Medical Diagnostics*, 2009, 3(2):157-165

30. **Gevaert O.**, Pochet N., De Smet F., Engelen K., Van Gorp T., Amant F., De Moor B., Timmerman D., Vergote I., Expression profiling to predict the clinical behaviour of ovarian cancer fails independent evaluation, *BMC Cancer*, 2008 (18),pp1-26, 2008
 31. **Gevaert O.**, Van Vooren S., De Moor B., A framework for elucidating regulatory networks based on prior information and expression data, *Annals of the New York Academy of Sciences*, 1115, pp.240-248, 2007.
 32. **Gevaert O.**, De Smet F., Timmerman D., Moreau Y., and De Moor B. Predicting the prognosis of breast cancer by integrating clinical and microarray data with Bayesian networks, *Bioinformatics*, 22(14):e184-190, 2006
 33. **Gevaert O.**, De Smet F., Kirk E., Van Calster B., Bourne T., Van Huffel S., Moreau Y., Timmerman D., De Moor B and Condous G., Predicting the outcome of pregnancies of unknown location: Bayesian networks with expert prior information compared to logistic regression, *Human Reproduction*, 21(7), pp1824-1831, 2006
- Co-author 2018
 34. Bakr S, **Gevaert O**, Echegaray S, Ayers K, **Zhou M**, Shafiq M, **Zheng H**, Benson J, Zhang W, Leung A, Kadoch M, Shrager J, Quon A, Rubin D, Plevritis S, Napel S. A radiogenomic dataset of non-small cell lung cancer, *Scientific Data*, 2018, *Sci Data*. 2018 Oct 16;5:180202. doi: 10.1038/sdata.2018.202.
Dr. Gevaert was involved in creating, processing and annotating this radiogenomic data set and supervised two postdocs that were involved in specific aspects of this project.
 35. Han Y, Xie Z, Zang Y, Zhang S, Gu D, Zhou M, Gevaert O, Wei J, Li C, Chen H, Du J, Liu Z, Dong D, Tian J, Zhou D. Non-invasive genotype prediction of chromosome 1p/19q co-deletion by development and validation of an MRI-based radiomics signature in lower-grade gliomas. *J Neurooncol*. 2018 Aug 10. doi: 10.1007/s11060-018-2953-y.
Dr. Gevaert discussed ideas with the senior authors regarding the concept and planning of this project. He provided expertise and mentoring to graduate students regarding radiomics analysis of brain tumors and was involved in the editing of the manuscript.
 36. Campbell JD*, Yau C*, Bowlby R*, Liu Y*, **Brennan K***, Fan H*, Taylor A*, Wang C*, Walter V*, Akbani R*, Averett B*, Creighton CJ*, Coarfa C*, Shih J, Cherniack AD, **Gevaert O**, Shen H, ANur P, Chen J, Cheng H, Hayes N, Bullman S, Peadamallu S, Ojesina A, Sadeghi S, Mungall K, Benz C, Schultz A, Kanchi R, Gay CM, Hegde A, Diao L, Wang J, Sumazin P, Gunaratne P, Donehower L, Rader JS, Zuna R, Al-Ahmadie H, Lazar A, Drill E, Shen R, Won C, The Cnacer Genome Atlas Network, Stuart JM, Larid PW, Hoadley K, Weinstein J, Peto M, Pickering CR, Chen Z, Van Waes C. Genomic, pathway network and immunologic features distinguishing squamous carcinomas. *Cell Reports* 2018, In Press.
Dr. Gevaert supervised Dr. Brennan and together they provided multi-omics analysis of pan-squamous cancers in the TCGA cohort. Specifically, they worked on analyzing DNA methylation data to identify subtypes of squamous carcinomas including the development of methods to identify DNA methylation of microRNAs.
 37. Malta M, Sokolov A, Gentles AJ, Burzykowski T, Poisson L, Weinstein JN, Kaminska B, Huelsken J, Larsson O, **Gevaert O**, Colaprico A, Czerwinska P, Mauzrek S, Mishra L, Heyn H, Krasnitz A, Godwin A, Lazar A, The Cancer Genome Atlas Research Network, Stuart JM, Hoadley KA, Laird PW, Noushmehr H, Wiznerowicz M. Comprehensive analysis of cancer stemness. *Cell*. 2018, In Press.
Dr. Gevaert provided analysis of multi-omics data using computational algorithms for data fusion to characterize stemness of cancer patients across the entire Cancer Genome Atlas database (TCGA).
 38. Williams LM, Pines A, Goldstein-Piekarski AN, Rosas LG, Kullar M, Sacchet MD, **Gevaert O**, Bailenson J, Lavori PW, Dagum P, Wandell B, Correa C, Greenleaf W, Suppes T, Perry LM, Smyth JM, Lewis MA, Venditti EM, Snowden M, Simmons JM, Ma J. The ENGAGE study: Integrating neuroimaging, virtual reality and smartphone sensing to understand self-regulation for managing depression and obesity in a precision medicine model. *Behav Res Ther*. 2018 Feb;101:58-70. doi: 10.1016/j.brat.2017.09.012. Epub 2017 Oct 7.

Dr. Gevaert is responsible for the overall data fusion strategy proposed in this randomized clinical trial.

- Co-author 2017

39. Yan KS, **Gevaert O**, Probert CS, Zheng GXY, Larkin KA, Davies PS, Cheng Z, Kaddis JS, Wilhelmy J, Grimes S, Han A, Roelf K, Corney D, Terry JM, Belgrader P, Mikkelsen TS, Wang F, von Furstenberg RJ, Chrissy M, Cartwright CA, Niland JC, Hong Y, Carrington J, Breault D, Epstein J, Houchen CW, Lynch JP, Martin MG, Curtis CM, Ji HP, Li L, Henning SJ, Wong MH, Kuo CJ. Mature enteroendocrine cells possess injury-inducible reserve stem cell function. *Cell Stem Cell*, 2017 Jul 6;21(1):78-90.e6. doi: 10.1016/j.stem.2017.06.014. Dr. Gevaert was responsible for the overall bioinformatics analysis of this work by contributing to the conception, design, analysis and interpretation of a large compendium of intestinal stem cells analyzed with RNA-sequencing. Dr. Gevaert was involved in drafting the manuscript.
40. Minamimoto R, Jamali M, **Gevaert O**, Echegaray S, Khuong A, Hoang CD, Shrager JB, Plevritis SK, Rubin DL, Leung AN, Napel S, Quon A. Prediction of EGFR and KRAS mutation in non-small cell lung cancer using quantitative 18F FDG-PET/CT metrics. *Oncotarget*. 2017 May 10. doi: 10.18632/oncotarget.17782. PubMed PMID: 28538213. Dr. Gevaert contributed bioinformatics and radiogenomics expertise to develop a statistical model using PET features to predict EGFR and KRAS mutation status. Dr. Gevaert provided critical revision of the manuscript for important intellectual content.

- Co-author 2016

41. Cancer Target Discovery and Development Network. Transforming Big Data into Cancer-Relevant Insight: An Initial, Multi-Tier Approach to Assess Reproducibility and Relevance. *Mol Cancer Res*. 2016 Aug;14(8):675-82. doi: 10.1158/1541-7786.MCR-16-0090. Epub 2016 Jul 11. PubMed PMID: 27401613; PubMed Central PMCID: PMC4987219. Dr. Gevaert is listed as a contributor of the Cancer Target Discovery and Development (CTD2) network. Dr. Gevaert contributed to manuscript writing proposing a multi-tier framework for reporting novel therapeutic targets.
42. Liu TT, Achrol AS, Mitchell LA, Rodriguez SA, Feroze A; Michael Iv., Kim C, Chaudhary N, **Gevaert O**, Stuart JM, Harsh GR, Chang SD, Rubin DL. Magnetic resonance perfusion image features uncover an angiogenic subgroup of glioblastoma patients with poor survival and better response to antiangiogenic treatment. *Neuro Oncol*. 2016 Dec 22. pii: now270. doi: 10.1093/neuonc/now270. Dr. Gevaert co-supervised graduate student Liu TT to analyze MRI and molecular data to identify novel subgroups of glioblastoma patients based on perfusion imaging. Dr. Gevaert contributed to manuscript writing and critical revision of the manuscript.
43. Dubey R., Lebensohn A., Bahrami-Nejad Z., Marceau C., **Champion M.**, **Gevaert O.**, Sikic B.I., Carette J.E., Rohatgi R. Chromatin-remodeling complex SWI/SNF controls multidrug resistance by transcriptionally regulating the drug efflux pump ABCB1. *Cancer Res*. 2016 Aug 8. pii: canres.0716.2016. Dr. Gevaert supervised postdoc (M. Champion), to analyze, interpret and report of publicly available gene expression data from The Cancer Genome Atlas (TCGA) to conform experimental findings. Dr. Gevaert contributed to manuscript drafting.
44. Willis S, Villalobos VM, **Gevaert O**, Abramovitz M, Williams C, Sikic BI, Leyland-Jones B. Single Gene Prognostic Biomarkers in Ovarian Cancer: A Meta-Analysis. *PLoS One*. 2016 Feb 17;11(2):e0149183. doi:10.1371/journal.pone.0149183. Dr. Gevaert contributed expertise to analyze publicly available gene expression data of ovarian cancer patients to predict prognosis. Dr. Gevaert contributed to manuscript writing.
45. Echegaray S, Nair V, Kadoch M, Leung A, Rubin D, **Gevaert O**, Napel S. A rapid segmentation-insensitive “digital biopsy” method for radiomic feature extraction: method and pilot study using CT images of non-small cell lung cancer. *Tomography*. 2016 Dec;2(4):283-94. Dr. Gevaert co-supervised the graduate student that implemented this algorithm. He provided expertise in analyzing CT image data of lung cancer patients, and developed

statistical algorithms to assess robustness of image features using intra-class correlation analysis.

- Co-author 2015

46. Echegaray S, **Gevaert O**, Shah R, Kamaya A, Louie J, Kothary N, Napel S. Core samples for radiomics features that are insensitive to tumor segmentation: method and pilot study using CT images of hepatocellular carcinoma. *J Med Imaging (Bellingham)*. 2015 Oct;2(4):041011. PMID: 26587549; PMCID: PMC4650964.

Contributed data analysis of radiomics biopsies, manuscript writing and interpretation of the results.

47. Musen MA, Bean CA, Cheung KH, Dumontier M, Durante KA, **Gevaert O**, Gonzalez-Beltran A, Khatri P, Kleinstein SH, O'Connor MJ, Pouliot Y, Rocca-Serra P, Sansone SA, Wiser JA; CEDAR team. The center for expanded data annotation and retrieval. *J Am Med Inform Assoc*. 2015 Nov;22(6):1148-52. doi:10.1093/jamia/ocv048. Epub 2015 Jun 25. PubMed PMID: 26112029.

Contributed manuscript writing to present the Stanford Center for Expanded Data Annotation and Retrieval (CEDAR) to the main public.

48. Verstraete M, Debucquoy A, Dekervel J, van Pelt J, Verslype C, Devos E, Chiritiescu G, Dumon K, D'Hoore A, **Gevaert O**, Sagaert X, Van Cutsem E, Haustermans K. Combining bevacizumab and chemoradiation in rectal cancer. Translational results of the AXEBEAM trial. *Br J Cancer*. 2015 Apr 14;112(8):1314-25. doi: 10.1038/bjc.2015.93. Epub 2015 Mar 17. PubMed PMID: 25867261; PubMed Central PMCID: PMC4402460.

Contributed bioinformatics expertise and carried out the core data analysis including microarray data analysis, pathway analysis and statistical analysis. Contributed to manuscript writing for all data analysis sections, interpretation and conclusions.

49. Litovkin K, Van Eynde A, Joniau S, Lerut E, Laenen A, Gevaert T, **Gevaert O**, Spahn M, Kneitz B, Gramme P, Helleputte T, Isebaert S, Haustermans K, Bollen M. DNA methylation-guided prediction of clinical failure in high-risk prostate cancer. *PLoS One*. 2015 Jun;10(6):e0130651.

Dr. Gevaert provided expertise for DNA methylation data analysis leading to the identification of DNA methylation signature for prediction of clinical failure of prostate cancer. Dr. Gevaert was further involved in univariate and multivariate Cox model analysis used to investigate the prognostic value of the DNA methylation.

50. Nicolasjilwan M, Hu Y, Yan C, Meerzaman D, Holder CA, Gutman D, Jain R, Colen R, Rubin DL, Zinn PO, Hwang SN, Raghavan P, Hammoud DA, Scarpace LM, Mikkelsen T, Chen J, **Gevaert O**, Buetow K, Freymann J, Kirby J, Flanders AE, Wintermark M; TCGA Glioma Phenotype Research Group. Addition of MR imaging features and genetic biomarkers strengthens glioblastoma survival prediction in TCGA patients. *J Neuroradiol*. 2015 Jul;42(4):212-21.

Dr. Gevaert provided expertise in data fusion of MR imaging features and molecular biomarkers for the prediction of survival analysis in TCGA patients, as part of the TCGA imaging glioma working group.

- Co-author 2014

51. Nicolasjilwan M, Hu Y, Yan C, Meerzaman D, Holder CA, Gutman D, Jain R, Colen R, Rubin DL, Zinn PO, Hwang SN, Raghavan P, Hammoud DA, Scarpace LM, Mikkelsen T, Chen J, **Gevaert O**, Buetow K, Freymann J, Kirby J, Flanders AE, Wintermark M; TCGA Glioma Phenotype Research Group. Addition of MR imaging features and genetic biomarkers strengthens glioblastoma survival prediction in TCGA patients. *J Neuroradiol*. 2014 Jul 2

52. Litovkin K, Joniau S, Lerut E, Laenen A, **Gevaert O**, Spahn M, Kneitz B, Isebaert S, Haustermans K, Beullens M, Van Eynde A, Bollen M. Methylation of PITX2, HOXD3, RASSF1 and TDRD1 predicts biochemical recurrence in high-risk prostate cancer. *J Cancer Res Clin Oncol*. 2014 Jun 18.

53. Li X, Nadauld L, Ootani A, Corney DC, Pai RK, **Gevaert O**, Cantrell MA, Rack PG, Neal JT, Chan CW, Yeung T, Gong X, Yuan J, Wilhelmy J, Robine S, Attardi LD, Plevritis SK, Hung

- KE, Chen CZ, Ji HP, Kuo CJ. Oncogenic transformation of diverse gastrointestinal tissues in primary organoid culture. *Nature Medicine*. 2014 Jul;20(7):769-77.
54. Zuurbier L, Gutierrez A, Mullighan CG, Canté-Barrett K, **Gevaert O**, de Rooij J, Li Y, Smits WK, Buijs-Gladdines JG, Sonneveld E, Look AT, Horstmann M, Pieters R, Meijerink JP. Immature MEF2C-dysregulated T-cell leukemia patients have an early T-cell precursor acute lymphoblastic leukemia gene signature and typically have non-rearranged T-cell receptors. *Haematologica*. 2014 Jan;99(1):94-102. doi:10.3324/haematol.2013.090233.
- Co-author 2013
 55. Nair VS, **Gevaert O**, Davidzon G, Plevritis SK, West R. NF-kB protein expression associates with (18)F-FDG PET tumor uptake in non-small cell lung cancer: A radiogenomics validation study to understand tumor metabolism. *Lung Cancer*. 2013 Nov 13. pii: S0169-5002(13)00511-4.
 56. Van Bockstal M, Lambein K, **Gevaert O**, De Wever O, Praet M, Cocquyt V, Van den Broecke R, Braems G, Denys H, Libbrecht L. Stromal architecture and periductal decorin are potential prognostic markers for ipsilateral locoregional recurrence in ductal carcinoma in situ of the breast. *Histopathology*. 2013 Oct;63(4):520-33. doi: 10.1111/his.12188.Co-Author 2012
 57. Vicent S, Sayles L.C., Vaka D., Khatri P., **Gevaert O.**, Chen R., Zheng Y, Gillespie A., Clarke N., Xu Y., Shrager J., Hoang C., Plevritis S., Butte A., Sweet-Cordero A., Cross-species functional analysis of cancer-associated fibroblasts identifies a critical role for CLCF1 and IL6 in non-small cell lung cancer in vivo. *Cancer Res*. 2012 Nov 15;72(22):5744-56.
 58. Fassbender A., Verbeeck N., Börnigen D., Kyama CM, Bokor A., Vodolazkaia A., Peeraer K., Tomassetti C., Meuleman C., **Gevaert O.**, Van de Plas R., Ojeda F., De Moor B., Moreau Y., Waelkens E., D'Hooghe TM. Combined mRNA microarray and proteomic analysis of eutopic endometrium of women with and without endometriosis. *Human Reproduction* 2012, Jul;27(7):2020-9
 59. Vodolazkaia A., El-Aalamat Y., Popovic D., Mihalyi A., Bossuyt X., Kyama CM., Fassbender A., Bokor A., Schols D., Huskens D., Meuleman C., Peeraer K., Tomassetti C., **Gevaert O.**, Waelkens E., Kasran A., De Moor B., D'Hooghe T. Evaluation of a panel of 28 biomarkers for a non-invasive diagnosis of endometriosis. *Human Reproduction* 2012, Sep;27(9):2698-711.
 60. Fassbender A, Waelkens E, Verbeeck N, Kyama CM, Bokor A, Vodolazkaia A, Van de Plas R, Meuleman C, Peeraer K, Tomassetti C, **Gevaert O**, Ojeda F, De Moor B, D'Hooghe T. Proteomics analysis of plasma for early diagnosis of endometriosis. *Obstetrics & Gynecology*, 119:276-85
 - Co-Author, 2011
 61. Beert E, Brems H, Daniëls B, De Wever I, Van Calenbergh F, Schoenaers J, Debiec-Rychter M, **Gevaert O**, De Raedt T, Van Den Bruel A, de Ravel T, Cichowski K, Kluwe L, Mautner V, Sciot R, Legius E. Atypical neurofibromas in neurofibromatosis type 1 are premalignant tumors. *Genes Chromosomes Cancer*. 2011 Dec;50(12):1021-32
 62. Smeets A, Daemen A, Vanden Bempt I, **Gevaert O**, Claes B, Wildiers H, Drijkoningen R, Van Hummelen P, Lambrechts D, De Moor B, Neven P, Sotiriou C, Vandorpe T, Paridaens R, Christiaens MR. Prediction of lymph node involvement in breast cancer from primary tumor tissue using gene expression profiling and miRNAs. *Breast Cancer Research and Treatment*, 2011 Oct; 129(3):767-76.
 63. Kyama CM., Mihalyi A., **Gevaert O.**, Waelkens E., Simsa P., Van de Plas R., Meuleman C., De Moor B., D'Hooghe TM. Evaluation of endometrial biomarkers for semi-invasive diagnosis of endometriosis, Sterility and Fertility, 2011 Mar 15;95(4):1338-43.e1-3
 - Co-Author 2010
 64. Kirk E, Van Calster B, Condous G, Papageorghiou AT, **Gevaert O**, Van Huffel S, De Moor B, Timmerman D, Bourne T. Ectopic pregnancy: using the hCG ratio to select women for expectant or medical management. *Acta Obstet Gynecol Scand*. 2011 Mar;90(3):264-272
 65. Fassbender A., Simsa P., Kyama C.M., Waelkens E, Mihalyi A., Meuleman C., **Gevaert O.**, Van de Plas R., De Moor B., D'Hooghe T.M. TRIzol treatment of secretory phase endometrium allows combined proteomic and mRNA microarray analysis of the same sample

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- Co-Author 2009
 69. Gravendeel L, Kouwenhoven M, **Gevaert O.**, de Rooi J., Stubbs A., Duijm J., Daemen A., Bleeker F., Bralten L., Kloosterhof N., De Moor B., van der Spek P., Kros J., Sillevs Smitt P., van den Bent M., French P. Intrinsic gene expression profiles of gliomas are a better predictor of survival than histology. *Cancer Research*, 2009, 69(23):9065-72
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 - Co-Author 2008
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 - Co-Author 2005
 75. Condous G., Kirk E., Lu C., Van Huffel S., **Gevaert O.**, De Moor B., De Smet F., Timmerman D., Bourne T. Diagnostic accuracy of varying discriminatory zones for the prediction of ectopic pregnancy in women with a pregnancy of unknown location, *Ultrasound in Obstetrics and Gynecology* 26,(7), pp.770-775, 2005.

Peer Reviewed publications: Letters to the editor.

- **Gevaert O.**, Napel S. Radiogenomics Map: A Novel Approach for Noninvasive Identification of Molecular Properties? Response. *Radiology*, Dec 2017, Vol. 285: 1060–1061
- **Gevaert O.**, Pochet N., De Smet F., Van Gorp T., De Moor B., Timmerman D., Amant F., Vergote I., Molecular profiling of platinum resistant ovarian cancer: use of the model in clinical practice, *International Journal of Cancer*, 119(6), pp1511-1512, 2006
- Van den Bosch T., Verguts J., Daemen A., **Gevaert O.**, Domali E., Claerhout F., Vandenbroucke V., De Moor B., Deprest J., Timmerman D. In reply: Pain experienced during transvaginal ultrasound, saline contrast sonohysterography, hysteroscopy and office sampling: a comparative study, *Ultrasound in Obstetrics and Gynecology*, 32(1), pp.118-119,2008

Book chapters

- De Moor B., **Gevaert O.**, "ICT and eHealth: New roads for science", in Lessons for the 21st Century, Translated: "ICT en eHealth. Nieuwe wegen voor de wetenschap", in XXI lessen voor de eenentwintigste eeuw, (Pattyn B., and Raymaekers B., eds.), Universitaire Pers (Leuven, Belgium), 2010, pp. 15-26.
- Daemen A., **Gevaert O.**, Leunen K., Vanspauwen V., Michils G., Legius E., Vergote I., De Moor B. Genome-wide computational study of copy number variations to classify familial ovarian cancer, in Chapter 9, Investigating Human Cancer with Computational Intelligence Techniques, (Vellido A., and Lisboa PJG., eds.), Future Technology Press (Shoreham-by-sea, UK), 2009, pp. 107-118
- Van Calster B., **Gevaert O.**, Van Holsbeke C., De Moor B, Van Huffel S., Timmerman D. Clinical decision support for ovarian tumor diagnosis using Bayesian models: Results from the IOTA study. Computational intelligence in bioengineering, Essays in memory of Antonina Starita. Edited by Masulli F., Micheli A. and Sperduti A. IOS Press, Frontiers in Artificial Intelligence and Applications, Volume 196, 2009, pp 111-128.

Conference papers with peer review

Lab members and PI in bold.

- Last author
 - **Darvin Y., Zhou M.,** Chen A., **Gevaert O.** 3-D Convolutional Neural Networks for Glioblastoma Segmentation. Accepted for presentation at the Multimodal Learning for Clinical Decision Support, MICCAI 2016, Athens.
 - **Panahiazar M.,** Dumontier M., **Gevaert O.** Context aware recommendation engine for metadata submission. K-CAP Workshop on Capturing Scientific Knowledge. 2015, Palisades, NY
 - Manolakos A., Ochoa I., Venkat K., Goldsmith A., **Gevaert O.** CaMoDi: A new method for fast Cancer Module Discovery. 25th International Conference on Genome Informatics (GIW/ISCB-Asia), Tokyo, Japan 2014.
- First author
 - **Gevaert O.,** Plevritis S. Identifying regulators of cancer and their downstream targets by integrating genomic and epigenomic features. Pacific Symposium on Biocomputing 2013.
 - **Gevaert O.,** Van Vooren S., De Moor B. Integration of microarray and textual data improves the prognosis prediction of breast, lung and ovarian cancer patients, In Pacific Symposium on Biocomputing (PSB), Kohala Coast, Hawaii, pp. 279-290, 2008.
 - **Gevaert O.,** De Smet F., Timmerman D., Moreau Y., and De Moor B. Integration of clinical and microarray data using Bayesian networks. In Proceedings of the 14th IFAC Symposium on System Identification (SYSID), Newcastle, Australia, March 2006.
 - **Gevaert O.,** Van Vooren S., De Moor B., "The use of prior distributions for learning genetic networks", in Proc. of the workshop on Probabilistic Modeling and Machine Learning in Structural and Systems Biology (PMSB), Helsinki, Finland, Jun. 2006, pp. 103-107.
- Co-author
 - Martínez-Romero M, O'Connor MJ, Shankar RD, Panahiazar M, Willrett D, Egyedi AL, **Gevaert O,** Graybeal J, Musen MA. Fast and Accurate Metadata Authoring Using Ontology-Based Recommendations. AMIA Annual Symposium 2018
 - Wang S., **Mu Z., Gevaert O.,** Tang Z., Dong D., Liu Z., Tian J., A Multi-view Deep Convolutional Neural Networks for Lung Nodule Segmentation, 39th Annual International Conference of the IEEE Engineering in Medicine & Biology Society (EMBC'17), South Korea, July 2017.
 - Yu D, **Mu Z.,** Yang F., **Gevaert O.,** Liu Z., Shi J., Tian J. Convolutional Neural Networks for Predicting Molecular Profiles of Non-Small Cell Lung Cancer. International Symposium on Biomedical Imaging (ISBI'17) Melbourne, Australia, April, 2017.

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- Daemen A., **Gevaert O.**, Leunen K., Vanspauwen V., Michils G., Legius E., Vergote I., De Moor B., Classification of sporadic and BRCA1 ovarian cancer based on a genome-wide study of copy number variations, In Proceedings of 12th International Conference on Knowledge-Based and Intelligent Information and Engineering Systems (KES), Zagreb, Croatia, 2008
- Daemen A., **Gevaert O.**, De Bie T., Debucquoy A., Machiels J.-P., De Moor B., Haustermans K., Integrating microarray and proteomics data to predict the response on cetuximab in patients with rectal cancer, In Pacific Symposium on Biocomputing (PSB), Kohala Coast, Hawaii, pp. 166-177, 2008.
- De Moor B., Van Delm W., **Gevaert O.**, Engelen K., Coessens B., Systems Biology, Come Forth! In Foundations of Systems Biology in Engineering (FOSBE), Stuttgart, Germany, 2007

Digital publications

- Gevaert O (2017). MethylMix: MethylMix: Identifying methylation driven cancer genes. R package version 2.4.0. <https://www.bioconductor.org/packages/release/bioc/html/MethylMix.html>

Abstracts at conferences with peer review (oral presentations)

- 2018
 - Itakura H. **Gevaert O.** Multi-omics data integration strategy improves survival prognostication in renal cell carcinoma. AMIA Translational Bioinformatics Symposium, San Francisco, CA. 2018
 - Wang Z., Zhou M, Tranvinh E, Lanzman B, Shpanskaya K, Poussaint T, Iv M, Yeom K, **Gevaert O.** Development of MRI-based Radiomics Signature for Predicting Molecular Subtypes in Medulloblastoma. AMIA Translational Bioinformatics Symposium, San Francisco, CA. 2018
- 2016
 - Champion M., **Gevaert O.**, Pancancer module analysis captures major oncogenic pathways and identifies master regulator of immune response. Keystone Symposia on The Cancer Genome, Banff, Alberta, Canada, 2016
 - Zhou M., Napel S., Echegaray S., Leung A., **Gevaert O.** Radiogenomics Mapping of Non-small Cell Lung Cancer Shows Strong Correlations between Semantic Image Features and Metagenes. 102nd Scientific Assembly and Annual Meeting of the Radiological Society of North America (RSNA) 2016. Chicago, IL
 - Zhou M., Yi D., Tranvih E., Lanzman B.A., Vayapeyam S., Poussaint T.Y., Iv M., Yeom K.W., **Gevaert O.** A Pilot Study of Integrating Computational Image Features and Molecular Subtypes in Medulloblastoma. 102nd Scientific Assembly and Annual Meeting of the Radiological Society of North America (RSNA) 2016. Chicago, IL
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- 2015
 - Brennan K., Koenig J., Sunwoo J., **Gevaert O.** Methylation-Driven Subtyping of Head and Neck Squamous Cell Carcinoma", 4th Cancer Epigenetics Conference, November 16-17, 2015 in San Francisco, CA.
 - **Gevaert O.**, S. Napel, S. Echegaray, A. Khuong, C. D. Hoang, J. Shrager, S. Plevritis, and A. N. Leung. 2015. "Radiogenomics Mapping of Non-Small Cell Lung Cancer Identifies

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- **Gevaert O.**, Echegaray S., Napel S., Kothary N. Predictive modeling of microvascular invasion using triphasic quantitative imaging of hepatocellular carcinoma. 101th Scientific Assembly and Annual Meeting of the Radiological Society of North America (RSNA) 2015. Chicago, IL.
 - Itakura H., **Gevaert O.** Partial integration strategy of heterogeneous datasets to prognosticate survival in glioblastoma. AMIA Translational Bioinformatics Symposium, San Francisco, CA. 2015
 - Sweeney T., Chen A., **Gevaert O.** COmbined Mapping of Multiple cUsteriNg ALgorithms (COMMUNAL): A Robust Method for Selection of Cluster Number K. AMIA Translational Bioinformatics Symposium, San Francisco, CA. 2015
 - Planey K. **Gevaert O.** Definition and Exploration of LUAD-LUSC Hybrid Subtype via Integrative Omics Module Networks. AMIA Translational Bioinformatics Symposium, San Francisco, CA. 2015
 - 2014
 - **Gevaert O.** Glioblastoma subtypes defined by quantitative imaging map to different canonical signaling pathways. European Association of Neuro-Oncology (EANO), Turin, Italy
 - **Gevaert O.** Pancancer analysis of DNA-methylation driven genes. International Conference on Systems Biology (ICSB), Melbourne, Australia
 - **Itakura H.**, Achrol A., Liu TT., Echegaray S., Loya J., Feroze AH., Mitchell L.A., Rodriguez S., Westbrook E., Cheshier S.H., Steinberg G.K., Rubin D., Yeom K., Napel S., Harsh G.R., **Gevaert O.** Development and validation of a quantitative image signature that predicts clinical survival in glioblastoma. 100th Scientific Assembly and Annual Meeting of the Radiological Society of North America (RSNA) 2014. Chicago, IL
 - 2013
 - **Gevaert O.**, Mitchell L., Achrol A., Xu J., Steinberg G., Cheshier S., Napel S., Zaharchuk G., Plevritis S. Creating a Radiogenomics map of multi-omics and quantitative image features in glioblastoma multiforme. 99th Scientific Assembly and Annual Meeting of the Radiological Society of North America (RSNA) 2013. Chicago, IL.
 - **Gevaert O.**, Achrol A., Chang S., Harsh G., Steinberg G., Cheshier S., Plevritis S. GLIOMETH: A novel DNA methylation signature predicts overall survival in glioblastoma multiforme. 4th Quadrennial Meeting of the World Federation of Neuro-Oncology, 18th Annual Meeting of the Society for Neuro-Oncology, November 21-24, 2013, San Francisco, California.
 - **Gevaert O.**, Achrol A., Gholamin S., Mitra S., Westbrook E., Loya J., Mitchell L., Chang S., Harsh G., Steinberg G., Plevritis S., Cheshier S. Cancer stem cell transcriptional subtyping of glioblastoma multiforme correlates with clinically relevant molecular and imaging phenotypes. 4th Quadrennial Meeting of the World Federation of Neuro-Oncology, 18th Annual Meeting of the Society for Neuro-Oncology, November 21-24, 2013, San Francisco, California.
 - **Gevaert O.**, Mitchell L., Achrol A., Xu J., Steinberg G., Cheshier S., Napel S., Zaharchuk G., Plevritis S., Creating a radiogenomics map of multi-omics and quantitative image features in glioblastoma multiforme. 4th Quadrennial Meeting of the World Federation of Neuro-Oncology, 18th Annual Meeting of the Society for Neuro-Oncology, November 21-24, 2013, San Francisco, California.
 - 2012
 - **Gevaert O.**, Plevritis S. Identifying a landscape of DNA methylation-driven genes in breast cancer using MethylMix. RECOMB Conference on regulatory and Systems Genomics, San Francisco 2012.

- **Gevaert O.**, Mitchell L., Xu J., Yu C., Rubin D., Zaharchuk G., Napel S., Plevritis S. Radiogenomic analysis indicates MR images are potentially predictive of EGFR mutation status in glioblastoma multiforme. AACR 103rd annual meeting, Chicago, April 2012.
- Adam S., Yetil A., **Gevaert O.**, Jojic V., Gentles A., Felsher DW. Distinct roles of p53 and p19ARF in MYC-dependent tumor oncogene addiction. AACR 103rd annual meeting, Chicago, April 2012.
- 2011
 - **Gevaert O.**, Xu J., Hoang C., Leung A., Quon A., Rubin D., Napel S., Plevritis S. Integrating medical images and transcriptomic data in non-small cell lung cancer. AACR 102nd annual meeting, Orlando, April 2011.
 - **Gevaert O.**, Gentles A., Stubbs A., Kremer A., van der Spek P., Plevritis S., Meijerink J. Modeling the regulatory network of pediatric T cell acute lymphoblastic leukemia. AACR-NCI Conference on Systems Biology: Confronting the Complexity of Cancer, San Diego, February 2011.
 - Napel S., Hoang C., Xu J., **Gevaert O.**, Rubin D., Plevritis S., Xu Y., Leung A., Quon A. Computational and semantic annotation of CT and PET images and integration with genomic assays of tumors in non-small cell lung cancer (NSCLC) for decision support and discovery: method and preliminary results. Radiological Society of North America (RSNA), Chicago, November 2011.
 - Plevritis S., **Gevaert O.**, Xu J., Hoang C., Leung A., Xu Y., Quon A., Rubin D., Napel S. Rapid Identification of Prognostic Imaging Biomarkers for Non-small Cell Lung Carcinoma (NSCLC) by Integrating Image Features and Gene Expression and Leveraging Public Gene Expression Databases. Radiological Society of North America (RSNA), November 2011 Chicago.
 - Hoang C., Napel S., **Gevaert O.**, Xu Y., Rubin D., Leung A., Merritt R., Whyte R., Shrager J., Plevritis S. NSCLC Gene Profiles Correlate with Specific CT Characteristics: “Image-omics”. American Association for Thoracic Surgery (AATS) 2011 Philadelphia.
- 2010
 - Beert E., Brems H., **Gevaert O.**, De Wever I., Van Calenbergh F., Kluwe L., Mautner V., Sciot R., Legius E. Chromosomal abnormalities in high grade MPNSTs from NF microdeletion versus non-microdeletion patients. 14th Annual European Neurofibromatosis meeting location, September 2010, Oslo, Norway.
- 2008
 - **Gevaert O.**, Van Holsbeke C., Fruscio R., Guerriero S., Czekierdowski A., Savelli L., Testa A., Fischerova D., Jurkovic D., Bourne T., Neven P., Valentin L., De Moor B., Timmerman D. Multicenter prospective testing to predict malignancy in adnexal masses using Bayesian network models, In 18th World Congress on Ultrasound in Obstetrics and Gynecology (ISUOG), Chicago, Illinois, Aug. 2008
 - **Gevaert O.**, Testa A., Daemen A., Van Holsbeke C., Fruscio R., Epstein E., Leone FPG., Czerkierdowski A., Valentin L., Savelli L., Bourne T., Amant F., De Moor B., Timmerman D. Investigation of the performance of mathematical models on small ovarian masses on IOTA phase 1 and 2 data. In 18th World Congress on Ultrasound in Obstetrics and Gynecology (ISUOG), Chicago, Illinois, Aug. 2008
 - Kyama CM., Mihalyi A., **Gevaert O.**, Simsa P., Waelkens E., Van de Plas R., Mwenda JM., Meuleman C., De Moor B., D’Hooghe TM. Proteomics in translational research: an integrated approach in the pathogenesis and diagnosis of endometriosis. In The 10th world congress on endometriosis, Melbourne, Australia, March 2008
 - Daemen A., Van Holsbeke C., **Gevaert O.**, Fruscio R., Guerriero S., Czekierdowski A., Valentin L., Savelli L., Testa A., Fischerova D., Bourne T., Vergote I., De Moor B., Timmerman D. Prospective comparison of one-step and two-step models for the classification of adnexal masses as benign or malignant, In 18th World Congress on Ultrasound in Obstetrics and Gynecology (ISUOG), Chicago, Illinois, Aug. 2008
 - Machiels J.H., Debuquoy A., **Gevaert O.**, Daemen A., Sempoux C., McBride W., Stroh C., Vlassak S., Haustermans K. Prediction of pathological response to preoperative

chemoradiotherapy with cetuximab in rectal cancer. Annual Meeting of American Society of Clinical Oncology (ASCO), J Clin Oncol, Suppl, Chicago, Illinois, May-June 2008

- 2007
 - **Gevaert O.**, Van Vooren S., De Moor B. Integration of expression and textual data enhances the prediction of prognosis in breast cancer. International workshop on Probabilistic Modeling in Computational Biology: Probabilistic methods for Active Learning and Data Integration in Computational Biology, Vienna, July 2007
 - **Gevaert O.**, De Moor B., Timmerman D., Optimizing variable selection and cost using a genetic algorithm for modeling adnexal masses with Bayesian networks, In 17th World Congress on Ultrasound in Obstetrics and Gynecology (ISUOG), Firenze, Italy, Oct 2007
 - Kyama CM., Mihalyi A., **Gevaert O.**, Simsa P., Waelkens E., Van de Plas R., Mwenda JM., Meuleman C., De Moor B., D'Hooghe TM. Endometrial biomarkers for semi-invasive diagnosis of endometriosis, In 23rd Annual Meeting of the European Society for Human Reproduction and Embryology (ESHRE), Lyon, France, 2007
 - Van den Bosch T., Daemen A., **Gevaert O.**, Timmerman D. Mathematical decision trees versus clinician based algorithms in the diagnosis of endometrial disease In 17th World Congress on Ultrasound in Obstetrics and Gynecology (ISUOG), Firenze, Italy, Oct 2007
 - Daemen A., Bottomley C., **Gevaert O.**, De Moor B., Timmerman D., Bourne T. Predicting early pregnancy loss with Functional Linear Discriminant Analysis (FLDA) In 17th World Congress on Ultrasound in Obstetrics and Gynecology (ISUOG), Firenze, Italy, Oct 2007
 - Daemen A., **Gevaert O.**, De Moor B. Integration of clinical and microarray data with kernel methods, In 29th Annual International Conference of the IEEE Engineering in Medicine and Biology Society, Lyon, France, Aug. 2007.
- 2005
 - Kirk E., **Gevaert O.**, Haider Z., Condous G., Bourne T. Can the hCG ratio be used to predict the likelihood of success of conservative management of ectopic pregnancies? In 15th World Congress on Ultrasound in Obstetrics and Gynecology (ISUOG), Vancouver, Canada, Sept. 2005

Editorial service

Editorial board membership

- Data Science, June 2017: Data Science is an interdisciplinary journal that addresses the development that data has become a crucial factor for a large number and variety of scientific fields <https://datasciencehub.net/>

Refereeing (dates refer to most recent review)

- Journals
 - Bioinformatics (01-2017), Biostatistics (05-2013), BMC Bioinformatics (11-2016), BMC Cancer (01-2017), BMC genomics (03-2015), BMC medical genomics (01-2016), Genome Medicine (December 2016), Scientific Reports (March 2016), PLoS ONE (May 2016), IEEE Transactions on computational biology (June 2017), Journal of Medical Imaging (April 2016), Medical Image Analysis (March 2017), Nucleic Acids Research (March, April, June 2017), Neurocomputing (February 2016), Neuroradiology (November 2016), Oncotarget (February 2017), Cell Systems (February 2017), Nature Communications (November 2017, March 2018), JCO Precision Oncology (January 2018), Clinical Cancer Research (2017)
 - Full profile: <https://publons.com/author/426239/olivier-gevaert#profile>
- Conference program committee/reviewer:
 - Pacific Symposium on Biocomputing, (2015, 2017, 2018).
- Program Committee.
 - European Conference on Computational Biology, Basel Switzerland (ECCB 2012, 2014, 2016)
 - International Conference on Intelligent Systems for Molecular Biology, Boston, USA (ISMB 2010, 2017, 2018)

- American Medical Informatics Association annual symposium (AMIA 2016).
- RECOMB Conference on Regulatory and Systems Genomics, with DREAM challenges, San Francisco 2012.
- Neural Information Processing Systems Conference, Vancouver, Canada (NIPS 2009, 2010)

Grants

Current funding

- R01 EB020527 (Gevaert) 2/15/15 – 1/31/19
 NIH/NIBIB
 Radiogenomics Framework for Non-invasive Personalized Medicine
 The major goal of this project is to capture quantitatively the 3D morphology of tumors on medical images and apply frameworks that identify cancer driver genes from genomic and transcriptomic data.
 Role: PI
- U01 DE025188 (Kuo/Sunwoo/Gevaert) 7/1/15 – 4/30/19
 NIH/NIDCR
 Identification of Cooperative Genetic Alterations in the Pathogenesis of Oral Cancer
 The major goals of this project are to use bioinformatics algorithms to integrate genomic data in Oral Squamous Cell Carcinoma TCGA data sets to identify master regulators of biologic processes.
 Role: PI
- U01 CA198943 (Milenkovic/Weissman) 6/1/15 – 5/31/18
 NIH/NCI
 Genomic Compression: From Information Theory to Parallel Algorithms
 The major goal of this project is to develop novel algorithms to compress DNA sequence data for more optimized storage and transmission and apply them on cancer data from The Cancer Genome Atlas project.
 Role: Co-Investigator
- U01 CA187947 (Napel/Rubin) 7/1/15 – 6/30/20
 NIH/NCI
 Computing, Optimizing and Evaluating Quantitative Cancer Imaging Biomarkers
 The major goal of this project is to develop a cloud-based resource for generating image features of tumors and evaluating their absolute and relative efficacy for predicting dependent variables, such as response, survival, and cancer genomics.
 Role: Co-Investigator
- U01 CA217851 (Kuo) 9/1/17 – 8/31/22
 NIH/NCI
 Organoid-Based Discovery of Oncogenic Drivers and Treatment Resistance Mechanisms
 The major goal of this proposal is to use bioinformatics strategies to identify novel cancer targets that will subsequently be modeled in organoid cultures of mouse and human tissues.
 Role: Co-Investigator
- U01 CA199241 (Kuo) 4/14/16 – 3/31/20
 NIH/NCI
 Colon Organoid Investigation of KRAS-Dependent Synthetic Lethality
 This project aims to identify new synthetic lethal targets in KRAS-driven human colon organoid models using multiple technology platforms including CRISPRi and proteomic kinase profiling.
 Role: Co-Investigator

U54 CA199075 (Gambhir) 9/1/15 – 7/31/20
 NIH/NCI
 Center for Cancer Nanotechnology Excellence for Translational Diagnostics (CCNE-TD)
 The major goal of this project is to discriminate malignant from benign disease, using methods to interrogate the contribution of individual blood and image features.
 Role: Co-Investigator

UH2 HL13268 (Williams) 9/15/15 – 6/30/20
 University of Illinois at Chicago
 Engaging self-regulation targets to understand the mechanisms of behavior change and improve mood and weight outcomes
 The major goal of this clinical trial is to use multi-modal data (imaging, physiological, emotional etc.) and predict treatment outcomes.
 Role: Co-Investigator

DE-AC52-07NA27344 (Cheshier) 3/24/17– 9/30/22
 Department of Defense / Lawrence Livermore
 National Laboratory
 Optimizing human neuronal cultures for analysis and model development
 This project aims to study neuronal function in an ex-vivo system that models the cellular composition and architectural relevance of the human brain.
 Role: Co-Investigator

Pending funding

R01 EB020527 (Gevaert) 2/1/19 – 1/31/24
 NIH/NCI
 Radiogenomics Framework for Non-invasive Personalized Medicine (Renewal)
 The major goal of this project is to capture quantitatively the 3D morphology of tumors on medical images and apply frameworks that identify cancer driver genes from genomic and transcriptomic data.
 Role: PI

U01 DE028228 (Sunwoo/Gevaert) 9/1/18 – 8/31/23
 NIH/NIDCR
 Understanding predictors of immune cell infiltration in head and neck cancer.
 We will use computational analysis of multi-scale data to discover mechanisms for assessing response of immune checkpoint blockade therapies in head and neck cancer patients.
 Role: MPI

U01 CA228069-01 (Kothary/Gevaert) 4/1/18 – 3/31/23
 NIH/NCI
 Radiomic signature of biologically aggressive hepatocellular carcinoma
 The major goal of this project is to develop a radiomic signature that reflects aggressive characteristics of hepatocellular carcinoma and that is robust to digital and molecular heterogeneity.
 Role: MPI

Prior Funding

R01 CA160251 (Napel/Plevritis) 9/1/11 – 7/31/17
 NIH/NCI
 Tools for Linking and Mining Image and Genomic Data in Non-Small Cell Lung Cancer
 Major Goals: To develop tools for creating an integrated database of imaging, clinical, and genomic features in non-small cell lung cancer and to mine it for relationships to prognosis.

Role: Co-Investigator

U01 CA176299 (Kuo/Ji)
NIH/NCI

5/2/13 – 4/30/17

Functional Analysis of Oncogenic Networks and Drug Response in Primary Organoids

The major goal of this project is to use novel statistical methods to pre-filter the enormous amount of mutational data from human cancers and directly validate these mutations as relevant to cancer in "organoid" cultures.

Role: Co-Investigator

U01 DK085527 (Kuo)
NIH/NIDDK

9/22/09 – 8/31/19 (inactive)

Regulation of Actively Proliferating and Quiescent Intestinal Stem Cells

The major goal of this project is to identify and molecularly characterize intestinal stem cells by identifying processes that control proliferation and differentiation of quiescent stem cells.

Role: Co-Investigator

Previous fellowships

- Post-Doc Fellowship (Research Foundation Flanders, Belgium (FWO))
- Post-Doc Fellowship Belgian American Educational Foundation (BAEF)
- PhD Fellowship (Applied Research Foundation Flanders, Belgium, (IWT))

Service as Grant Reviewer

USA

- National Institutes of Health
 - Medical Imaging (MEDI, 2016)
 - Surgical Sciences, Biomedical Imaging, and Bioengineering (SBIB, 2016)
 - Systems Biology of Aging (2017)
 - Development of Informatics Technologies for Cancer Research and Management (ITCR) (2018)
- City College of New York (CCNY) and Memorial Sloan Kettering Cancer Center (MSK) partnership (2017)
- Kentucky Science and Engineering Foundation (2016)

United Kingdom

- UK Cancer Research
- Sir Henry Dale Fellowship (2015)
- UK Medical Research Council UK (2015, 2017)

Europe

- European Research Council (ERC starting grant, 2016)
- NWO Netherlands Organization for Scientific Research (2016)
- Fund for Scientific Research Flanders (FWO 2013-2017)
- Swiss Cancer League (2015),
- Science Foundation Ireland (2015),
- Israel Science Foundation (2016)
- French Cancer Foundation (2016)

International

- National Science Foundation, South Africa (2016)

Patents

- WO2013149904A1: Marker gene based diagnosis, staging and prognosis of prostate cancer. Filing year 2013.
- WO2010127417: Hepatocellular Carcinoma: kit and in vitro method for the evaluation of the biological stage of an HCC tumor, based on the expression profile of 7 genes. Filing year 2010
- WO2008049175A1: High discriminating power biomarker diagnosing. Filing year. 2007.

Membership

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| • Society for Neuro-Oncology (SNO) | 2013-current |
| • International Society for Computational Biology (ISCB) | 2006-current |
| • American Medical Informatics Association | 2014-current |
| • American Association for Cancer Research (AACR) | 2010-current |

Invited presentations

- 2018
 - Multi-scale modeling of lung cancer. Fifth AACR-IASLC International Joint Conference: Lung Cancer Translational Science from the Bench to the Clinic. San Diego, CA, January 8-11. 2018
- 2017
 - Multi-scale AI for modeling complex diseases. XYZ Technology Forum. December 15, San Francisco.
 - Deep Learning for Lung Cancer Images, GTC 2017, May 2017, Santa Clara, CA.
 - Machine learning and bioinformatics approaches to combine imaging with non-imaging data for outcome prediction, ESTRO 36, May 2017, Vienna, Austria.
 - Radiogenomics in Neuro-oncology, International Society for Magnetic Resonance in Imaging (ISMRM), April 2017, Honolulu, HI,
 - Deep learning in Biomedicine: Challenges and Opportunities, DEVOXX USA, April 2017, Santa Clara US.
 - Full talk here: <https://www.youtube.com/watch?v=9uBRKvbjofk&t=805s>
 - Biomedical multi-scale data fusion for cancer data: applications linking imaging with molecular data, China Radiomics Summit, February 2017, Guangzhou, China.
- 2016
 - Pancancer Identification of DNA Methylation Driven Genes for Target Discovery and Subtyping, 4th Cancer Epigenetics Conference, San Francisco, CA
 - Radiomics and radiogenomics in neuro-oncology. Section of Biomedical Image Analysis. University of Pennsylvania, Philadelphia.
- 2015
 - “Radiomics for tumours: The future for personalised radiotherapy?”, 5th European Lung Cancer Conference (ELCC), Geneva Switzerland, April 2015
 - “Neuroinformatics for Brain Tumors”, American Society for Neuroradiology (ASNR), Omics and Big Data for Neuroradiology Symposium, Chicago April 2015,
- 2014
 - “Glioblastoma subtypes defined by quantitative imaging map to different canonical signaling pathways”, European Association of Neuro-Oncology Meeting, Turin, Italy, October 2014s

- “Multi-omics analysis of colorectal cancer and beyond”, Colon Cancer Family Registry, Kauai, Hawaii, September 2014
- “Integrative Informatics for Brain Tumor Gene Expression: Correlation with Imaging”, ASNR 52nd Annual Meeting, Montreal, Canada, May 2014
- “MethylMix: Identifying methylation driven genes in cancer”, Cancer Target Discovery and Development (CTD²) workshop, Bethesda, MD, April 2014
- “RNA sequencing pipeline for Intestinal Stem Cell profiling”, Intestinal Stem Cell consortium (ISCC) workshop, Washington DC, March 2014
- 2013
 - “Integrative Cancer Systems Biology”, UCLA, Los Angeles, CA, January 2013.
 - “Radiogenomics of Non-Small Cell Lung Cancer”, Radiomics Workshop, Moffitt Cancer Center, Tampa, FL, October 2013.
 - Gevaert O. Radiogenomics in lung cancer. AAPM 2013, Indianapolis, IN
- 2012
 - “Radiogenomics of Lung Cancer: Linking Molecular, Cellular and Tissue Cancer Data”, Ohio State University Cancer Center, Columbus OH, August 2012
- 2011
 - “Integrating Medical Images and Transcriptomic Data in Non-Small Cell Lung Cancer”, Molecular Profiling Colloquium, Brown Lab, February 2011, Stanford, CA
 - “Integrating Medical Images and Transcriptomic Data in Non-Small Cell Lung Cancer”, Information Sciences in Imaging Seminar (ISIS) Series, January 2011, Stanford, CA
- 2010
 - “Integrating Medical Images and Transcriptomic Data in Non-Small Cell Lung Cancer”, BCATS Symposium, November 2010, Stanford, CA

Mentoring/advising

- PhD thesis: Committee membership:
 - Christina Delimitrou, Electrical Engineering 2015 (Chair)
 - Idoia Ochoa, Electrical Engineering 2016
 - Jiwei Li, Computer Science, 2017 (Chair)
- PhD thesis: Primary advisor, Stanford University
 - Katie Planey, “Unsupervised learning across multiple datasets”, Stanford University, 2015
 - Haruka Itakura, “Multi-scale data integration frameworks for predicting outcomes in cancer”, Stanford University, 2016
- PhD thesis: advisor
 - Tiffany Ting Liu, “Integrated analysis using molecular-scale and imaging-scale data to identify prognostic subgroups in glioblastoma”, 2015
- PhD thesis mentorship:
 - Anneleen Daemen, Design of clinical decision support systems for cancer based upon clinical and molecular data, 2006-2010. Now scientist at Genentech, San Francisco, CA
- MS thesis: primary advisor, Stanford University
 - Marcos Prunello, “BAREGA: a bivariate mixture model to identify DNA methylation driven and transcriptionally predictive genes”, 2016, Stanford University
- Master thesis mentorship, KU Leuven, Belgium
 - Paolo Pillozzi, Modularized Learning of Genetic Networks, Master of Artificial Intelligence, 2005-06, continued to PhD, Computer Science, KU Leuven Belgium
 - Joachim Jacobs, Data mining in health insurance, Master of Electrical Engineering, 2006-07
 - Nico Verbeeck, Learning cancer biology: the combination of Bayesian networks and prior information, Master of Artificial Intelligence, 2008-09, now Postdoc at Delft University
- Undergraduate Pre-major advisor, Stanford University, 2015-2017

Teaching

- Stanford Graduate classes:
 - BIOMEDIN 217: Translational Bioinformatics:
 - Core faculty Winter 2015-2016, Winter 2016-2017
 - BIOMEDIN 205: Precision practice with big data
 - Guest lecture Fall 2014: Multi-scale data fusion
 - Guest lecture Fall 2015: Multi-scale data fusion.
 - C BIO 243: Principles of Cancer Systems Biology:
 - Guest lecture 2013/2014: Multi-omics data modeling.
 - Guest lecture 2014/2015: Multi-omics data modeling.
 - HRP 236: Epidemiology Research Seminars
 - Guest lecture Fall 2014: Multi-scale data fusion in glioblastoma multiforme
- Presenter, Bioinformatics tutorial seminar
 - ETumour FP6 European Framework Project: “Introduction to bioinformatics”, KU Leuven, Leuven, Belgium, 2006.
- Teaching Assistant:
 - Problem solving & design 3, Bachelor of Science in Engineering, Katholieke Universiteit Leuven, Belgium