

Anthony Mathelier, Ph.D.

Group Leader

✉ anthony.mathelier@ncmm.uio.no | 📞 +47 228-40-561 | 🐦 @AMathelier

Currently

Group Leader, Computational Biology & Gene Regulation Group at the Centre for Molecular Medicine Norway (NCMM), Nordic EMBL Partner for Molecular Medicine, University of Oslo, and **Adjunct Researcher**, Dept. of Medical Genetics, Oslo University Hospital, Oslo, Norway.

Employment

- 2016- **Group Leader**, Centre for Molecular Medicine Norway (NCMM), Oslo, Norway
- 2020- **Adjunct Researcher**, Dept. of Medical Genetics, Oslo University Hospital, Oslo, Norway
- 2016-19 **Adjunct Researcher**, Dept. of Cancer Genetics, Institute for Cancer Research, Oslo University Hospital, Oslo, Norway
- 2013-16 **Deputy Group Leader**, Wasserman laboratory, Centre for Molecular Medicine and Therapeutics (CMMT), Child and Family Research Institute (CFRI), University of British Columbia (UBC), Vancouver, Canada
- 2011-13 **Postdoctoral fellow**, Wasserman laboratory, CMMT, CFRI, UBC, Vancouver, Canada
- 2006-10 **Teaching assistant**, Université Pierre et Marie Curie (UPMC), Paris, France
- 2006-10 **Ph.D. student**, Laboratory of Computational and Quantitative Biology, Analytical Genomics Group, UPMC, Paris, France

Education

- 2006-10 **Ph.D.** in Computer Science and Bioinformatics (supervisor: Dr. Alessandra Carbone), UPMC, Paris, France
- 2004-06 **M.Sc.** in Computer Science, UPMC, Paris, France

Grants and Awards

- 2021-25 **Renewal package from the NCMM** after external evaluation to support the Computational Biology & Gene Regulation Group with NOK 13.5 millions over 4 years
- 2021-25 Open call on **personalized breast cancer treatments** from the **Rosa sløfe (Pink Ribbon) campaign, Norwegian Cancer Society**, for the project "Cis-regulatory signatures for improved identification and stratification of breast cancer subtypes": NOK 4.999 millions over 4 years
- 2019-22 **Young Research Talents grant from the Research Council of Norway** for the project "Characterisation of cis-regulatory variations that dysregulate driver microRNAs in cancer": NOK 7.352 millions over 3 years
- 2019-23 **Open Call grant from the Norwegian Cancer Society** for the project "Characterisation of cis-regulatory variations that dysregulate driver microRNAs in cancer": with NOK 1.968 millions over 4 years
- 2019-20 Two NCMM internal grants in collaboration with Dr. Russnes and Dr. Skotheim (NOK 710K)
- 2018 Åsgard Research Mobility Program. Funding for spending one week in France developing new scientific interactions (NOK 15.5K)
UiO:Life Science event support for the Sven Furberg Seminars in Bioinformatics and Statistical Genomics (NOK 20K)
- 2017-18 NCMM internal grant in collaboration with Dr. Russnes (NOK 480K)
UiO:Life Science event support for the Sven Furberg Seminars in Bioinformatics and Statistical Genomics (NOK 49K)
- 2016-21 **Start-up package from the NCMM** to launch the Computational Biology & Gene Regulation Group with NOK 18 millions over 5 years
- 2006-09 Ministry of National Education, Research and Technology Ph.D. scholarship attributed by the President of Paris 6 University

Publications

- Preprints 2020 J.A. Castro-Mondragon, M. Ragle Aure, O.C. Lingjærde, A. Langerød, J.W.M. Martens, A.-L. Børresen-Dale, V. Kristensen, **A. Mathelier**. Cis-regulatory mutations associate with transcriptional and post-transcriptional deregulation of the gene regulatory program in cancers. bioRxiv, doi:10.1101/2020.06.25.170738.
- Peer-reviewed 2021 R. Riudavets Puig, A. Khan, P. Boddie, J.A. Castro-Mondragon, **A. Mathelier**. UniBind: maps of high-confidence direct TF-DNA interactions across nine species. BMC Genomics, doi:10.1186/s12864-021-07760-6.
M. Ragle Aure, T. Fleischer, S. Bjørklund, J. Ankill, J.A. Castro-Mondragon, OSBREAC, A.-L. Børresen-Dale, K.K. Sahlberg, **A. Mathelier**, X. Tekpli, V.N. Kristensen. Crosstalk between microRNA expression and DNA methylation drive the hormone-dependent phenotype of breast cancer. Genome Medicine, doi:10.1186/s13073-021-00880-4.
E. Mileti, K.H.M. Kwok, D.P. Andersson, **A. Mathelier**, A. Raman, J. Bäckdahl, J. Jalkanen, L. Massier, A. Thorell, H. Gao, P. Arner, N. Mejhert, C.O. Daub, M. Rydén. Human white adipose tissue displays selective insulin resistance in the obese state. Diabetes, doi:10.2337/db21-0001.
A.J. Korecki, J.L. Cueva-Vargas, O. Fornes, J. Agostinone, R.A. Farkas, J.W. Hickmott, S.L. Lam, **A. Mathelier**, M. Zhou, W.W. Wasserman, A. Di Polo, E.M. Simpson. Human MiniPromoters for ocular-rAAV expression in ON bipolar, cone,

- corneal, endothelial, Müller glial, and PAX6 cells. *Gene Therapy*, doi:10.1038/s41434-021-00227-z.
- 2020 A. Khan, R. Riudavets Puig, P. Boddie, **A. Mathelier**. BiasAway: command-line and web server to generate nucleotide composition-matched DNA background sequences. *Bioinformatics*. doi:10.1093/bioinformatics/btaa928.
- A.V. Pladsen, G. Nilsen, O.M. Rueda, M.R. Aure, Ø. Borgan, K. Liestøl, V. Vitelli, A. Frigessi, A. Langerød, OSBREAC, **A. Mathelier**, O. Engebråten, D.C. Wedge, P. Van Loo, C. Caldas, A.-L. Børresen-Dale, H.G. Russnes, O.C. Lingjærde. Copy number motifs expose genome instability type and predict driver events and disease outcome in breast cancer. *Communications Biology*, doi:10.1038/s42003-020-0884-6.
- O. Fornes*, J.A. Castro-Mondragon*, A. Khan*, R. van der Lee, X. Zhang, P.A. Richmond, B.P. Modi, S. Correard, M. Gheorghe, D. Baranašić, W. Santana-Garcia, G. Tan, J. Chèneby, B. Ballester, F. Parcy, A. Sandelin+, B. Lehnard+, W.W. Wasserman+, and **A. Mathelier**+. JASPAR 2020: update of the open-access database of transcription factor binding profiles. *Nucleic Acids Research*, doi:10.1093/nar/gkz1001.
- B. Fromm, D. Domanska, E. Hoye, V. Ovchinnikov, W. Kang, E. Aparicio-Puerta, M. Johansen, K. Flatmark, **A. Mathelier**, E. Hovig, M. Hackenberg, M.R. Friedlander, K.J. Peterson. MirGeneDB2.0: the curated microRNA Gene Database. *Nucleic Acids Research*, doi:10.1093/nar/gkz885.
- 2019 S. Salvatore, K.D. Rand, I. Grytten, E. Ferkingstad, D. Domanska, L. Holden, M. Gheorghe, **A. Mathelier**, I. Glad, G.K. Sandve. Beware the Jaccard: the choice of metric is important and non-trivial in genomic colocalisation analysis. *Briefings in Bioinformatics*, 2019, doi:10.1093/bib/bbz083.
- T.J. Ha, P.G.Y. Zhang, R. Robert, J. Yeung, D.J. Swanson, **A. Mathelier**, W.W. Wasserman, S. Im, M. Itoh, H. Kawaji, T. Lassmann, C.O. Daub, E. Arner, The FANTOM Consortium, P. Carninci, Y. Hayashizaki, A.R.R. Forrest, and D. Goldowitz. Identification of novel cerebellar developmental transcriptional regulators with motif activity analysis. *BMC Genomics*, doi:10.1186/s12864-019-6063-9
- H.M. Itkonen, A. Urbanucci, S.E.S. Martin, A. Khan, **A. Mathelier**, B. Thiede, S. Walker, I.G. Mills. High OGT activity is essential for MYC-driven proliferation of prostate cancer cells. *Theranostics*, doi:10.7150/thno.30834.
- A.J. Korecki, J.W. Hickmott, S.L. Lam, L. Dreolini, **A. Mathelier**, O. Baker, C. Kuehne, R.J. Bonaguro, J. Smith, C.-V. Tan, M. Zhou, D. Goldowitz, J.M. Deussing, A.F. Stewart, W.W. Wasserman, R.A. Holt, and E.M. Simpson. Twenty-Seven Tamoxifen-Inducible iCre-Driver Mouse Strains for Eye and Brain; Including Seventeen Carrying a New Inducible-First Constitutive-Ready Allele. *Genetics*, doi:10.1534/genetics.119.301984.
- 2018 M. Gheorghe, G.K. Sandve, A. Khan, J. Chèneby, B. Ballester, and **A. Mathelier**. A map of direct TF-DNA interactions in the human genome. *Nucleic Acids Research*, doi:10.1093/nar/gky1210.
- A. Khan, **A. Mathelier**, X. Zhang. Super-enhancers are transcriptionally more active and cell type-specific than stretch enhancers. *Epigenetics*, doi:10.1080/15592294.2018.1514231.
- O. Fornes*, M. Gheorghe*, P.A. Richmond, D.J. Arenillas, W.W. Wasserman+, and **A. Mathelier**+. MANTA2, update of the Mongo database for the analysis of transcription factor binding site alterations. *Scientific Data*, doi:10.1038/sdata.2018.141.
- E. Simpson, A.J. Korecki, O. Fornes, T.J. McGill, J.L. Cueva-Vargas, J. Agostinone, R.A. Farkas, J.W. Hickmott, S.L. Lam, **A. Mathelier**, L.M. Renner, J. Stoddard, M. Zhou, A. Di Polo, M. Neuringer, W.W. Wasserman. New MiniPromoter Ple345 (NEFL) Drives Strong and Specific Expression in Retinal Ganglion Cells of Mouse and Primate Retina. *Human Gene Therapy*, doi:10.1089/hum.2018.118.
- R.A.G. De Souza*, N. Kosior*, S.B. Thomson, **A. Mathelier**, A.W. Zhang, K. Becanovic, W.W. Wasserman, and B.R. Leavitt. Computational Analysis of Transcriptional Regulation Sites at the HTT Gene Locus. *Journal of Huntington's Disease*, doi:10.3233/JHD-170272.
- C.-H. Lecellier+, W.W. Wasserman, and **A. Mathelier**+. Human enhancers harboring specific sequence composition, activity, and genome organization are linked to the immune response. *Genetics*, doi:10.1534/genetics.118.301116.
- A. Khan, A. Montenegro-Montero, and **A. Mathelier**. Put science first and formatting later. *EMBO Reports*, doi:10.15252/embr.201845731.
- D. Sugjaman-Trapman, M. Vitezic, E.-M. Jouhilahti, **A. Mathelier**, G. Lauter, S. Misra, C.O. Daub, J. Kere, and P. Swoboda. Characterization of the human RFX transcription factor family by regulatory and target gene analysis. *BMC Genomics*, doi:10.1186/s12864-018-4564-6.
- 2017 A. Khan and **A. Mathelier**. JASPAR RESTful API: accessing JASPAR data from any programming language. *Bioinformatics*, doi:10.1093/bioinformatics/btx804.
- A. Khan*, O. Fornes*, A. Stigliani*, M. Gheorghe, J.A. Castro-Mondragon, R. van der Lee, A. Bessy, J. Chèneby, S.R. Kulkarni, G. Tan, D. Baranašić, D.J. Arenillas, A. Sandelin+, K. Vandepoele, B. Lehnard+, B. Ballester, W.W. Wasserman+, F. Parcy, and **A. Mathelier**+. JASPAR 2018: update of the open-access database of transcription factor binding profiles and its web framework. *Nucleic Acids Research*, doi:10.1093/nar/gkx1126.
- T. Fleischer*, X. Tekpli*, **A. Mathelier**, S. Wang, D. Nebdal, H.P. Dhakal, K. Kleivi Sahlberg, E. Schlichting, Oslo Breast Cancer Research Consortium (OSBREAC), A.-L. Børresen-Dale, E. Borgen, B. Naume, R. Eskeland, A. Frigessi, J. Tost, A. Hurtado, and V.N. Kristensen. DNA methylation at enhancers identifies distinct breast cancer lineages. *Nature Communications*, doi:10.1038/s41467-017-00510-x.
- J. Chèneby, M. Gheorghe, M. Artufel, **A. Mathelier**, and B. Ballester. ReMap 2018: an updated atlas of regulatory regions from an integrative analysis of DNA-binding ChIP-seq experiments. *Nucleic Acids Research*, doi:10.1093/nar/gkx1092.
- D. de Rie, ..., **A. Mathelier**, ..., M.J.L. de Hoon (70 authors). An integrated expression atlas of miRNAs and their promoters in human and mouse. *Nature Biotechnology*, doi:10.1038/nbt.3947.
- A. Khan and **A. Mathelier**. Intervene: a tool for intersection and visualization of multiple gene or genomic region sets. *BMC Bioinformatics*, doi:10.1186/s12859-017-1708-7.
- 2016 C.-Y. Chen, W. Shi, B.P. Balaton, A.M. Matthews, Y. Li, D.J. Arenillas, **A. Mathelier**, M. Itoh, H. Kawaji, T. Lassmann, Y. Hayashizaki, P. Carninci, A.R.R. Forrest, C.J. Brown, and W.W. Wasserman. YY1 binding association with sex-biased

transcription revealed through X-linked transcript levels and allelic binding analyses. *Scientific Reports*, doi:10.1038/srep37324.

M. Lizio, J. Harshbarger, I. Abugessaisa, S. Noguchi, A. Kondo, J. Severin, C. Mungall, D. Arenillas, **A. Mathelier**, Y.A. Medvedeva, A. Lennartsson, F. Drablos, J.A. Ramilowski, O. Rackham, J. Gough, R. Andersson, A. Sandelin, H. Ienasescu, H. Ono, H. Bono, Y. Hayashizaki, P. Carninci, A.R.R. Forrest, T. Kasukawa+ and H. Kawaji+. Update of the FANTOM web resource: high resolution transcriptome of diverse cell types in mammals. *Nucleic Acids Research*, doi: 10.1093/nar/gkw995.

A. Mathelier, B. Xin, T.-P. Chiu, L. Yang, R. Rohs, and W.W. Wasserman. DNA Shape Features Improve Transcription Factor Binding Site Predictions In Vivo. *Cell Systems*, doi:10.1016/j.cels.2016.07.001.

J.W. Hickmott, C.-Y. Chen, D.J. Arenillas, A.J. Korecki, S.L. Lam, L.L. Molday, R.J. Bonaguro, M. Zhou, A.Y. Chou, **A. Mathelier**, S.L. Boye, W.W. Hauswirth, R.S. Molday, W.W. Wasserman, and E.M. Simpson. PAX6 MiniPromoters drive restricted expression from rAAV in the adult mouse retina. *Molecular therapy - Methods & Clinical Development*, doi:10.1038/mtm.2016.51.

W. Shi, O. Fornes, **A. Mathelier**, and W.W. Wasserman. Evaluating the impact of single nucleotide variants on transcription factor binding. *Nucleic Acids Research*, doi:10.1093/nar/gkw691.

D.J. Arenillas, A. Forrest, H. Kawaji, T. Lassman, the FANTOM consortium, W.W. Wasserman+, and **A. Mathelier**+. CAGED-oPOSSUM: motif enrichment analysis from CAGE-derived TSSs. *Bioinformatics*, doi:10.1093/bioinformatics/btw337.

S. Klein*, L.C. Dieterich*, **A. Mathelier**, C. Chong, A. Sliwa-Primorac, Y.-K. Hong, J.W. Shin, M. Lizio, M. Itoh, H. Kawaji, T. Lassmann, C.O. Daub, E. Arner, the FANTOM consortium, P. Carninci, Y. Hayashizaki, A.R.R. Forrest, W.W. Wasserman, and M. Detmar. DeepCAGE transcriptomics identify HOXD10 as transcription factor regulating lymphatic endothelial responses to VEGF-C. *Journal of Cell Science*, doi:10.1242/jcs.186767.

R.A.G. De Souza, S.A. Islam, L.M. McEwen, **A. Mathelier**, A. Hill, S.M. Mah, W.W. Wasserman, M.S. Kobor, and B.R. Leavitt. DNA methylation profiling in human Huntington's disease brain. *Human Molecular Genetics*, doi:10.1093/hmg/ddw076.

A. Mathelier, O. Fornes, D.J. Arenillas, C.-Y. Chen, G. Denay, J. Lee, W. Shi, C. Shyr, G. Tan, R. Worsley-Hunt, A.W. Zhang, F. Parcy, B. Lenhard, A. Sandelin, and W.W. Wasserman. JASPAR 2016: a major expansion and update of the open-access database of transcription factor binding profiles. *Nucleic Acids Research*, doi:10.1093/nar/gkv1176.

2015 L.C. Dietrich*, S. Klein*, **A. Mathelier**, A. Primorac, Q. Ma, Y.-K. Hong, J.W. Shin, M. Hamada, M. Lizio, M. Itoh, H. Kawaji, T. Lassman, C.O. Daub, E. Arner, P. Carninci, Y. Hayashizaki, the FANTOM5 consortium, A.R.R. Forrest, W.W. Wasserman, and M. Detmar. The transcription factor MAFB links VEGFR-3 signaling with PROX1 expression in lymphatic endothelial cells. *Cell Reports*, doi:10.1016/j.celrep.2015.10.002.

A. Mathelier, C. Lefebvre, A.W. Zhang, D.J. Arenillas, J. Ding, W.W. Wasserman, and S.P. Shah. Cis-Regulatory Somatic Mutations and Gene-Expression Alteration in B-cell Lymphomas. *Genome Biology*, doi:10.1186/s13059-015-0648-7.

A. Mathelier, W. Shi, and W.W. Wasserman. Identification of altered cis-regulatory elements in human diseases. *Trends in Genetics*, doi:10.1016/j.tig.2014.12.003.

2014 A. Saumet, **A. Mathelier**, and C.H. Lecellier. The potential of microRNAs in personalized medicine against cancers. *Biomed Research International*, doi:10.1155/2014/642916.

R. Worsley-Hunt, **A. Mathelier**, L. Del Peso, and W.W. Wasserman. Improving detection and analysis of transcription factor binding sites within ChIP-seq data based on topological motif enrichment. *BMC Genomics*, doi:10.1186/1471-2164-15-472.

A.R. Forrest, ..., **A. Mathelier**, ..., Y. Hayashizaki, The FANTOM5 Consortium (~275 authors). A promoter level mammalian expression atlas. *Nature*, doi:10.1038/nature13182.

L. Yang, T. Zhou, I. Dror, **A. Mathelier**, W.W. Wasserman, R. Gordan, and R. Rohs. TFBSshape: a motif database for DNA shape features of transcription factor binding sites. *Nucleic Acids Research*, doi:10.1093/nar/gkt1087.

A. Mathelier*, X. Zhao*, A.W. Zhang, F. Parcy, R. Worsley-Hunt, D.J. Arenillas, S. Buchman, C.-Y. Chen, A. Chou, H. Ienasescu, J. Lim, C. Shyr, G. Tan, M. Zhou, B. Lenhardt, A. Sandelin, and W.W. Wasserman. JASPAR 2014: an extensively expanded and updated open-access database of transcription factor binding profiles. *Nucleic Acids Research*, doi:10.1093/nar/gkt997.

2013 **A. Mathelier** and W.W. Wasserman. The next generation of transcription factor binding site prediction. *PLOS Computational Biology*, doi:10.1371/journal.pcbi.1003214.

A. Mathelier and A. Carbone. Large scale chromosomal mapping of human microRNA structural clusters. *Nucleic Acids Research*, doi:10.1093/nar/gkt112.

2012 J.-F. Schmouth, K.G. Banks, **A. Mathelier**, C.Y. Gregory-Evans, M. Castellarin, R. Holt, K. Gregory-Evans, W.W. Wasserman and E.M. Simpson. Retina restored and brain abnormalities ameliorated by single-copy knock-in of Human NR2E1 in null mice. *Molecular and Cellular Biology*, doi:10.1128/MCB.06016-11.

2010 **A. Mathelier** and A. Carbone. MiReNA: finding microRNAs with high accuracy and no learning at genome scale and from deep sequencing data. *Bioinformatics*, doi:10.1093/bioinformatics/btq329.

A. Mathelier and A. Carbone. Chromosomal periodicity and positional networks of genes in Escherichia coli. *Molecular Systems Biology*, doi:10.1038/msb.2010.21.

Presentations

Conference / Symposium /
Workshop talks (last 5

years)	2021	Symposium "Where are we in the search for DNA motifs involved in transcriptional regulation?" at the JOBIM conference, invited speaker (Virtual) Workshop "Genomic Regulation: Focus on Cancer", invited speaker (Virtual)
	2019	EMBL conference - Perspectives in Translational Medicine, invited speaker (Barcelona, Spain)
	2018	NuGOweek 2018 - Mitochondria, Nutrition, and Health, keynote speaker (Newcastle, UK) French Bioinformatics Conference (JOBIM) (Marseille, France) Anniversary RSAT / GINsim workshop, invited speaker (Paris, France)
	2017	Oslo Epigenetics Mini Symposium, invited speaker (Oslo, Norway)
	2016	European Conference on Computational Biology, highlight talk (The Hague, The Netherlands)
	2015	Basel Computational Biology Conference, highlight talk (Basel, Switzerland) Basel Computational Biology Conference, Workshop "Beyond position weight matrices" (Basel, Switzerland)

Invited seminar talks

(last 5 years)

2019	Institute for Cancer Research seminars (Oslo, Norway)
2018	Institut Curie (Paris, France) Molecular Genetics Institute of Montpellier (Montpellier, France) EMBL Heidelberg blue seminars (Heidelberg, Germany)
2017	Gene Regulation Ensemble Effort for the Knowledge Commons meeting (Lisbon, Portugal) VIB - KU Leuven seminars (Leuven, Belgium)
2016	Department of Cancer Genetics, Oslo University Hospital (Oslo, Norway) Furberg CLS seminar series (Oslo, Norway)

Supervision

Current	Hallvard Wæhler (Ph.D. student since 2021, co-supervision with Dr. Ragnhild Eskeland) Katalin Ferenc (Ph.D. student since 2021) Ieva Rauluseviciute (Ph.D. student since 2020) Rafael Riudavets Puig (Ph.D. student since 2019) Vipin Kumar (Postdoctoral fellow since 2020) Roza Berhanu Lemma (Postdoctoral fellow since 2019) Jaime Castro-Mondragon (Postdoctoral fellow since 2017) Dina Aronsen (Lab technician since 2021) Paul Boddie (Software developer since 2020)
Alumni	Aziz Khan (2016-2019, postdoctoral fellow, moved to a researcher position in Christina Curtis' group, Stanford University) Marius Gheorghe (2016-2019, PhD student, moved to a senior bioinformatician position for the NEC Oncolmmunity company) Timothée Launay (Master student, 4 months) Solveig Klokkerud (Master student, 10 months) Arnaud Stigliani (visiting Ph.D. student, 3 months) Kübra Altinel (Master student, 10 months) Victor Laigle (Master student, 3 months) Eleftherios Pavlos (Master student, Erasmus plus programme, 3 months)

Academic activities

Conference / Workshop /

Seminar Series organizer	2017-	Sven Furberg Seminars in Bioinformatics and Statistical Genomics (Oslo, Norway).
	2021	ISMB Regulatory and Systems Genomics, ISMB/ECCB 2021 conference (virtual).
	2020	ISMB Regulatory and Systems Genomics, ISMB 2020 conference (virtual).
	2019	ISMB Regulatory and Systems Genomics, ISMB/ECCB 2019 conference (Basel, Switzerland)
	2018	Nordic EMBL Partnership meeting (Oslo, Norway)

2012 European Conference on Computational Biology, Workshop "Detecting transcription factor binding sites with ChIP-seq data and predicting damaging cis-regulatory variations" (Basel, Switzerland)

Referee activities

Ph.D. defense and

committee

2021 Opponent for the Ph.D. defense of Raphael Romero (supervisor Charles-Henri Lecellier), Institut de Génétique Moléculaire de Montpellier (Montpellier, France).

2020 Opponent and reviewer for the Ph.D. defense of Axel Thieffry (supervisor Albin Sandelin), Bioinformatics Centre, Copenhagen University (Copenhagen, Denmark).

Committee member of the mid-term Ph.D. evaluation of Ping-Han Hsieh (supervisor Marieke Kuijjer), Centre for Molecular Medicine Norway, University of Oslo (Oslo, Norway).

2019 Opponent and reviewer for the Ph.D. defense of Bram Van de Sande (supervisor Stein Aerts), VIB (Leuven, Belgium).

2018 Opponent and reviewer for the Ph.D. defense of Chloé Bessièrè (supervisor Charles-Henri Lecellier), Institut de Génétique Moléculaire de Montpellier (Montpellier, France).

2017 Committee member of the mid-term Ph.D. evaluation of Jonas Meier Stromme (supervisor Rolf Skotheim), Oslo University Hospital (Oslo, Norway).

Committee member of the mid-term Ph.D. evaluation of Fatima Heinicke (supervisor Benedicte Lie), University of Oslo (Oslo, Norway).

2016 First opponent for the Ph.D. defense of Rezvan Ehsani (supervisor Finn Drablos), Norwegian University of Science and Technology (Trondheim, Norway).

First opponent for the Ph.D. defense of Bjarne Johannessen (supervisor Rolf I. Skotheim), Oslo University Hospital (Oslo, Norway).

Recruitment committee

2019 Member of the selection committee for the recruitment of a Group Leader at NCMM

2018 Member of the selection committee for the recruitment of a Group Leader at NCMM

2013 Member of the Canada Research Chairs Tier 2 / Associate Professor recruitment committee in Statistical Genetics at the University of British Columbia (Vancouver, Canada).

Journals and conferences

Associate Editor for the journal Bioinformatics, Oxford University Press since 2019

77 reviews for 20 international peer-reviewed journals

Member of reviewing committee for RECOMB/ISCB conference on Regulatory & Systems Genomics (2020), Journées Ouvertes Biologie, Informatique et Mathématique (2020), ISMB Regulatory and Systems Genomics (2019, 2020)

Teaching activities

Ph.D. Systems medicine approaches in cancer, NCMM Molecular Medicine Research Course (Oslo, Norway)

Master Statistics in bioinformatics and algorithms on sequences, UPMC (Paris, France)

Bachelor Recursive programming in Scheme, UPMC (Paris, France)



Imperative programming and data structures in C, UPMC (Paris, France)

Discrete structures, UPMC (Paris, France)

Imperative programming in Visual Basic, UPMC (Paris, France)

Types and data structures in Caml, UPMC (Paris, France)

Links

 anthony.mathelier@ncmm.uio.no
 @AMathelier

 scholar
 Pubmed
 Publons

 CBGR
 amathelier

Footer

Last updated: Oct. 20th 2021