

Pierre Neuvial

CNRS director of research

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Research interests

- Post-hoc/post-selection inference: see ANR project SansSouci and CNRS 80' project DDisc
- Multiple testing: theory and applications
- Statistical methods for high-dimensional data analysis
- Performance evaluation of statistical methods
- Applications to genomics and neuroimaging
- Reproducible research

Experience

- 2021-present CNRS researcher (DR) - CID 51. Institut de Mathématiques de Toulouse
- 2016-2021 CNRS researcher (CR) - section 41. Institut de Mathématiques de Toulouse
- 2011-2016 CNRS researcher (CR) - section 41. UMR CNRS 8071 (Évry)
- 2010-2011 Post-doc. UMR CNRS 8071 (Évry)
- 2008-2010 Post-doc. UC Berkeley - Department of Statistics (USA)
- 2003-2005 Research engineer in statistics and bioinformatics. Institut Curie Bioinformatics (Paris)
- 2001-2002 Intern statistician. Groupe de Recherche Opérationnelle, Crédit Lyonnais (Paris)

Education

- 2021 **Qualification PR**, *CNU Section 26*.
- 2020 **Habilitation à Diriger des Recherches (HDR)**, *Université Paul Sabatier*.
 - Manuscript: Contributions to statistical inference from genomic data
- 2009 **Qualification MCF**, *CNU Section 26*.
- 2004-2008 **PhD in Applied Mathematics**, *Université Paris Diderot (Paris 7)*.
 - Manuscript: Contributions to the statistical analysis of DNA microarray data
- 2002-2003 **M. S. in Stochastic models**, *Université Paris Diderot (Paris 7)*.
- 1999-2003 **ENSAE Paris**.

Teaching

For mathematicians/statisticians (M.Sc. level)

- 2022-2024 Asymptotic statistics (15h). Univ. Paul Sabatier/ISAE (Toulouse)
- 2017-2024 Statistical methods for genomic data analysis (12h). ENSAI (Rennes)
- 2018-2020 Asymptotic statistics (15h). Univ. Paul Sabatier/ISAE (Toulouse)
- 2015-2018 Statistical methods for genomic data analysis (3h). Institut des Actuaire (Paris)
- 2015-2016 Programming for genomics (15h). Université d'Évry val d'Essonne
- 2011-2015 Statistical methods for molecular biology (8h). ENSAE ParisTech
- 2011 Statistical methods for genomic data analysis (10h). ENSAI (Rennes)
- 2011-2012 Introduction to Statistical methods for molecular biology (6h). École Centrale Paris
- 2005-2008 Statistical methods for molecular biology (8h). ENSAE Paris
- 2004-2008 Mathematical Statistics (24h). ENSAE Paris (practicals)

For biologists/bioinformaticians (M.Sc. level)

- 2013-2015 Statistical tests (20h). Université d'Évry val d'Essonne
- 2011-2015 Statistical methods for genomic data analysis (18h). Univ. Paris Sud / Orsay
- 2011-2012 Statistical tests (16.5h). Université d'Évry val d'Essonne (practicals)
- 2004-2007 DNA copy number analysis (3h). Université Paris Diderot / Paris 7

Other

- 2020-2022 Introduction to shiny (12h). Plateforme biostatistique Génomoul
- 2020-2022 Introduction to ggplot2 (12h). Plateforme biostatistique Génomoul
- 2020-2021 Approfondissement en statistique (avec R) (12h). Plateforme biostatistique Génomoul
- 2017-2021 Supervision of student projects (4th and 5th year) (8h). INSA Toulouse
- 2017 Tests multiples pour la biologie et la médecine (4h). Groupe de travail INSERM Interstats

Postdoc supervision

- 2018-05 **Magali Champion**, *Funded by ANR SansSouci*.
 - ○ Subject: Post hoc inference
- 2018-08 ○ Current position: Assistant Professor at Université de Paris
- 2019-09 **Marie Perrot-Dockès**, *Funded by ANR SansSouci*.
 - ○ Subject: Post hoc false discovery proportion inference under a Hidden Markov Model
- 2020-08 ○ Co-supervised by Gilles Blanchard and Etienne Roquain
- Current position: Assistant Professor at Université de Paris
- 2021-11 **Samuel Davenport**, *Funded by ANR SansSouci*.
 - ○ Subject: False discovery proportion control in multivariate linear models using the bootstrap
- 2021-08 ○ Co-supervised by Bertrand Thirion
- Current position: postdoc at University of California San Diego

Student supervision

Current students

- Since **Javier González Delgado (50%)**, *Funded by Labex CIMI*.
2020-10 ○ Subject: Statistical models and methods for the structural analysis of intrinsically disordered proteins
○ Co-supervised by Juan Cortés (LAAS)
- Since **Nicolas Enjalbert-Courech (50%)**, *Funded by CNRS 80' project DDisc*.
2021-10 ○ Subject: Post-clustering inference for single-cell RNA sequencing data
○ Co-supervised by Cathy Maugis-Rabusseau
- Since **Alexandre Blain (50%)**, *Funded by UDOPIA (Paris Saclay)*.
2021-11 ○ Subject: Reliable statistical inference: controlling the false discovery proportion in high-dimensional multivariate estimators
○ Co-supervised by Bertrand Thirion

Past students

- 2012-2015 **Alia Dehman (50%)**, *Funded by École doctorale GAO, University of Évry*.
○ Subject: “Spatial clustering of Linkage Disequilibrium Blocks for Genome-Wide Association Studies”
○ Co-supervised by Christophe Ambroise
○ Current position: Data scientist at Aviwell in Toulouse.
- 2013-2016 **Morgane Pierre-Jean (100%)**, *Funded by École doctorale GAO, University of Évry*.
○ Subject: “Statistical methods for the analysis of structured genomic data. Applications in cancerology.”
○ Co-supervised by Catherine Matias
○ Current position: Data scientist at Data Scientist at CHU de Rennes.
- 2013-2017 **Benjamin Sadacca (50%)**, *Funded by Institut Curie*.
○ Subject: “Tumoral microenvironment and treatment response in breast cancers” (50%)
○ Co-supervised by Fabien Reyal
○ Current position: Principal Scientist in Bioinformatics at Mnemo Therapeutics
- 2015-2018 **Guillermo Durand (50%)**, *Funded by École doctorale des Sciences Mathématiques de Paris Centre*.
○ Subject: “Multiple testing and post hoc bounds for heterogeneous data”
○ Co-supervised by Etienne Roquain
○ Current position: Assistant professor at Université Paris-Saclay
- 2018-2021 **Nathanaël Randriamihamison (30%)**, *Funded by INRA/Inria*.
○ Subject: Adjacency-constrained hierarchical agglomerative clustering with application to Hi-C studies
○ Co-supervised by Nathalie Vialaneix & Marie Chavent & Sylvain Foissac
○ Current position: Assistant Professor at Université de Paris

Selected research funding (as PI or co-PI)

- 2017-2019 [CNRS "Osez l'Interdisciplinarité !"] **SCALES: Multi-scale and data-driven inference for genomic data (105k€)**.
○ with INRAE MIAT+GenPhySE and CRCT Oncopole

- 2016-2021 [ANR JCJC] **SansSouci: Post-hoc approaches for large scale multiple testing (192k€).**
 - includes funding for a 2 year post doc
- 2021-2022 [CNRS 80 Prime] **DDisc: Post-clustering inference for single cell RNAseq studies (143k€).**
 - includes funding for a 3-year PhD thesis (2021-2024)
 - with INRAE, LIPME and RESTORE
- 2023-2026 [ANR] **CORNFLEX: Computational Design of Intrinsically Disordered Proteins: Application to Flexible Linkers (151k€).**
 - PI: Juan Cortés (LAAS)

Participation to other grants

- 2021-2023 [INRAE DIGIT-Bio] **PEERSIM: Planification d'expériences pour l'Étude de la Réponse aux Stress-multiples et l'Intégration Multi-omique..**
 - PI: Guillem Rigail (INRAE/LaMME)
- 2021-2024 [ANR JCJC] **GAP: Gaussian Processes for computer experiments and machine learning: more guarantees and broader applications..**
 - PI: François Bachoc (IMT)

Software development

Contribution to the development and technical support of R packages within open source and collaborative projects of statistical/bioinformatics tools, including:

- sanssouci: R and python implementations (github), IIDEA R/shiny application,
- acnr, jointseg, adjclust, tmle.npvi (CRAN),
- MANOR, DEGraph (Bioconductor),
- aroma.cn, aroma.cn.eval (the Aroma Project).

See <https://www.math.univ-toulouse.fr/~pneuvial/software>

Editorial boards

Since 2021 **Computo**, *Associate Editor*.

2015-2020 **The International Journal of Biostatistics**, *Associate Editor*.

Review activities

Review for journals in Statistics/Machine Learning

American Statistician (2016), Annals of Applied Statistics (2009, 2011), Annals of Statistics (2013, 2015, 2016, 2017), Australian & New Zealand Journal of Statistics (2019), Bernoulli (2022), Computational Learning Theory (2018), Electronic Journal of Statistics (2012, 2023), Journal de la Société Française de Statistique (2014), Journal of Machine Learning Research (2008, 2019), Journal of the American Statistical Association (2016, 2017), Scandinavian journal of Statistics (2015), Statistica Sinica (2015), Statistics (2013, 2021), Statistics and Probability Letters (2019).

Review for journals in applied statistics/bioinformatics

Advances in Bioinformatics (2012), BMC Bioinformatics (2011, 2014 x2), BMC Genomics (2012), Bioinformatics (2014 x3, 2018, 2020), Biostatistics (2011), Briefings in Bioinformatics (2020, 2021, 2022), EURASIP Journal on Bioinformatics and Systems Biology (2014), Genome Research (2009), PLoS One (2012), Statistics in Medicine (2009, 2017).

Review for funding agencies

European Research Council (ERC), French National Research Agency (ANR), German-Israeli Foundation for Scientific Research and Development, Grenoble-Alpes University IRGA, Ile de France DIM Elicit, Netherlands Organisation for Scientific Research, U.S.-Israel Binational Science Foundation, i-Site MUSE (Montpellier University).

Conference organization

- Nov 2015 **Statistical analysis of Massive genomic data**, Évry.
 - Co-organized with Christophe Ambroise & Bernard Prum
 - ~ 80 participants
- Feb 2018 **Post-selection inference and multiple testing**, Toulouse.
 - Co-organized with Mélisande Albert & Gilles Blanchard & Etienne Roquain
 - ~ 40 participants
- Apr 2019 **“Journées IMAG-IMT”**, Toulouse.
 - Co-organized with Marcello Bernardara & Florent Chazel & Alice Cleynen & Clément Dupont
 - ~ 100 participants
- Jul 2019 **useR!2019**, Toulouse.
 - Member of the local organization committee and vice-chair of the scientific committee
 - ~ 1200 participants
- Dec 2019 **Workshop Chromatin conformation and Hi-C data**, Toulouse.
 - Co-organized with Nathalie Vialaneix and Sylvain Foissac
 - ~ 50 participants
- Jul 2021 **Mini symposium at JOBIM 2021: post-selection inference for bioinformatics**, virtual.
 - Co-organized with Chloé-Agathe Azencott and Cathy Maugis-Rabusseau
 - 4 invited talks (Y. Benjamini/M. Ebrahimpour/L. Gao/A. Villié)

- Mar 2022 **Workshop « Post-selection inference for genomic and neuroimaging data »**, Toulouse.
- 15 participants
- Oct 2022 **Workshop « Statistical challenges in scRNA-seq data analysis » (program)**, Toulouse.
- Co-organized with Cathy Maugis-Rabusseau and Nicolas Enjalbert-Courrech
 - 15 participants

Scientific committees

- GDR MathSAV: MATHématiques, SANTé, sciences de la Vie (since 2021)
- Statistical Methods for Post-Genomic Data (SMPGD) workshop (since 2020)
 - Organization of the session “Machine Learning for Protein Design’ ’ at SMPGD2021
- Génomol Bioinformatics/Biostatistics day (since 2018)

Comités de sélection

- 2023 Professor. Université Paul Sabatier (Toulouse 3)/IMT. Role: Vice-president
- 2022 Assistant Professor. Univ. Jean-Jaurès (Toulouse 2)/IMT. Role: Vice-president
- 2022 Professor. Université de Paris/MAP5
- 2022 Two Research Scientists (CR). INRAE (MathNum department)
- 2021 Assistant Professor. Institut National des Sciences Appliquées (INSA) Toulouse/IMT
- 2021 Two Research Scientists (CR). INRAE (MathNum department)
- 2020 Assistant Professor. Université Paul Sabatier (Toulouse 3)/IMT
- 2017 Assistant Professor. Institut National des Sciences Appliquées (INSA) Toulouse/IMT
- 2016 Assistant Professor. Université de Bordeaux/Institut de santé publique d'épidémiologie et de développement (ISPED)
- 2013 Assistant Professor. Université Paris-Sud

Thesis reports

PhD theses

- 2021 **Marine Gauthier**, Université de Bordeaux.
- Title: Méthodes statistiques pour l'analyse différentielle de données RNA-seq en masse et en cellule unique appliquées en immunologie
 - Supervised by Boris Hejblum & Rodolphe Thiébaud (SISTM - Inria & INSERM Bordeaux)
- 2021 **Anna Vesely**, University of Padova (Italy).
- Title: Resampling-based methods for multiple testing on high-dimensional data
 - Supervised by J. Goeman (Leiden University - Netherlands) & Livio Finos (University of Padova - Italy)

- 2022 **Wencan Zhu**, AgroParisTech.
 ○ Title: Development of machine learning approaches in precision medicine for the identification of prognostic and predictive biomarkers based on high-dimensional omics data
 ○ Supervised by Céline Lévy-Leduc (AgroParisTech) & Nils Ternès (Sanofi)
- 2022 **Perrine Lacroix**, Université Paris Saclay.
 ○ Title: Contributions à la sélection de variables en grande dimension et ses utilisations en biologie
 ○ Supervised by Pascal Massart & Marie-Laure Martin-Magniette
- 2023 **Antoine Villié**, Université Lyon 1.
 ○ Title: Quantifier l'Incertitude de l'Explicabilité en Apprentissage Automatique : Inférence Post-Sélection sur des Caractéristiques Biologiques Interprétables.
 ○ Supervised by Laurent Jacob & Yohann de Castro

Habilitation theses

- 2022 **Cyril Dalmasso**, University of Evry.
 ○ Title: Contributions à l'analyse statistique de données génomiques de grande dimension dans le domaine de la santé

Thesis defenses

- 2017 **Victor Bellon**, Paris Sciences Lettres University.
 ○ Title: Personalized drug adverse side effect prediction
 ○ Supervised by Chloé-Agathe Azencott & Véronique Stoven
- 2018 **Marine Roux**, Université Grenoble Alpes.
 ○ Title: Graph Inference by Multiple Testing with Application to Neuroimaging
 ○ Supervised by Sophie Achard & Pierre Borgnat & Irène Gannaz & Etienne Roquain
- 2018 **Marta Cousido-Rocha**, Universita de Vigo (Spain).
 ○ Title: New contributions to the statistical analysis of high-dimensional data under dependence
 ○ Supervised by Jacobo de Uña Álvarez
- 2019 **Marie Perrot-Dockès**, Université Paris Saclay.
 ○ Title: Méthodes régularisées pour l'analyse de données multivariées en grande dimension : théorie et applications
 ○ Supervised by Julien Chiquet & Céline Lévy-Leduc & Laure Sansonnet
- 2019 **Florian Hébert**, Université de Bretagne-Loire.
 ○ Title: Prise en compte de la dépendance pour des problèmes de test global et de prédiction
 ○ Supervised by David Causeur & Mathieu Emily
- 2020 **Lotfi Slim**, Mines ParisTech.
 ○ Title: Detection of Epistasis in Genome Wide Association Studies with Machine Learning Methods for Therapeutic Target Identification
 ○ Supervised by supervised by Chloé-Agathe Azencott & Clément Chatelain
- 2020 **Wei Jiang**, Université Paris Saclay.
 ○ Title: Statistical inference with incomplete and high-dimensional data—modeling polytraumatized patients
 ○ Supervised by Julie Josse & Marc Lavielle

- 2020 **Jérôme-Alexis Chevalier**, Université Paris Saclay.
- Title: Contrôle statistique de modèles parcimonieux en grande dimension
 - Supervised by Joseph Salmon & Bertrand Thirion
- 2021 **Marine Gauthier**, Université de Bordeaux.
- Title: Méthodes statistiques pour l'analyse différentielle de données RNA-seq en masse et en cellule unique appliquées en immunologie
 - Supervised by Boris Hejblum & Rodolphe Thiébaud (SISTM - Inria & INSERM Bordeaux)
- 2022 **Wencan Zhu**, AgroParisTech.
- Title: Development of machine learning approaches in precision medicine for the identification of prognostic and predictive biomarkers based on high-dimensional omics data
 - Supervised by Céline Lévy-Leduc (AgroParisTech) & Nils Ternès (Sanofi)
- 2023 **Antoine Villié**, Université Lyon 1.
- Title: Quantifier l'Incertitude de l'Explicabilité en Apprentissage Automatique : Inférence Post-Sélection sur des Caractéristiques Biologiques Interprétables.
 - Supervised by Laurent Jacob & Yohann de Castro

External member for the PhD thesis committee(s) of 12 PhD students since 2013.

Habilitation theses

Research management

- since 2020: “Responsable d'équipe” for the Statistics and Optimization team at IMT
- since 2019: local contact for the Mathematics, Biology and Health group at IMT
- 01/2014-06/2016: “Adjoint au directeur” at Laboratoire de Mathématiques et Modèles Aléatoires d'Évry (LaMME)

Seminars, workgroups, local scientific animation

- 2018-2019: co-organization of the Statistics seminar at IMT
- fall 2018: co-organization of the “journée des doctorants” at IMT-ESP
- 2018: co-organization of the Mathematics for Biology seminar at IMT
- 2017-2018: Workgroup “Post-selection inference” at Institut de Mathématiques de Toulouse
- 2017: Workgroup “Multiple testing” at Institut de Mathématiques de Toulouse
- 2012: Organization of the “Fête de la science” for the Department of Mathematics of the University of Évry

Other responsibilities

- Since 2019: Commission Administrative Paritaire (CAP) du CNRS:
 - Since 2023: membre nommé (suppléant) de la CAP 1 (CR et DR)
 - 2019-2022: membre nommé (suppléant) de la CAP 2 (CR)
- 2018-2020: référent HAL pour l'IMT

Publications

Preprints

1. Gonzalez-Delgado, J., Mier, P., Bernado, P., Neuvial, P., & Cortes, J. (2022). *Statistical tests to detect differences between codon-specific ramachandran plots*. <https://www.biorxiv.org/content/10.1101/2022.11.29.518303>
2. Davenport, S., Thirion, B., & Neuvial, P. (2022). *FDP control in multivariate linear models using the bootstrap*. <https://doi.org/10.48550/ARXIV.2208.13724>
3. Perrot-Dockès, M., Blanchard, G., Neuvial, P., & Roquain, E. (2021). *Post hoc false discovery proportion inference under a hidden markov model*. <https://hal.archives-ouvertes.fr/hal-03214472>

To appear

1. González-Delgado, J., González-Sanz, A., Cortés, J., & Neuvial, P. (2021). Two-sample goodness-of-fit tests on the flat torus based on wasserstein distance and their relevance to structural biology. *Electronic Journal of Statistics*. <https://hal.archives-ouvertes.fr/hal-03369795v2>
2. González-Delgado, J., Sagar, A., Zanon, C., Lindorff-Larsen, K., Bernadó, P., Neuvial, P., & Cortés, J. (2023). WASCO: A wasserstein-based statistical tool to compare conformational ensembles of intrinsically disordered proteins. *Journal of Molecular Biology*, 168053. <https://doi.org/https://doi.org/10.1016/j.jmb.2023.168053>

International journals

1. González-Delgado, J., Bernadó, P., Neuvial, P., & Cortés, J. (2022). Statistical proofs of the interdependence between nearest neighbor effects on polypeptide backbone conformations. *Journal of Structural Biology*, 214(4), 107907.
2. Enjalbert-Courrech, N., & Neuvial, P. (2022). Powerful and interpretable control of false discoveries in differential expression studies. *Bioinformatics*, 38(23), 5214–5221. <https://doi.org/10.1093/bioinformatics/btac693>
3. Blain, A., Thirion, B., & Neuvial, P. (2022). Notip: Non-parametric True Discovery Proportion control for brain imaging. *Neuroimage*, 260. <https://doi.org/10.1016/j.neuroimage.2022.119492>
4. Champion, M., Chiquet, J., Neuvial, P., Elati, M., Radvanyi, F., & Birmelé, E. E. (2021). Identification of Deregulated Mechanisms Specific to Bladder Cancer Subtypes. *Journal of Bioinformatics and Computational Biology*, 19(1), 2140003. <https://doi.org/10.1142/S0219720021400035>
5. Randriamihamison, N., Vialaneix, N., & Neuvial, P. (2021). Applicability and Interpretability of Ward Hierarchical Agglomerative Clustering With or Without Contiguity Constraints. *Journal of Classification*. <https://doi.org/https://dx.doi.org/10.1007/s00357-020-09377-y>
6. Blanchard, G., Neuvial, P., & Roquain, E. (2020). Post hoc confidence bounds on false positives using reference families. *Annals of Statistics*, 48(3), 1281–1303. <https://projecteuclid.org/euclid.aos/1594972818>
7. Pont, F., Tosolini, M., Gao, Q., Perrier, M., Madrid-Mencía, Huang, T. S., Neuvial, P., Ayyoub, M., Nazor, K., & Fournié, J.-J. (2020). Single-Cell Virtual Cytometer allows user-friendly and versatile analysis and visualization of multimodal single cell RNAseq datasets. *NAR Genomics and Bioinformatics*. <https://www.biorxiv.org/content/10.1101/843946v1>
8. Durand, G., Blanchard, G., Neuvial, P., & Roquain, E. (2020). Post hoc false positive control for structured hypotheses. *Scandinavian Journal of Statistics*, 47(4), 1114–1148. <https://doi.org/10.1111/sjos.12453>

9. Ambroise, C., Dehman, A., Neuvial, P., Rigaiil, G., & Vialaneix, N. (2019). Adjacency-constrained hierarchical clustering of a band similarity matrix with application to Genomics. *Algorithms for Molecular Biology*, 14(22). <https://almob.biomedcentral.com/track/pdf/10.1186/s13015-019-0157-4>
10. Bachoc, F., Blanchard, G., & Neuvial, P. (2018). On the post selection inference constant under restricted isometry properties. *Electron. J. Statist.*, 12(2), 3736–3757. <https://doi.org/10.1214/18-EJS1490>
11. Sadacca, B., Hamy-Petit, A.-S., Laurent, C., Gestraud, P., Bonsang-Kitzis, H., Pinheiro, A., Abecassis, J., Neuvial, P., & Reyat, F. (2017). New insight for pharmacogenetics studies from the transcriptional analysis of two large-scale cancer cell line panels. *Scientific Reports*, 7, 15126. <https://www.nature.com/articles/s41598-017-14770-6>
12. Picchetti, T., Chiquet, J., Elati, M., Neuvial, P., Nicolle, R., & Birmelé, E. (2015). A model for gene deregulation detection using expression data. *BMC Systems Biology*. <http://bmcsystbiol.biomedcentral.com/articles/10.1186/1752-0509-9-S6-S6>
13. Chambaz, A., & Neuvial, P. (2015). Tmle.npvi: Targeted, integrative search of associations between DNA copy number and gene expression, accounting for DNA methylation. *Bioinformatics*, 31(18), 3054–3056. <https://academic.oup.com/bioinformatics/article/31/18/3054/241218>
14. Pierre-Jean, M., Rigaiil, G. J., & Neuvial, P. (2015). Performance evaluation of DNA copy number segmentation methods. *Briefings in Bioinformatics*, 4, 600–615. <https://academic.oup.com/bib/article/16/4/600/347347>
15. Dehman, A., Ambroise, C., & Neuvial, P. (2015). Performance of a blockwise approach in variable selection using linkage disequilibrium information. *BMC Bioinformatics*. <http://bmcbioinformatics.biomedcentral.com/articles/10.1186/s12859-015-0556-6>
16. Brito, I., Hupé, P., Neuvial, P., & Barillot, E. (2013). Stability-based comparison of class discovery methods for array-CGH profiles. *PLoS One*, 8(12), e81458. <http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0081458>
17. Neuvial, P. (2013). Vers une médecine personnalisée grâce à la recherche en génomique. *Variances*, 48, 31–33.
18. Neuvial, P. (2013). Asymptotic results on adaptive false discovery rate controlling procedures based on kernel estimators. *Journal of Machine Learning Research*, 14, 1423–1459. <http://jmlr.org/papers/v14/neuvial13a.html>
19. Neuvial, P., & Roquain, E. (2012). On false discovery rate thresholding for classification under sparsity. *Annals of Statistics*, 40(5), 2572–2600. <https://projecteuclid.org/euclid.aos/1359987531>
20. Chambaz, A., Neuvial, P., & Laan, M. J. van der. (2012). Estimation of a non-parametric variable importance measure of a continuous exposure. *Electron. J. Statist.*, 6, 1059–1099. <https://projecteuclid.org/euclid.ejs/1340369355>
21. Ortiz-Estevéz, M., Aramburu, A., Bengtsson, H., Neuvial, P., & Rubio, A. (2012). CalMaTe: A method and software to improve Allele-Specific copy number of SNP arrays for downstream segmentation. *Bioinformatics*, 28(13), 1793–1794. <https://academic.oup.com/bioinformatics/article/28/13/1793/234984/>
22. Jacob, L., Neuvial, P., & Dudoit, S. (2012). More power via graph-structured tests for differential expression of gene networks. *Annals of Applied Statistics*, 6(2), 561–600. <https://projecteuclid.org/euclid.aos/1339419608>

23. Heiser, L. M., Sadanandam, A., Kuo, W. L., Benz, S. C., Goldstein, T. C., Ng, S., Gibb, W. J., Wang, N. J., Ziyad, S., Tong, F., Bayani, N., Hu, Z., Billig, J. I., Dueregger, A., Lewis, S., Jakkula, L., Korkola, J. E., Durinck, S., Pepin, F., ... Spellman, P. T. (2012). Subtype and pathway specific responses to anticancer compounds in breast cancer. *Proceedings of the National Academy of Sciences*, *109*(8), 2724–2729. <http://www.pnas.org/content/109/8/2724.long>
24. Neuvial, P. (2011). Tests multiples en génomique. *La Gazette Des Mathématiciens*, *130*, 71–76. <http://smf4.emath.fr/Publications/Gazette/2011/130/>
25. Olshen, A. B., Bengtsson, H., Neuvial, P., Spellman, P. T., Olshen, R. A., & Seshan, V. E. (2011). Parent-specific copy number in paired tumor-normal studies using circular binary segmentation. *Bioinformatics*, *27*(15), 2038–2046. <https://academic.oup.com/bioinformatics/article-lookup/doi/10.1093/bioinformatics/btr329>
26. The Cancer Genome Atlas Research Network. (2011). Integrated genomic analyses of ovarian carcinoma. *Nature*, *474* (7353), 609–615. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3163504/>
27. Noushmehr, H., Weisenberger, D. J., Diefes, K., Phillips, H. S., Pujara, K., Berman, B. P., Pan, F., Pelloski, C. E., Sulman, E. P., Bhat, K. P., Verhaak, R. G. W., Meyerson, M. L., Hoadley, K. A., Hayes, D. N., Perou, C. M., Schmidt, H. K., Ding, L., Wilson, R. K., Van Den Berg, D., ... Aldape, K. (2010). Identification of a CpG island methylator phenotype that defines a distinct subgroup of glioma. *Cancer Cell*, *17*(5), 510–522. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2872684/>
28. Bengtsson, H., Neuvial, P., & Speed, T. P. (2010). TumorBoost: Normalization of allele-specific tumor copy numbers from a single pair of tumor-normal genotyping microarrays. *BMC Bioinformatics*, *11*(1), 245. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2894037/>
29. Neuvial, P., & Bourguignon, P.-Y. (2009). Problématiques statistiques à l’heure de la post-génomique. *Variations*, *35*, 56–60. <https://hal.archives-ouvertes.fr/hal-01201651>
30. Neuvial, P. (2008). Asymptotic properties of false discovery rate controlling procedures under independence. *Electron. J. Statist.*, *2*, 1065–1110. <https://projecteuclid.org/euclid.ejs/1227287693>
31. Neuvial, P. (2009). Corrigendum to ‘asymptotic properties of false discovery rate controlling procedures under independence’. *Electron. J. Statist.*, *3*, 1083. <https://doi.org/10.1214/09-EJS519>
32. Bollet, M. A., Servant, N., Neuvial, P., Decraene, C., Lebigot, I., Meyniel, J.-P., De Rycke, Y., Savignoni, A., Rigai, G., Hupé, P., Fourquet, A., Sigal-Zafrani, B., Barillot, E., & Thiery, J.-P. (2008). High-resolution mapping of DNA breakpoints to define true recurrences among ipsilateral breast cancers. *J Natl Cancer Inst*, *100*(1), 48–58. <https://academic.oup.com/jnci/article-lookup/doi/10.1093/jnci/djm266>
33. Elati, M., Neuvial, P., Bolotin-Fukuhara, M., Barillot, E., Radvanyi, F., & Rouveirol, C. (2007). LICORN: LearnIng COoperative Regulation Networks. *Bioinformatics*, *23*(18), 2407–2414. <https://academic.oup.com/bioinformatics/article/23/18/2407/236890>
34. La Rosa, P., Viara, E., Hupé, P., Pierron, G., Liva, S., Neuvial, P., Brito, I., Lair, S., Servant, N., Robine, N., Manié, E., Brennetot, C., Janoueix-Lerosey, I., Raynal, V., Gruel, N., Rouveirol, C., Stransky, N., Stern, M.-H., Delattre, O., ... Barillot, E. (2006). VAMP: visualization and analysis of array-CGH, transcriptome and other molecular profiles. *Bioinformatics*, *22*(17), 2066–2073. <https://academic.oup.com/bioinformatics/article-lookup/doi/10.1093/bioinformatics/btl359>

35. Liva, S., Hupé, P., Neuvial, P., Brito, I., Viara, E., La Rosa, P., & Barillot, E. (2006). CAPweb: a bioinformatics CGH array Analysis Platform. *Nucleic Acids Res*, 34(Web Server issue), 477–481. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1538852/>
36. Neuvial, P., Hupé, P., Brito, I., Liva, S., Manié, E., Brennetot, C., Radvanyi, F., Aurias, A., & Barillot, E. (2006). Spatial normalization of array-CGH data. *BMC Bioinformatics*, 7(1), 264. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1523216/>

Book chapters

1. Neuvial, P., Foissac, S., & Vialaneix, N. (2023). Comprendre l'organisation spatiale de l'ADN à l'aide de la statistique. In *L'interdisciplinarité. Voyages au-delà des disciplines*.
2. Neuvial, P., Bengtsson, H., & Speed, T. P. (2011). Statistical analysis of single nucleotide polymorphism microarrays in cancer studies. In H. H.-S. Lu, B. Schölkopf, & H. Zhao (Eds.), *Handbook of statistical bioinformatics*. Springer. https://link.springer.com/chapter/10.1007%2F978-3-642-16345-6_11
3. Blanchard, G., Neuvial, P., & Roquain, E. (2021). On agnostic post hoc approaches to false positive control. In X. Cui, T. Dickhaus, Y. Ding, & J. C. Hsu (Eds.), *Handbook of multiple comparisons* (1st Edition). <https://hal.archives-ouvertes.fr/hal-02320543>

Theses

1. Neuvial, P. (2020). *Contributions to statistical inference from genomic data* [Habilitation thesis, Université Toulouse III (France)]. <https://tel.archives-ouvertes.fr/tel-02969229>
2. Neuvial, P. (2008). *Contributions à l'analyse statistique des données de puces à ADN* [PhD thesis, Institut Curie et Université Paris VII (France)]. <https://tel.archives-ouvertes.fr/tel-00433045>

Technical reports

1. Hauvuy, E., Lebrave, B., & Neuvial, P. (2003). *Analyse statistique du lien entre les plages homogènes de séquences d'ADN de différentes bactéries* [Master's thesis]. ENSAE Paristech et Université Paris Diderot.
2. Elie, R., Frachot, A., Georges, P., & Neuvial, P. (2002). *A Model of Prepayment for the French Residential Loan Market*. Groupe de Recherche Opérationnelle, Crédit Lyonnais, France.

Software

Main contributions

1. Blanchard, G., Durand, G., Neuvial, P., & Roquain, E. (2019). *Sanssouci: Post hoc multiple testing inference*. <https://pneuvial.github.io/sanssouci>
2. Ambroise, C., Chaturvedi, S., Dehman, A., Neuvial, P., Rigaille, G., & Vialaneix, N. (2018). *Adjclust: Adjacency-constrained clustering of a block-diagonal similarity matrix*. <https://CRAN.R-project.org/package=adjclust>
3. Pierre-Jean, M., & Neuvial, P. (2017). *Acnr: Annotated copy-number regions*. <https://CRAN.R-project.org/package=acnr>
4. Pierre-Jean, M., Rigaille, G., & Neuvial, P. (2019). *Jointseg: Joint segmentation of multivariate (copy number) signals*. <https://CRAN.R-project.org/package=jointseg>
5. Chambaz, A., & Neuvial, P. (2015). *Targeted learning of a non-parametric variable importance measure of a continuous exposure*. <http://CRAN.R-project.org/package=tmle.npvi>

6. Jacob, L., & Neuvial, P. (2012). *DEGraph: Two-sample tests on a graph*. <https://bioconductor.org/packages/DEGraph>
7. Neuvial, P., & Hupé, P. (2006). *MANOR: Micro-Array data NORmalization*.

Contributions to other software

1. Neuvial, P., & Hupé, P. (2006). *MANOR: Micro-Array data NORmalization*.
2. Dehman, A., & Neuvial, P. (2015). *BALD: A block-wise approach using linkage disequilibrium information*. R package, <http://www.math-evry.cnrs.fr/logiciels/bald>.
3. Liva, S. et al. (2006). *CAPweb: Copy Number Microarray Analysis Platform*.
4. La Rosa, P. et al. (2006). *VAMP: Visualisation and Analysis of Molecular Profiles*.
5. Neuvial, P., & Gestraud, P. (2008). *GTCA: Genome-transcriptome correlation analysis*.
6. Elati, M., & Neuvial, P. (2008). *LICORN: Learning Co-Operative Regulation Networks*.
7. Bengtsson, H., & Neuvial, P. (2010). *Aroma.cn: Analysis of copy-number estimates obtained from various platforms*.
8. Bengtsson, H., & Neuvial, P. (2010). *Aroma.cn.eval: Evaluating copy-number estimates*.
9. Olshen, A. et al. (2011). *PSCBS: Analysis of parent-specific DNA copy numbers*.
10. Ortiz-Estevéz, M. et al. (2011). *CalMaTe: A post-calibration process to improve allele-specific copy number estimates from SNP microarrays*.