Pierre Neuvial

CNRS director of research

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Research interests

- Post-hoc/post-selection inference: see project SansSouci
- Multiple testing: theory and applications
- Statistical methods for genomic and neuroimaging data analysis
- Performance evaluation of statistical methods
- Reproducible research: see the Computo journal

Experience

2021-present	CNRS researcher (DR) - section 41 and CID 51. Institut de Math. 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 (selected)

- 2022-2025: course "Asymptotic statistics" for 2nd year MSc students in Applied Mathematics at Université de Toulouse and ISAE: 15h/y
- 2017-2024: course "Statistical methods for genomic data analysis" for 2nd year MSc students in Statistics at ENSAI (Rennes): 12h/y
- since 2020: training for biologists/bioinformaticians via the Génotoul Biostatistics plaftorm

Postdoc supervision

2023 — 2025	**Simon Bartels**, *Funded by ANR CORNFLEX.* ○ Subject: Bayesian optimization for the computational design of flexible linkers ○ Co-supervised by François Bachoc and Juan Cortés ○ Current position: Machine Learning Engineer at Component AI
2020-11 — 2021-08	**Samuel Davenport**, *Funded by ANR SansSouci.* ○ Subject: False discovery proportion control in multivariate linear models using the bootstrap ○ Co-supervised by Bertrand Thirion ○ Current position: Postdoc at University of California San Diego
2019-09 — 2020-08	**Marie Perrot-Dockès**, *Funded by ANR SansSouci.* ○ Subject: Post hoc false discovery proportion inference under a Hidden Markov Model ○ Co-supervised by Gilles Blanchard and Etienne Roquain ○ Current position: Assistant Professor at Université de Paris
2018-05 — 2018-08	**Magali Champion**, *Funded by ANR SansSouci.* ○ Subject: Post hoc inference ○ Current position: Assistant Professor at Université de Paris

PhD student supervision

Current students

Since 2024-10	**Sara Fallet (50%)**, *Funded by PEPR Santé Numérique: MultiScale AI for SingleCell-Based Precision Medicine.* ○ Subject: Analyse différentielle par groupes de gènes de données scRNA-seq issues déchantillons multiples ○ Co-supervised by Boris Hejblum
Since 2024-10	**Angel Reyero Lobo (50%)**, *Funded by ANR VITE.* ○ Subject: Inferring variable importance in high-dimensional settings ○ Co-supervised by Bertrand Thirion
Since 2023-11	**Elise Jorge (33%)**, *Funded by INRAE.* ○ Subject: Comparative analysis of 3-dimensional genomic data ○ Co-supervised by Nathalie Vialaneix & Sylvain Foissac

Past students

2021-2024	**Nicolas Enjalbert-Courrech (50%)**, *Funded by CNRS 80' project DDisc.* ○ Subject: Post-clustering inference for single-cell RNA sequencing data ○ Co-supervised by Cathy Maugis-Rabusseau ○ Current position: Research Engineer at INRAE MIAT

2021-2024 **Alexandre Blain (50%)**, *Funded by UDOPIA (Paris Saclay).*
- ○ Subject: Reliable statistical inference: controlling the false discovery proportion in high-dimensional multivariate estimators
- ○ Co-supervised by Bertrand Thirion
- ○ Current position: NA

2020-2023 **Javier González Delgado (50%)**, *Funded by Labex CIMI.*
- ○ Subject: Statistical models and methods for the structural analysis of intrinsically disordered proteins
- ○ Co-supervised by Juan Cortés (LAAS)
- ○ Current position: Postdoc at Mc Gill University

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: High-school math teacher

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

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: Associate Director in Bioinformatics at Mnemo Therapeutics

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: Research Engineer at CHU de Rennes

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: Senior Biostatistician at Comac Medical

Selected research funding (as PI or co-PI)

2023-2027 **[ANR] VITE: Explainable AI through variable importance tests (150k).**
- ○ PI: Bertrand Thirion

2023-2026 **[ANR] CORNFLEX: Computational Design of Intrinsically Disordered Proteins: Application to Flexible Linkers (151k).**
- ○ PI: Juan Cortés (LAAS)

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

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

Participation to other grants

2023-2027 **[ANR] BACKUP: Bayesian nonparametrics, complex models and kernels, uncertainty quantification and deep methods**.
  ○ PI: Ismaël Castillo

2023-2026 **[ANR (PEPR Santé numérique)] AI4scMed: Multiscale AI for single cell-based prediction medicine**.
  ○ PI: Franck Picard

2021-2024 **[ANR JCJC] GAP: Gaussian Processes for computer experiments and machine learning: more guarantees and broader applications.**.
  ○ PI: François Bachoc (IMT)

2021-2023 **[INRAE DIGIT-Bio] PEERSIM: Planification dexpériences pour lEtude de la Réponse aux Stress-multiples et lIntégration Multi-omique.**.
  ○ PI: Guillem Rigaill (INRAE/LaMME)

Software development

Contribution to the development and technical support of R packages within open source and collaborative projects of statistical/bioinformatics tools:
○ sanssouci: R and python implementations (github), IIDEA R/shiny application,
○ acnr, jointseg, adjclust, hicream, tmle.npvi (CRAN),
○ MANOR, DEGraph (Bioconductor),
○ aroma.cn, aroma.cn.eval (the Aroma Project).
See `https://pneuvial.github.io/software`

Editorial boards

Since 2025 **PCI Statistics and Machine Learning**, *Recommender*.

Since 2021 **Computo**, *Co-founder and 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), Biometrical journal (2023), 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, 2024), 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, 2023), Biostatistics (2011), Briefings in Bioinformatics (2020, 2021, 2022, 2025, 2025), EURASIP Journal on Bioinformatics and Systems Biology (2014), Genome Research (2009), NAR Genomics and Bioinformatics (2025), PCI Genomics (2024), PLoS One (2012), Statistics in Medicine (2009, 2017).

Review for funding agencies

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

Conference organization (since 2022)

2026-06 **Rencontres R 2026**, Nantes.
- Member of the scientific committee

2026-01 **Workshop SMPGD2026**, Grenoble.
- Session "Next-generation hypothesis testing"

2025-12 **Workshop Explanability for high-dimensional statistics**, Montpellier.
- Co-organized with Joseph Salmon and Bertrand Thirion

2024-06 **JOBIM 2024**, Toulouse.
- Co-head of program committee with Géraldine Pascal
- 470 participants - 36 talks - 184 posters 8 mini-symposia

2022-10 **Workshop "Statistical challenges in scRNA-seq data analysis"**, Toulouse.
- Co-organized with Cathy Maugis-Rabusseau and Nicolas Enjalbert-Courrech
- 15 participants

2022-03 **Workshop "Post-selection inference for genomic and neuroimaging data"**, Toulouse.
- 15 participants

Scientific committees

- PEPR ADAAPT (since 2025)

- Réseau Thématique (RT) Mathématiques, Biologie, Santé (since 2024)
- GDR MathSAV: MATHématiques, SAnté, sciences de la Vie (2021-2023)
- Statistical Methods for Post-Genomic Data (SMPGD) workshop (since 2020)
    - Organizer of the session "Machine Learning for Protein Design'' at SMPGD2021
    - Organizer of the session "Next-generation hypothesis testing'' at SMPGD2026
- Génotoul Bioinformatics/Biostatistics day (since 2018)

Comités de sélection

2024	Chaire de Professeur Junior "Santé publique de précision". Université de Bordeaux
2024	Professor. Univ. Jean-Jaurès (Toulouse 2)/IMT
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 committees, reports and defenses

PhD thesis committees

Member for the PhD thesis committee(s) of 15 PhD students since 2013.

PhD theses

Examiner at the defense of 21 PhD students since 2013, including 8 as a referee. Recently:

- **2025** **Aurélie Mercadié (president)**, Université de Toulouse.
    - Title: Intégration de données omiques de la peau issues d'expériences multi-groupes
    - Supervised by Nathalie Vialaneix and Céline Brouard (INRAE)
- **2025** **Annaig de Walsche (referee)**, Université Paris Saclay.
    - Title: Development of statistical methods for meta-analysis of genome-wide association studies, applications in plant genetics
    - Supervised by Tristan Mary-Huard and Alain Charcosset (INRAE)
- **2025** **Damien Remot (president)**, Université de Toulouse.
    - Title: Sensitivity analysis & Machine Learning and their applications to accelerate the evaluation of analog semiconductor circuits performances against multiple sources of parametric variations
    - Supervised by Clément Pellegrini & Reda Chhaibi & Fabrice Gamboa

2024 **Liudmila Pischagina (examiner)**, Université Paris Saclay.
  ○ Title: Geometric functional pruning for change point detection in low-dimensional exponential family models
  ○ Supervised by Guillem Rigaill & Vincent Runge

2024 **Benjamin Hivert (examiner)**, Université de Bordeaux.
  ○ Title: Clustering et analyse différentielle de données dexpression génique
  ○ Supervised by Boris Hejblum & Rodolphe Thiébaut (SISTM - Inria & INSERM Bordeaux)

2023 **Antoine Villié (referee)**, Université Lyon 1.
  ○ Title: Quantifier lIncertitude de lExplicabilité en Apprentissage Automatique : Inférence Post-Sélection sur des Caractéristiques Biologiques Interprétables.
  ○ Supervised by Laurent Jacob & Yohann de Castro

2023 **Arnaud Liehrmann (examiner)**, Univesité Paris Saclay.
  ○ Title: Multiscale analysis of transcriptome: methodological and algorithmic developments
  ○ Supervised by Guillem Rigaill & Benoît Castandet

2023 **Ludivine Obry (referee)**, Université Paris Saclay.
  ○ Title: Weighted multiple testing procedures in genome wide association studies
  ○ Supervised by Cyril Dalmasso

2023 **Thi Thanh Yen Nguyen (referee)**, Université Paris Cité.
  ○ Title: Optimal transport-based machine learning with applications to genomics and actuarial science
  ○ Supervised by Antoine Chambaz & Olivier Bouaziz

2022 **Wencan Zhu (referee)**, 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 (referee)**, 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

Habilitation theses

2024 **Boris Hejblum (referee)**, Université de Bordeaux.
  ○ Title: Statistical methods for leveraging high-dimensional data from high-throughput measurements in vaccine clinical development

2023 **Sophie Lèbre (examiner)**, Université de Montpellier.
  ○ Title: Statistique appliquée pour une recherche pluridisciplinaire à linterface entre statistique, informatique et biologieă: étude des mécanismes de régulation des gènes

2022 **Raphaël Mourad (president)**, University Toulouse Paul Sabatier.
  ○ Title: Data analyses and bioinformatic models for genomics

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

2022 **Cathy Maugis-Rabusseau (mentor)**, Université Toulouse Paul Sabatier.
  ○ Title: Quelques contributions autour des modèles de mélange et pour lanalyse de données transcriptomiques

Research management

○ 2020-2024: "Responsable d'équipe" for the Statistics and Optimization team at IMT
○ since 2019: local contact for the Mathematics, Biology and Health group at IMT
○ 2014-2016: "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
○ 2018-2021: co-organization of the Mathematics for Biology and Health 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 Math Department at Univ. Évry

Other responsibilities

○ 2024-2025: Comité National de la Recherche Scientifique (section 41: Mathématiques et interactions des mathématiques)
○ 2019-2023: Commission Administrative Paritaire (CAP) du CNRS:
  - 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

Full text available from `https://cv.hal.science/pierre-neuvial`

Preprints

1. Peyrouset, N., Neuvial, P., & Thirion, B. (2025). *Cluster size matters: A comparative study of notip and pARI for post hoc inference in fMRI.* `https://arxiv.org/abs/2511.02422`
2. Reyero-Lobo, A., Neuvial, P., & Thirion, B. (2025). *A principled approach for comparing variable importance.* `https://arxiv.org/abs/2507.17306`
3. Bontemps, D., Bachoc, F., & Neuvial, P. (2025). *Inference post region selection.* `https://hal.science/hal-05109459`
4. Blain, A., Reyero Lobo, A., Linhart, J., Thirion, B., & Neuvial, P. (2025). *When knockoffs fail: Diagnosing and fixing non-exchangeability of knockoffs.* `https://doi.org/10.48550/arXiv.2407.06892`
5. González-Delgado, J., Deronzier, M., Cortés, J., & Neuvial, P. (2025). *Post-clustering inference under dependency.* `https://doi.org/10.48550/arXiv.2310.11822`

To appear

1. Enjalbert Courrech, N., Maugis-Rabusseau, C., & Neuvial, P. (2025). Review of post-clustering inference methods. *International Statistical Review*. `https://hal.science/hal-05053220`

International journals

1. González-Delgado, J., Mier, P., Bernado, P., Neuvial, P., & Cortés, J. (2025). The dependence of the amino acid backbone conformation on the translated synonymous codon is not statistically significant. *Proceedings of the National Academy of Sciences*, *122*(24), e2503264122. `https://doi.org/10.1073/pnas.2503264122`

2. Bachoc, F., Maugis-Rabusseau, C., & Neuvial, P. (2025). Selective inference after convex clustering with l1 penalization. *ESAIM Probability and Statistics*, *29*, 204–242. `https://doi.org/10.1051/ps/2025004`

3. Davenport, S., Thirion, B., & Neuvial, P. (2025). FDP control in mass-univariate linear models using the residual bootstrap. *Electron. J. Statist.*, *19*(1), 1313–1336. `https://doi.org/10.1214/25-EJS2354`

4. Jorge, É., Foissac, S., Neuvial, P., Zytnicki, M., & Vialaneix, N. (2025). A comprehensive review and benchmark of differential analysis tools for Hi-C data. *Briefings in Bioinformatics*, *26*(2), bbaf074. `https://doi.org/10.1093/bib/bbaf074`

5. González-Delgado, J., Bernadó, P., Neuvial, P., & Cortés, J. (2024). Weighted families of contact maps to characterize conformational ensembles of (highly-)flexible proteins. *Bioinformatics*, *40*(11), btae627. `https://doi.org/10.1093/bioinformatics/btae627`

6. Neuvial, P., Randriamihamison, N., Chavent, M., Foissac, S., & Vialaneix, N. (2024). A two-sample tree-based test for hierarchically organized genomic signals. *Journal of the Royal Statistical Society, Series C*. `https://doi.org/10.1093/jrsssc/qlae011`

7. Perrot-Dockès, M., Blanchard, G., Neuvial, P., & Roquain, E. (2023). Selective inference for false discovery proportion in a hidden markov model. *TEST*, *32*, 1365–1391. `https://doi.org/10.1007/s11749-023-00886-7`

8. González-Delgado, J., González-Sanz, A., Cortés, J., & Neuvial, P. (2023). Two-sample goodness-of-fit tests on the flat torus based on wasserstein distance and their relevance to structural biology. *Electronic Journal of Statistics*, *17*, 1547–1586. `https://doi.org/10.1214/23-EJS2135`

9. 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`

10. 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.

11. 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`

12. 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`

13. 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`

14. 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`

15. 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`

16. 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`

17. 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`

18. Ambroise, C., Dehman, A., Neuvial, P., Rigaill, 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`

19. 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`

20. Sadacca, B., Hamy-Petit, A.-S., Laurent, C., Gestraud, P., Bonsang-Kitzis, H., Pinheiro, A., Abecassis, J., Neuvial, P., & Reyal, 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`

21. 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`

22. 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`

23. Pierre-Jean, M., Rigaill, 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`

24. Dehman, A., Ambroise, C., & Neuvial, P. (2015). Performance of a block-wise approach in variable selection using linkage disequilibrium information. *BMC Bioinformatics*. `http://bmcbioinformatics.biomedcentral.com/articles/10.1186/s12859-015-0556-6`

25. 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`

26. 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`

27. 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`

28. 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`

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▬▬▬ Software

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