

International journal papers with external peer review

1. Di Camillo B, Giugno R. From translational bioinformatics computational methodologies to personalized medicine. **J Biomed Inform.** 2024 Mar;151:104619.
2. Discriminative power of DNA-based, volatilome, near infrared spectroscopy, elements and stable isotopes methods for the origin authentication of typical Italian mountain cheese using sPLS-DA modeling. Cardin M, Mounier J, Coton E, Cardazzo B, Perini M, Bertoldi D, Pianezze S, Segato S, Di Camillo B, Cappellato M, Coton M, Carraro L, Currò S, Lucchini R, Mohammadpour H, Novelli E. **Food Res Int.** 2024;178:113975.
3. Trescato I, Roversi C, Vettoretti M, Di Camillo B, Facchinetti A. A model to forecast the two-year variation of subjective wellbeing in the elderly population. **BMC Med Inform Decis Mak.** 2023 Nov 8;23(1):253.
4. Guazzo A, Longato E, Fadini GP, Morieri ML, Sparacino G, Di Camillo B. Deep-learning-based natural-language-processing models to identify cardiovascular disease hospitalisations of patients with diabetes from routine visits' text. **Sci Rep.** 2023 Nov 5;13(1):19132.
5. Lee Y, Cappellato M, **Di Camillo B**. Machine learning-based feature selection to search stable microbial biomarkers: application to inflammatory bowel disease. **Gigascience.** 2023 28;12:giad083.
6. Bellato M, Cappellato M, Longhin F, Del Vecchio C, Brancaccio G, Cattelan AM, Brun P, Salaris C, Castagliuolo I, Di Camillo B. Uncover a microbiota signature of upper respiratory tract in patients with SARS-CoV-2 + . **Sci Rep.** 2023 6;13(1):16867.
7. Bossi LE, Palumbo C, Trojani A, Melluso A, Di Camillo B, Beghini A, Samataro LM, Cairoli R. A Nine-Gene Expression Signature Distinguished a Patient with Chronic Lymphocytic Leukemia Who Underwent Prolonged Periodic Fasting. **Medicina (Kaunas).** 2023 31;59(8):1405.
8. Spolverato G, Fassan M, Scarpa M, Stepanyan A, De Simoni O, Scognamiglio F, Chiminazzo V, De Nardi C, Tamponi G, Negro S, Angriman I, Kotsafti A, Ruffolo C, Vignotto C, Zizzo M, Marchegiani F, Facci L, Bergamo F, Brignola S, Businello G, Guzzardo V, Dal Santo L, Salmaso R, Ceccon C, Massani M, Pozza A, Cataldo I, Stecca T, Dei Tos AP, Zagonel V, Pilati P, Franzato B, Scapinello A, Pirozzolo G, Recordare A, Merenda R, Bordignon G, Laurino L, Guerriero S, Romiti C, Portale G, Cipollari C, Candioli S, Gavagna L, Pozza G, Godina M, Mondì I, Noaro G, Ortenzi M, Guerrieri M, Tagliente G, Tomassi M, Tedeschi U, Porzionato A, Agostini M, Maretto I, Bao QR, Cavallin F, Di Camillo B, Bardini R, Castagliuolo I, Pucciarelli S, Scarpa M; IMMUNOREACT Study Group. IMMUNOREACT 6: weak immune surveillance characterizes early-onset rectal cancer. **Br J Surg.** 2023 Oct 10;110(11):1490-1501. doi: 10.1093/bjs/znad219.
9. Tavazzi E, Longato E, Vettoretti M, Aidos H, Trescato I, Roversi C, Martins AS, Castanho EN, Branco R, Soares DF, Guazzo A, Birolo G, Pala D, Bosoni P, Chiò A, Manera U, de Carvalho M, Miranda B, Gromicho M, Alves I, Bellazzi R, Dagliati A, Fariselli P, Madeira SC, Di Camillo B. Artificial intelligence and statistical methods for

- stratification and prediction of progression in amyotrophic lateral sclerosis: A systematic review. **Artif Intell Med.** 2023;142:102588.
10. Panariello F, Gagliano O, Luni C, Grimaldi A, Angiolillo S, Qin W, Manfredi A, Annunziata P, Slovin S, Vaccaro L, Riccardo S, Bouche V, Dionisi M, Salvi M, Martewicz S, Hu M, Cui M, Stuart H, Laterza C, Baruzzo G, Schiebinger G, Di Camillo B, Cacchiarelli D, Elvassore N. Cellular population dynamics shape the route to human pluripotency. **Nat Commun.** 2023;14(1):2829.
 11. Spolverato G, Fassan M, Capelli G, Scarpa M, Negro S, Chiminazzo V, Kotsafti A, Angriman I, Campi M, De Simoni O, Ruffolo C, Astghik S, Vignotto C, Scognamiglio F, Becherucci G, Rivella G, Marchegiani F, Facci L, Bergamo F, Brignola S, Businello G, Guzzardo V, Dal Santo L, Salmaso R, Massani M, Pozza A, Cataldo I, Stecca T, Dei Tos AP, Zagonel V, Pilati P, Franzato B, Scapinello A, Pirozzolo G, Recordare A, Merenda R, Bordignon G, Guerriero S, Romiti C, Portale G, Cipollari C, Zizzo M, Porzionato A, Agostini M, Cavallin F, Di Camillo B, Bardini R, Maretto I, Castagliuolo I, Pucciarelli S, Scarpa M. IMMUNOREACT 5: female patients with rectal cancer have better immune editing mechanisms than male patients - a cohort study. **Int J Surg.** 2023;109(3):323-332.
 12. Khachatryan L, Xiang Y, Ivanov A, Glaab E, Graham G, Granata I, Giordano M, Maddalena L, Piccirillo M, Manipur I, Baruzzo G, Cappellato M, Avot B, Stan A, Battey J, Lo Sasso G, Boue S, Ivanov NV, Peitsch MC, Hoeng J, Falquet L, Di Camillo B, Guarracino MR, Ulyantsev V, Siervo N, Poussin C. Results and lessons learned from the sbv IMPROVER metagenomics diagnostics for inflammatory bowel disease challenge. **Sci Rep.** 2023;13(1):6303.
 13. Baruzzo G, Serafini A, Finotello F, Sanavia T, Cioetto-Mazzabò L, Boldrin F, Lavezzo E, Barzon L, Toppo S, Provvedi R, Manganelli R, Di Camillo B. Role of the Extracytoplasmic Function Sigma Factor SigE in the Stringent Response of Mycobacterium tuberculosis. **Microbiol Spectr.** 2023;11(2):e0294422.
 14. Di Camillo B, Puricelli L, Iori E, Toffolo GM, Tessari P, Arrigoni G. Modeling SILAC Data to Assess Protein Turnover in a Cellular Model of Diabetic Nephropathy. **Int J Mol Sci.** 2023;24(3):2811.
 15. Tavazzi E, Gatta R, Vallati M, Cotti Piccinelli S, Filosto M, Padovani A, Castellano M, Di Camillo B. Leveraging process mining for modeling progression trajectories in amyotrophic lateral sclerosis. **BMC Med Inform Decis Mak.** 2023;22(Suppl 6):346.
 16. Cesaro G, Milia M, Baruzzo G, Finco G, Morandini F, Lazzarini A, Alotto P, da Cunha Carvalho de Miranda NF, Trajanoski Z, Finotello F, Di Camillo B. MAST: a hybrid Multi-Agent Spatio-Temporal model of tumor microenvironment informed using a data-driven approach. **Bioinformatics Advances.** 2022, 2(1) vbac092.
 17. Morieri ML, Longato E, Di Camillo B, Sparacino G, Avogaro A, Fadini GP. Management of type 2 diabetes with a treat-to-benefit approach improved long-term cardiovascular outcomes under routine care. **Cardiovasc Diabetol.** 2022; 21(1):274.
 18. Innocente G, Patuzzi I, Furlanello T, Di Camillo B, Bargelloni L, Giron MC, Facchin S, Savarino E, Azzolin M, Simionati B. Machine Learning and Canine Chronic Enteropathies: A New Approach to Investigate FMT Effects. **Vet Sci.** 2022; 9(9):502.

19. Cappellato M, Baruzzo G, Di Camillo B. Investigating differential abundance methods in microbiome data: A benchmark study. **PLoS Comput Biol**. 2022; 18(9):e1010467.
20. Longato E, Di Camillo B, Sparacino G, Avogaro A, Fadini GP. Time-resolved trajectory of glucose lowering medications and cardiovascular outcomes in type 2 diabetes: a recurrent neural network analysis. **Cardiovasc Diabetol**. 2022;21(1):159.
21. Pancotti C, Birolo G, Rollo C, Sanavia T, Di Camillo B, Manera U, Chiò A, Fariselli P. Deep learning methods to predict amyotrophic lateral sclerosis disease progression. **Sci Rep**. 2022;12(1):13738.
22. Longato E, Morieri ML, Sparacino G, Di Camillo B, Cattelan A, Lo Menzo S, Trevenzoli M, Vianello A, Guarnieri G, Lionello F, Avogaro A, Fioretto P, Vettor R, Fadini GP. Time-series analysis of multidimensional clinical-laboratory data by dynamic Bayesian networks reveals trajectories of COVID-19 outcomes. **Comput Methods Programs Biomed**. 2022;221:106873.
23. Guazzo A, Longato E, Morieri ML, Sparacino G, Franco-Novelletto B, Cancian M, Fusello M, Tramontan L, Battaglia A, Avogaro A, Fadini GP, Di Camillo B. Performance assessment across different care settings of a heart failure hospitalisation risk-score for type 2 diabetes using administrative claims. **Sci Rep**. 2022;12(1):7762.
24. Cappellato M, Baruzzo G, Patuzzi I, Di Camillo B. Modeling Microbial Community Networks: **Methods and Tools**. **Curr Genomics**. 2021;22(4):267-290.
25. Tavazzi E, Daberdaku S, Zandonà A, Vasta R, Nefussy B, Lunetta C, Mora G, Mandrioli J, Grisan E, Tarlarini C, Calvo A, Moglia C, Drory V, Gotkine M, Chiò A, Di Camillo B; Piemonte, Valle d'Aosta Register for ALS (PARALS), for the Emilia Romagna Registry for ALS (ERRALS). Predicting functional impairment trajectories in amyotrophic lateral sclerosis: a probabilistic, multifactorial model of disease progression. **J Neurol**. 2022 Jul;269(7):3858-3878.
26. Baruzzo G, Patuzzi I, Di Camillo B. Beware to ignore the rare: how imputing zero-values can improve the quality of 16S rRNA gene studies results. **BMC Bioinformatics**. 2022;22(Suppl 15):618.
27. Baruzzo G, Cesaro G, Di Camillo B. Identify, quantify and characterize cellular communication from single cell RNA sequencing data with scSeqComm. **Bioinformatics**. 2022 btac036.
28. Zorzan I, Del Favero S, Giaretta A, Manganelli R, Di Camillo B, Schenato L. Mathematical modelling of SigE regulatory network reveals new insights into bistability of mycobacterial stress response. **BMC Bioinformatics**. 2021;22(1):558.
29. Longato E, Di Camillo B, Sparacino G, Tramontan L, Avogaro A, Fadini GP. Cardiovascular outcomes after initiating GLP-1 receptor agonist or basal insulin for the routine treatment of type 2 diabetes: a region-wide retrospective study. **Cardiovasc Diabetol**. 2021;20(1):222. doi: 10.1186/s12933-021-01414-3.
30. Longato E, Bonora BM, Di Camillo B, Sparacino G, Tramontan L, Avogaro A, Fadini GP. Outcomes of patients with type 2 diabetes treated with SGLT-2 inhibitors versus

DPP-4 inhibitors. An Italian real-world study in the context of other observational studies. **Diabetes Res Clin Pract.** 2021;179:109024.

31. Pungolino E, D'adda M, De Canal G, Trojani A, Perego A, Elena C, Lunghi F, Turrini M, Borin L, Iurlo A, Latargia ML, Carraro MC, Spina F, Artale S, Anghilieri M, Molteni A, Caramella M, Baruzzo G, Nichelatti M, Di Camillo B, Cairoli R. Nilotinib-induced bone marrow CD34+/lin-Ph+ cells early clearance in newly diagnosed CP-Chronic Myeloid Leukemia: Final report of the PhilosoPhi34 study. **Eur J Haematol.** 2021;107(4):436-448.
32. Berlanda M, Innocente G, Simionati B, Di Camillo B, Facchin S, Giron MC, Savarino E, Sebastiani F, Fiorio F, Patuzzi I. Faecal Microbiome Transplantation as a Solution to Chronic Enteropathies in Dogs: A Case Study of Beneficial Microbial Evolution. **Animals (Basel).** 2021;11(5):1433.
33. Sanavia T, Huang C, Manduchi E, Xu Y, Dadi PK, Potter LA, Jacobson DA, Di Camillo B, Magnuson MA, Stoeckert CJ Jr, Gu G. Temporal Transcriptome Analysis Reveals Dynamic Gene Expression Patterns Driving β -Cell Maturation. **Front Cell Dev Biol.** 2021;9:648791.
34. Trojani A, Di Camillo B, Bossi LE, Leuzzi L, Greco A, Tedeschi A, Frustaci AM, Deodato M, Zamprogna G, Beghini A, Cairoli R. Identification of a Candidate Gene Set Signature for the Risk of Progression in IgM MGUS to Smoldering/Symptomatic Waldenström Macroglobulinemia (WM) by a Comparative Transcriptome Analysis of B Cells and Plasma Cells. **Cancers (Basel).** 2021;13(8):1837.
35. Longato E, Fadini GP, Sparacino G, Avogaro A, Tramontan L, Di Camillo B. A Deep Learning Approach to Predict Diabetes' Cardiovascular Complications From Administrative Claims. **IEEE J Biomed Health Inform.** 2021;25(9):3608-3617.
36. Longato E, Di Camillo B, Sparacino G, Tramontan L, Avogaro A, Fadini GP. Cardiovascular effectiveness of human-based vs. exendin-based glucagon like peptide-1 receptor agonists: a retrospective study in patients with type 2 diabetes. **Eur J Prev Cardiol.** 2021, 23;28(1):22-29.
37. Cassaro A, Grillo G, Notaro M, Gliozzo J, Esposito I, Reda G, Trojani A, Valentini G, Di Camillo B, Cairoli R, Beghini A. FZD6 triggers Wnt-signalling driven by WNT10B/VS1 expression and highlights new targets in T-cell acute lymphoblastic leukemia. **Hematol Oncol.** 2021, 26. doi: 10.1002/hon.2840. Epub ahead of print. PMID: 33497493.
38. Comin M, Di Camillo B, Pizzi C, Vandin F. Comparison of microbiome samples: methods and computational challenges. **Brief Bioinform.** 2021 Jan 18;22(1):88-95.
39. Ciccarese F, Grassi A, Pasqualini L, Rosano S, Noghero A, Montenegro F, Bussolino F, Di Camillo B, Finesso L, Toffolo GM, Mitola S, Indraccolo S. Genetic perturbation of IFN- α transcriptional modulators in human endothelial cells uncovers pivotal regulators of angiogenesis. **Comput Struct Biotechnol J.** 2020; 18:3977-3986.
40. Di Camillo B, Nicosia G, Buffa F, Lo B. Guest Editorial Data Science in Smart Healthcare: Challenges and Opportunities. **IEEE Journal of Biomedical and Health Informatics**, 2020; 24 (11), pp. 3041-3043,

41. Fadini GP, Morieri ML, Longato E, Bonora BM, Pinelli S, Selmin E, Voltan G, Falaguasta D, Tresso S, Costantini G, Sparacino G, Di Camillo B, Tramontan L, Cattelan AM, Vianello A, Fioretto P, Vettor R, Avogaro A. Exposure to dipeptidyl-peptidase-4 inhibitors and COVID-19 among people with type 2 diabetes: A case-control study. **Diabetes Obes Metab**. 2020; 22(10):1946-1950.
42. Longato E, Vettoretti M, Di Camillo B. A practical perspective on the concordance index for the evaluation and selection of prognostic time-to-event models. **J Biomed Inform**. 2020; 108:103496.
43. Vettoretti M, Longato E, Zandonà A, Li Y, Pagán JA, Siscovick D, Carnethon MR, Bertoni AG, Facchinetti A, Di Camillo B. Addressing practical issues of predictive models translation into everyday practice and public health management: a combined model to predict the risk of type 2 diabetes improves incidence prediction and reduces the prevalence of missing risk predictions. **BMJ Open Diabetes Res Care**. 2020; 8(1):e001223.
44. Longato E, Di Camillo B, Sparacino G, Tramontan L, Avogaro A, Fadini GP. Better cardiovascular outcomes of type 2 diabetic patients treated with GLP-1 receptor agonists versus DPP-4 inhibitors in clinical practice. **Cardiovasc Diabetol**. 2020; 19(1):74.
45. Tavazzi E, Daberdaku S, Vasta R, Calvo A, Chiò A, Di Camillo B. Exploiting mutual information for the imputation of static and dynamic mixed-type clinical data with an adaptive k-nearest neighbours approach. **BMC Med Inform Decis Mak**. 2020; 20(Suppl 5):174.
46. Longato E, Di Camillo B, Sparacino G, Gubian L, Avogaro A, Fadini GP. Cardiovascular outcomes of type 2 diabetic patients treated with SGLT-2 inhibitors versus GLP-1 receptor agonists in real-life. **BMJ Open Diabetes Res Care**. 2020; 8(1):e001451.
47. Longato E, Di Camillo B, Sparacino G, Saccavini C, Avogaro A, Fadini GP. Diabetes diagnosis from administrative claims and estimation of the true prevalence of diabetes among 4.2 million individuals of the Veneto region (North East Italy). **Nutr Metab Cardiovasc Dis**. 2020; 30(1):84-91.
48. Patuzzi I, Baruzzo G, Losasso C, Ricci A, Di Camillo B. metaSPARSim: a 16S rRNA gene sequencing count data simulator. **BMC Bioinformatics**. 2019; 20(Suppl 9):416.
49. Baruzzo G, Patuzzi I, Di Camillo B. SPARSim Single Cell: a count data simulator for scRNA-seq data. **Bioinformatics**. 2019 pii: btz752.
50. Morieri ML, Longato E, Mazzucato M, Di Camillo B, Cocchiglia A, Gubian L, Sparacino G, Avogaro A, Fadini GP, Vigili de Kreutzenberg S. Improved long-term cardiovascular outcomes after intensive versus standard screening of diabetic complications: an observational study. **Cardiovasc Diabetol**. 2019;18(1):117.
51. Trojani A, Pungolino E, Dal Molin A, Lodola M, Rossi G, D'Adda M, Perego A, Elena C, Turrini M, Borin L, Bucelli C, Malato S, Carraro MC, Spina F, Latargia ML, Artale S, Spedini P, Anghileri M, Di Camillo B, Baruzzo G, De Canal G, Iurlo A, Morra E, Cairoli R. Nilotinib interferes with cell cycle, ABC transporters and JAK-STAT signaling

pathway in CD34+/lin- cells of patients with chronic phase chronic myeloid leukemia after 12 months of treatment. **PLoS One**. 2019; 14(7):e0218444.

52. Zandonà A, Vasta R, Chiò A, Di Camillo B. A dynamic Bayesian network model for the simulation of amyotrophic lateral sclerosis progression. **BMC Bioinformatics**. 2019; 20(Suppl 4):118.
53. Dereli Eke E, Arga KY, Dikicioglu D, Eraslan S, Erkol E, Celik A, Kirdar B, Di Camillo B. Identification of Novel Components of Target-of-Rapamycin Signaling Pathway by Network-Based Multi-Omics Integrative Analysis. **OMICS**. 2019; 23(5):274-284.
54. Kueffner R, Zach N, Bronfeld M, Norel R, Atassi N, Balagurusamy V, Di Camillo B, Chio A, Cudkowicz M, Dillenberger D, Garcia-Garcia J, Hardiman O, Hoff B, Knight J, Leitner ML, Li G, Mangravite L, Norman T, Wang L; ALS Stratification Consortium, Xiao J, Fang WC, Peng J, Yang C, Chang HJ, Stolovitzky G.. Stratification of amyotrophic lateral sclerosis patients: a crowdsourcing approach" **Nature Scientific Reports** 2019; 9(1):690
55. Zorzan, I., Del Favero, S., Di Camillo, B., Schenato, L. Analysis of a minimal gene regulatory network for cell differentiation **IEEE Control Systems Letters** 2019 3(2),8467361, pp. 302-307.
56. Pauletto, M., Di Camillo, B, Miner, P., (...), Patarnello, T., Bargelloni, L. Understanding the mechanisms involved in the high sensitivity of Pecten maximus larvae to aeration 2018 **Aquaculture** 497, pp. 189-199.
57. Sambo F, Finotello F, Lavezzo E, Baruzzo G, Masi G, Peta E, Falda M, Toppo S, Barzon L, Di Camillo B Optimizing PCR primers targeting the bacterial 16S ribosomal RNA gene. **BMC Bioinformatics**. 2018; 19(1):343.
58. van Zuydam NR, Ahlqvist E, Sandholm N, Deshmukh H, Rayner NW, Abdalla M, Ladenvall C, Ziemek D, Fauman E, Robertson NR, McKeigue PM, Valo E, Forsblom C, Harjutsalo V; Finnish Diabetic Nephropathy Study (FinnDiane), Perna A, Rurali E, Marcovecchio ML, Igo RP Jr, Salem RM, Perico N, Lajer M, Käräjämäki A, Imamura M, Kubo M, Takahashi A, Sim X, Liu J, van Dam RM, Jiang G, Tam CHT, Luk AOY, Lee HM, Lim CKP, Szeto CC, So WY, Chan JCN; Hong Kong Diabetes Registry Theme-based Research Scheme Project Group, Ang SF, Dorajoo R, Wang L, Clara TSH, McKnight AJ, Duffy S; Warren 3 and Genetics of Kidneys in Diabetes (GoKinD) Study Group, Pezzolesi MG; GENIE (GENetics of Nephropathy an International Effort) Consortium, Marre M, Gyorgy B, Hadjadj S, Hiraki LT; Diabetes Control and Complications Trial (DCCT)/Epidemiology of Diabetes Interventions and Complications (EDIC) Research Group, Ahluwalia TS, Almgren P, Schulz CA, Orholm-Melander M, Linneberg A, Christensen C, Witte DR, Grarup N, Brandslund I, Melander O, Paterson AD, Tregouet D, Maxwell AP, Lim SC, Ma RCW, Tai ES, Maeda S, Lyssenko V, Tuomi T, Krolewski AS, Rich SS, Hirschhorn JN, Florez JC, Dunger D, Pedersen O, Hansen T, Rossing P, Remuzzi G; SUrrogate markers for Micro- and Macrovascular hard endpoints for Innovative diabetes Tools (SUMMIT) Consortium, (Di Camillo B within SUMMIT Consortium), Brosnan MJ, Palmer CNA, Groop PH, Colhoun HM, Groop LC, McCarthy MI. A Genome-Wide Association Study of Diabetic Kidney Disease in Subjects With Type 2 Diabetes. **Diabetes**. 2018; 67(7):1414-1427.

59. Finotello F, Mastrorilli E, Di Camillo B. Measuring the diversity of the human microbiota with targeted next-generation sequencing. **Brief Bioinform**. 2018; 19(4):679-692.
60. Pungolino E, Rossi G, De Canal G, Trojani A, D'adda M, Perego A, Orlandi EM, Lunghi F, Turrini M, Borin L, Iurlo A, Latargia ML, Carraro MC, Spina F, Lodola M, Artale S, Anghilieri M, Spedini P, Cantoni S, Di Camillo B, Morra E, Cairoli R. Nilotinib induced bone marrow CD34+/lin-Ph+ cells early clearance in newly diagnosed CP-chronic myeloid leukemia. **Am J Hematol**. 2018; 93(7):E162-E164.
61. Dal Molin A, Di Camillo B. How to design a single-cell RNA-sequencing experiment: pitfalls, challenges and perspectives. **Brief Bioinform**. 2018 Jan 31. doi: 10.1093/bib/bby007.
62. Di Camillo B, Hakaste L, Sambo F, Gabriel R, Kravic J, Isomaa B, Tuomilehto J, Alonso M, Longato E, Facchinetti A, Groop L, Cobelli C, Tuomi T. HAPT2D: High accuracy of prediction of T2D with a model combining basic and advanced data depending on availability. **Eur J Endocrinol**. 2018 EJE-17-0921. doi: 10.1530/EJE-17-0921.
63. Peta E, Sinigaglia A, Masi G, Di Camillo B, Grassi A, Trevisan M, Messa L, Loregian A, Manfrin E, Brunelli M, Martignoni G, Palù G, Barzon L. HPV16 E6 and E7 upregulate the histone lysine demethylase KDM2B through the c-MYC/miR-146a-5p axys. **Oncogene** 2018; 37(12):1654-1668.
64. Etna MP, Sinigaglia A, Grassi A, Giacomini E, Romagnoli A, Pardini M, Severa M, Cruciani M, Rizzo F, Anastasiadou E, Di Camillo B, Barzon L, Fimia GM, Manganelli R, Coccia EM. Mycobacterium tuberculosis-induced miR-155 subverts autophagy by targeting ATG3 in human dendritic cells. **PLoS Pathog**. 4;14(1):e1006790.
65. Trojani A, Pungolino E, Rossi G, D'Adda M, Lodola M, Di Camillo B, Perego A, Turrini M, Orlandi E, Borin L, Iurlo A, Malato S, Spina F, Latargia ML, Lanza F, Artale S, Anghilieri M, Carraro MC, Canal G, Morra E, Cairoli R. Wide-transcriptome analysis and cellularity of bone marrow CD34+/lin- cells of patients with chronic-phase chronic myeloid leukemia at diagnosis vs. 12 months of first-line nilotinib treatment. **Cancer Biomark**. 2017; 21(1):41-53.
66. Ferraresso S, Aricò A, Sanavia T, Da Ros S, Milan M, Cascione L, Comazzi S, Martini V, Giantin M, Di Camillo B, Mazzariol S, Giannuzzi D, Marconato L, Aresu L. DNA methylation profiling reveals common signatures of tumorigenesis and defines epigenetic prognostic subtypes of canine Diffuse Large B-cell Lymphoma. **Nat. Sci Rep**. 2017, 7(1):11591. doi: 10.1038/s41598-017-11724-w.
67. Dal Molin A, Baruzzo G and Di Camillo B. Single-Cell RNA-Sequencing: Assessment of Differential Expression Analysis Methods. **Front. Genet**. 2017, 8:62. doi: 10.3389/fgene.2017.00062
68. Giaretta A, Rocca B, Di Camillo B, Maria Toffolo G, Patrono C. In silico modeling of the antiplatelet pharmacodynamics of low-dose aspirin in health and disease. **Clin Pharmacol Ther**. 2017 Nov;102(5):823-83.
69. Franzin A, Sambo F, Di Camillo B. bnstruct: an R package for Bayesian Network structure learning in the presence of missing data. **Bioinformatics**, 2017; 33(8):1250-1252.

70. Baruzzo G, Hayer K, Ji Kim E, Di Camillo B, Fitzgerald G, Grant G. Simulation-Based Comprehensive Benchmark Analysis of RNA-Seq Aligners. **Nature Methods**, 2017; 14(2):135-139.
71. Peta E , Cappellesso R, Masi G, Sinigaglia A, Trevisan M, Grassi A, Di Camillo B, Vassarotto E, Fassina A, Palù G, Barzon L. Down-regulation of microRNA-146a is associated with high-risk human papillomavirus infection and epidermal growth factor receptor overexpression in penile squamous cell carcinoma. **Human Pathology**, 2017 Mar;61:33-40.
72. Sandholm N, Van Zuydam N, Ahlqvist E, Juliusdottir T, Deshmukh HA, Rayner NW, Di Camillo B, Forsblom C, Fadista J, Ziemek D, Salem RM, Hiraki LT, Pezzolesi M, Trégouët D, Dahlström E, Valo E, Oskolkov N, Ladenvall C, Marcovecchio ML, Cooper J, Sambo F, Malovini A, Manfrini M, McKnight AJ, Lajer M, Harjutsalo V, Gordin D, Parkkonen M; FinnDiane Study Group, Tuomilehto J, Lyssenko V, McKeigue PM, Rich SS, Brosnan MJ, Fauman E, Bellazzi R, Rossing P, Hadjadj S, Krolewski A, Paterson AD; DCCT/EDIC Study Group, Florez JC, Hirschhorn JN, Maxwell AP; GENIE Consortium, Dunger D, Cobelli C, Colhoun HM, Groop L, McCarthy MI, Groop PH; SUMMIT Consortium. The Genetic Landscape of Renal Complications in Type 1 Diabetes. **J Am Soc Nephrol**, 2017; 28(2):557-574.
73. Noren DP, Long BL, Norel R, Rrhissorakrai K, Hess K, Hu CW, Bisberg AJ, Schultz A, Engquist E, Liu L, Lin X, Chen GM, Xie H, Hunter GA, Boutros PC, Stepanov O, DREAM 9 AML-OPC Consortium (Di Camillo B within DREAM 9 AML-OPC Consortium), Norman T, Friend SH, Stolovitzky G, Kornblau S, Qutub AA. A Crowdsourcing Approach to Developing and Assessing Prediction Algorithms for AML Prognosis. **PLoS Comput Biol**, 2016; 28;12(6):e1004890
74. Di Camillo B, Carlon A, Eduati F, Toffolo G. A rule-based model of insulin signalling pathway. **BMC Systems Biology** 2016;10(1):38
75. Grassi A, Di Camillo B, Ciccarese F, Agnusdei V, Zanovello P, Amadori A, Finesso L, Indraccolo S, Toffolo GM. Reconstruction of gene regulatory modules from RNA silencing of IFN- α modulators: experimental set-up and inference method. **BMC Genomics**, 2016; 17(1):228
76. Milan M, Matozzo V, Pauletto M, Di Camillo B, Giacomazzo M, Boffo L, Binato G, Marin MG, Patarnello T, Bargelloni L. Can ecological history influence response to pollutants? Transcriptomic responses to heavy metal exposure in Manila clam collected in different Venice lagoon areas. **Aquatic Toxicology**, 2016; 174:123-33
77. Hill SM, Heiser LM, Cokelaer T, Unger M, Nesser NK, Carlin DE, Zhang Y, Sokolov A, Paull EO, Wong CK, Graim K, Bivol A, Wang H, Zhu F, Afsari B, Danilova LV, Favorov AV, Lee WS, Taylor D, Hu CW, Long BL, Noren DP, Bisberg AJ; HPN-DREAM Consortium (Di Camillo B within HPN-DREAM Consortium), Mills GB, Gray JW, Kellen M, Norman T, Friend S, Qutub AA, Fertig EJ, Guan Y, Song M, Stuart JM, Spellman PT, Koeppl H, Stolovitzky G, Saez-Rodriguez J, Mukherjee S. Inferring causal molecular networks: empirical assessment through a community-based effort. **Nat Methods**, 2016; 13(4):310-8

78. Marini S, Trifoglio E, Barbarini N, Sambo F, Di Camillo B, Malovini A, Manfrini M, Cobelli C, Bellazzi R. A Dynamic Bayesian Network model for long-term simulation of clinical complications in type 1 diabetes. **J Biomed Inform**, 2015; 57:369-76
79. Sanavia T, Finotello F, Di Camillo B. FunPat: function-based pattern analysis on RNA-seq time series. **BMC Genomics**, 2015, 16(Suppl 6):S2
80. Pegolo S, Di Camillo B, Montesissa C, Cannizzo FT, Biolatti B, Bargelloni L. Toxicogenomic markers for corticosteroid treatment in beef cattle: integrated analysis of transcriptomic data. **Food Chem Toxicol**, 2015; 77:1-11
81. Sinigaglia A, Lavezzo E, Trevisan M, Sanavia T, Di Camillo B, Peta E, Scarpa M, Castagliuolo I, Guido M, Sarcognato S, Cappellesso R, Fassina A, Cardin R, Farinati F, Palù G, Barzon L. Changes in microRNA expression during disease progression in patients with chronic viral hepatitis. **Liver Int**, 2015; 35(4):1324-33
82. Finotello F, Di Camillo B. Measuring differential gene expression with RNA-seq: challenges and strategies for data analysis. **Brief Funct Genomics**, 2015; 14(2):130-142
83. Visentin S, Grumolato F, Nardelli GB, Di Camillo B, Grisan E, Cosmi E. Early origins of adult disease: low birth weight and vascular remodeling. **Atherosclerosis**, 2014;237(2):391-9
84. Bansal M, Yang J, Karan C, Menden MP, Costello JC, Tang H, Xiao G, Li Y, Allen J, Zhong R, Chen B, Kim M, Wang T, Heiser LM, Realubit R, Mattioli M, Alvarez MJ, Shen Y; NCI-DREAM Community (Di Camillo B within NCI-DREAM Community), Gallahan D, Singer D, Saez-Rodriguez J, Xie Y, Stolovitzky G, Califano A. A community computational challenge to predict the activity of pairs of compounds. **Nat Biotechnol**, 2014;32(12):1213-22
85. Fadista J, Vikman P, Ottosson Laakso E, Mollet I, Esguerra J, Taneera J, Storm P, Osmark P, Ladenvall C, Prasad, R, Hansson K, Finotello F, Ofori J, Krus U, Di Camillo B, Hansson O, Eliasson L, Rosengren A, Renström E, Wollheim CB, Groop L. Global genomic and transcriptomic analysis of human pancreatic islets reveals novel genes influencing glucose metabolism. **Proc Natl Acad Sci**, 2014; 111(38):13924-9
86. Nasso S, Hartler J, Trajanoski Z, Di Camillo B, Mechtler K, Toffolo G. DSpectra:A 3-Dimensional Quantification Algorithm For LC-MS Labeled Profile Data. **Journal of Proteomics**, 2014;112:156-65
87. Sambo F, Di Camillo B, Toffolo G, Cobelli C. Compression and fast retrieval of SNP data. **Bioinformatics**, 2014, 30(21):3078-85
88. Costello JC, Heiser LM, Georgii E, Gönen M, Menden MP, Wang NJ, Bansal M, Ammad-Ud-Din M, Hintsanen P, Khan SA, Mpindi JP, Kallioniemi O, Honkela A, Aittokallio T, Wennerberg K; NCI DREAM Community (Di Camillo B within NCI-DREAM Community), Collins JJ, Gallahan D, Singer D, Saez-Rodriguez J, Kaski S, Gray JW, Stolovitzky G . A community effort to assess and improve drug sensitivity prediction algorithms. **Nat Biotechnol**, 2014; 32(12):1202-12
89. Sambo F, Malovini A, Sandholm N, Stavarachi M, Forsblom C, Mäkinen VP, Harjutsalo V, Lithovius R, Gordin D, Parkkonen M, Saraheimo M, Thorn LM, Tolonen N, Wadén

- J, He B, Osterholm AM, Tuomilehto J, Lajer M, Salem RM, McKnight AJ; The GENIE Consortium, Tarnow L, Panduru NM, Barbarini N, Di Camillo B, Toffolo GM, Tryggvason K, Bellazzi R, Cobelli C; The FinnDiane Study Group, Groop PH. Novel genetic susceptibility loci for diabetic end-stage renal disease identified through robust naive Bayes classification. **Diabetologia**, 2014; 57(8):1611-22
90. Di Camillo B, Eduati F, Nair SK, Avogaro A, Toffolo GM. Leucine modulates dynamic phosphorylation events in insulin signaling pathway and enhances insulin-dependent glycogen synthesis in human skeletal muscle cells. **BMC Cell Biol**, 2014; 15(1):9
 91. Finotello F, Lavezzo E, Bianco L, Barzon L, Mazzon P, Fontana P, Toppo S, Di Camillo B. Reducing bias in RNA sequencing data: a novel approach to compute counts. **BMC Bioinformatics**, 2014; 15(Suppl 1):S7
 92. Di Camillo B, Sambo F, Toffolo G, Cobelli C. ABACUS: an entropy based cumulative bivariate statistic robust to rare variants and different direction of genotype effect. **Bioinformatics**, 2014; 1(30): 384-91
 93. Lavezzo E, Toppo S, Franchin E, Di Camillo B, Finotello F, Falda M, Manganelli R, Palù G, Barzon L. Genomic comparative analysis and gene function prediction in infectious diseases: application to the investigation of a meningitis outbreak. **BMC Infectious Diseases**, 2013; 13(1):554
 94. Tarca AL, Lauria M, Unger M, Bilal E, Boue S, Kumar Dey K, Hoeng J, Koepl H, Martin F, Meyer P, Nandy P, Norel R, Peitsch M, Rice JJ, Romero R, Stolovitzky G, Talikka M, Xiang Y, Zechner C; IMPROVER DSC Collaborators (Di Camillo B within IMPROVER DSC Collaborators). Strengths and limitations of microarray-based phenotype prediction: lessons learned from the IMPROVER Diagnostic Signature Challenge. **Bioinformatics**, 2013; 29(22):2892-9
 95. Militello V, Lavezzo E, Costanzi G, Franchin E, Di Camillo B, Toppo S, Palù G, Barzon L. Accurate human papillomavirus genotyping by 454 pyrosequencing. **Clin Microbiol Infect**, 2013; 19(10): E428-34
 96. Zycinski G, Barla A, Squillario M, Sanavia T, Di Camillo B, Verri A. Knowledge Driven Variable Selection (KDVS): a new approach to enrichment analysis of gene signatures obtained from high-throughput data. **Source Code Biol Med**, 2013; 8(1):2
 97. Aghaeepour N, Finak G, FlowCAP Consortium, DREAM Consortium (Di Camillo B within DREAM Consortium), Hoos H, Mosmann TR, Brinkman R, Gottardo R, Scheuermann RH. Critical assessment of automated flow cytometry data analysis techniques. **Nat Methods**, 2013; 10(3):228-38
 98. Radivojac P, Clark WT, Oron TR, Schnoes AM, Wittkop T, Sokolov A, Graitl K, Funk C, Verspoor K, Ben-Hur A, Pandey G, Yunes JM, Talwalkar AS, Repo S, Souza ML, Piovesan D, Casadio R, Wang Z, Cheng J, Fang H, Gough J, Koskinen P, Törönen P, Nokso-Koivisto J, Holm L, Cozzetto D, Buchan DW, Bryson K, Jones DT, Limaye B, Inamdar H, Datta A, Manjari SK, Joshi R, Chitale M, Kihara D, Lisewski AM, Erdin S, Venner E, Lichtarge O, Rentzsch R, Yang H, Romero AE, Bhat P, Paccanaro A, Hamp T, Kaßner R, Seemayer S, Vicedo E, Schaefer C, Achten D, Auer F, Boehm A, Braun T, Hecht M, Heron M, Hönigschmid P, Hopf TA, Kaufmann S, Kiening M, Krompass D, Landerer C, Mahlich Y, Roos M, Björne J, Salakoski T, Wong A, Shatkay H,

- Gatzmann F, Sommer I, Wass MN, Sternberg MJ, Škunca N, Supek F, Bošnjak M, Panov P, Džeroski S, Šmuc T, Kourmpetis YA, van Dijk AD, ter Braak CJ, Zhou Y, Gong Q, Dong X, Tian W, Falda M, Fontana P, Lavezzo E, Di Camillo B, Toppo S, Lan L, Djuric N, Guo Y, Vucetic S, Bairoch A, Linial M, Babbitt PC, Brenner SE, Orengo C, Rost B, Mooney SD, Friedberg I. A large-scale evaluation of computational protein function prediction. **Nat Methods**, 2013; 10(3):221-7
99. Falda M, Toppo S, Pescarolo A, Lavezzo E, Di Camillo B, Facchinetti A, Cilia E, Velasco R, Fontana P. Argot2: a large scale function prediction tool relying on semantic similarity of weighted Gene Ontology terms. **BMC Bioinformatics**, 2012; 13 Suppl 4:S14
 100. Sambo F, Trifoglio E, Di Camillo B, Toffolo G, Cobelli C. Bag of Naïve Bayes: biomarker selection and classification from Genome-Wide SNP data. **BMC Bioinformatics**, 2012, 13 Suppl 14:S2
 101. Sambo F, Montes de Oca M A, Di Camillo B, Toffolo G, Stützle T. MORE: Mixed Optimization for Reverse Engineering. An application to modeling biological networks response via sparse systems of nonlinear differential equations. **IEEE/ACM Trans Comput Biol Bioinform**, 2012, 9(5):1459-71
 102. Eduati F, De Las Rivas J, Di Camillo B, Toffolo G, Saez-Rodriguez J. Integrating literature-constrained and data-driven inference of signalling networks. **Bioinformatics**, 2012, 28(18):2311-7
 103. Trojani A, Di Camillo B, Tedeschi A, Lodola M, Montesano S, Ricci F, Vismara E, Greco A, Veronese S, Orlacchio A, Martino S, Colombo C, Mura MA, Nichelatti M, Colosimo A, Scarpati B, Montillo M, Morra E. Gene Expression Profiling Identifies ARSD as a New Marker of Disease Progression in Chronic Lymphocytic Leukemia. **Cancer Biomarkers**, 2012; 11(1): 15-28
 104. Giobbe GG, Zagallo M, Riello M, Serena E, Masi G, Barzon L, Di Camillo B, Elvassore N. Confined 3D microenvironment regulates early differentiation in human pluripotent stem cells. **Biotechnol Bioeng**, 2012;109(12):3119-32
 105. Di Camillo B, Irving BA, Schimke J, Sanavia T, Toffolo G, Cobelli C, Nair KS. Function-based discovery of significant transcriptional temporal patterns in insulin stimulated muscle cells. **PLoS One**, 2012;7(3):e32391
 106. Sanavia T, Aiolfi F, Da San Martino G, Bisognin A, Di Camillo B. Improving biomarker list stability by integration of biological knowledge in the learning process. **BMC Bioinformatics**, 2012 Mar 28;13 Suppl 4:S22
 107. Eduati F, Di Camillo B, Karbiener M, Scheideler M, Corà D, Caselle M, Toffolo G. Dynamic modeling of miRNA-mediated feed forward loops. **J Comput Biol**, 2012;19(2):188-99
 108. Di Camillo B, Sanavia T, Martini M, Jurman G, Sambo F, Barla A, Squillario M, Furlanello C, Toffolo G, Cobelli C. Effect of size and heterogeneity of samples on biomarker discovery: synthetic and real data assessment. **PLoS One**, 2012;7(3):e32200

109. Badaloni S, Di Camillo B, Sambo F. Qualitative Reasoning for Biological Network Inference from Systematic Perturbation Experiments. **IEEE/ACM Trans Comput Biol Bioinform**, 2012, 9(5):1482-91
110. Martínez MR, Corradin A, Klein U, Álvarez MJ, Toffolo GM, Di Camillo B, Califano A, Stolovitzky GA. Quantitative modeling of the terminal differentiation of B cells and mechanisms of lymphomagenesis. **Proc Natl Acad Sci**, 2012, 109(7):2672-7
111. Finotello F, Lavezzo E, Fontana P, Peruzzo D, Albiero A, Barzon L, Falda M, Di Camillo B, Toppo S. Comparative analysis of algorithms for whole-genome assembly of pyrosequencing data. **Brief Bioinform**, 2012 13(3):269-80
112. De Palo G, Eduati F, Zampieri M, Di Camillo B, Toffolo G, Altafini C. Adaptation as a genome-wide autoregulatory principle in the stress response of yeast. **IET Systems Biology**, 2011; 5(4): 269-279
113. Di Camillo B, M Falda, G Toffolo, C Cobelli. SimBioNeT: A Simulator of Biological Network Topology. **IEEE/ACM Trans Comput Biol Bioinform**, 2012; 9(2):592-600
114. Guerra S, Boscarì F, Avogaro A, Di Camillo B, Sparacino G, De Kreutzenberg SV. Haemodynamics Assessed Via Approximate Entropy Analysis Of Impedance Cardiography Time Series: Effect Of Metabolic Syndrome. **American Journal of Physiology**, 2011, 301(2):H592-8
115. Corradin A, Di Camillo B, Ciminale V, Toffolo G, Cobelli C. Sensitivity analysis of retrovirus HTLV-1 transactivation. **J Comput Biol**, 2011; 18(2):183-93
116. Di Camillo B, Sanavia T, Iori E, Bronte V, Roncaglia E, Maran A, Avogaro A, Toffolo G, Cobelli C. The transcriptional response in human umbilical vein endothelial cells exposed to insulin: a dynamic gene expression approach. **PLoS One**, 2010; 5(12):e14390.
117. Eduati F, Corradin A, Di Camillo B, Toffolo G. A Boolean approach to linear prediction for signaling network modeling. **PLoS One**, 2010; 5(9): e12789
118. Lavezzo E, Toppo S, Barzon L, Cobelli C, Di Camillo B, Finotello F, Franchin E, Peruzzo D, Toffolo GM, Trevisan M, Palù G. Draft genome sequences of two *Neisseria meningitidis* serogroup C clinical isolates. **Journal of Bacteriology** 2010; 192 (19): 5270-5271
119. Bogner-Strauss Jg, Prokesch A, Sanchez-Cabo F, Rieder D, Hackl H, Duszka K, Krogsdam A, Di Camillo B, Walenta E, Klatzer A, Lass A, Pinent M, Wong Wc, Eisenhaber F, Trajanoski Z. Reconstruction of gene association network reveals a transmembrane protein required for adipogenesis and targeted by PPARgamma. **Cellular and Molecular Life Sciences** 2010; 67(23):4049-64
120. Nasso S, Silvestri F, Tisiot F, Di Camillo B, Pietracaprina A, Toffolo G. An Optimized Data Structure for High Throughput 3D Proteomics Data: mzRTree,. **Journal of Proteomics**, 2010; 73(6):1176-82
121. Di Camillo B, Toffolo G, Cobelli C. A Gene Network Simulator to Assess Reverse Engineering Algorithms. **Ann N Y Acad Sci**. 2009; 1158:125-42

122. Di Camillo B, Toffolo G, S K Nair, Greenlund L J, Cobelli, C Significance analysis of microarray transcript levels in time series experiments. **BMC Bioinformatics**, 2007; 8 S1: 1-13
123. Di Camillo B, Sanchez-Cabo F, Toffolo G, Nair Sk, Trajanoski Z, Cobelli C. A quantization method based on threshold optimization for microarray short time series. **BMC Bioinformatics**, 2005; 6: S11
124. Basu R, Di Camillo B, Toffolo G, Basu A, Shah P, Vella A, Rizza R, Cobelli C. Use of a Novel Triple-Tracer Approach to Assess Postprandial Glucose Metabolism. **American Journal of Physiology: Endocrinology and Metabolism**, 2003; 284: E55-E69

International congress papers with external peer review

1. Grisan E, Zandonà A, Di Camillo B. Deep Convolutional Neural Networks for Survival Estimation of ALS Patients. **European Symposium on Artificial Neural Networks, Computational Intelligence and Machine Learning** Bruges (Belgium), 24 - 26 April 2019.
2. Vettoretti M, Longato E, Di Camillo B, Facchinetti A. Importance of Recalibrating Models for Type 2 Diabetes Onset Prediction: Application of the Diabetes Population Risk Tool on the Health and Retirement Study. **Conf Proc IEEE Eng Med Biol Soc**. 2018 :5358-5361.
3. Giaretta A, Di Camillo B, Barzon L, Toffolo GM. Modeling HPV early promoter regulation. **Conf Proc IEEE Eng Med Biol Soc**, 2015; 2015:6493-6
4. Sambo F, Di Camillo B, Franzin A, Facchinetti A, Hakaste L, Kravic J, Fico G, Tuomilehto J, Groop L, Gabriel R, Tuomi T, Cobelli C. A Bayesian Network analysis of the probabilistic relations between risk factors in the predisposition to type 2 diabetes. **Conf Proc IEEE Eng Med Biol Soc**, 2015; 2015:2119-22
5. Sambo F, Facchinetti A, Hakaste L, Kravic J, Di Camillo B, Fico G, Tuomilehto J, Groop L, Gabriel R, Tuomi T, Cobelli C. A Bayesian network for probabilistic reasoning and imputation of missing risk factors in type 2 diabetes. In: **Proc. of the 15th Conference on Artificial Intelligence in Medicine, Lecture Notes in Computer Science**, 2015; 9105: 172-176
6. Trojani A, Greco A, Tedeschi A, Lodola M, Di Camillo B, Ricci F, Turrini M, Varettoni M, Rattotti S, Morra E. Microarray demonstrates different gene expression profiling signatures between Waldenström macroglobulinemia and IgM monoclonal gammopathy of undetermined significance. **Clin Lymphoma Myeloma Leuk**, 2013; 13(2):208-10
7. Zycinski G, Squillario M,, Barla A, Sanavia T, Verri A, Di Camillo B. Discriminant functional gene groups identification with machine learning and prior knowledge **European Symposium on Artificial Neural Networks, Computational Intelligence and Machine Learning**, Bruges Belgium, 25 - 27 April 2012

8. Sambo F, Di Camillo B. Minimizing Time when Applying Bootstrap to Contingency Tables Analysis of Genome-Wide Data. In: Hamadi, Y., Schoenauer, M. (eds.) **Learning and Intelligent Optimization. Lecture Notes in Computer Science**. Springer Berlin / Heidelberg, 2012; 7219: 175-189
9. Sambo F, Di Camillo B. Qualitative reasoning on systematic gene perturbation experiments. In: **Computational Intelligence Methods for Bioinformatics and Biostatistics. Lecture Notes in Bioinformatics**, Springer Berlin / Heidelberg, 2011; 6685: 135-146
10. Sambo F, Montes de Oca M A, Di Camillo B and Stützle T. On the difficulty of inferring gene regulatory networks: A study of the fitness landscape generated by relative squared error. In: Collet, P., Monmarché, N., Legrand, P., Schoenauer, M., Lutton, E. (eds.) **Artificial Evolution, Lecture Notes in Computer Science**, Springer Berlin / Heidelberg, 2010; 5975: 74-85
11. Corradin A, Di Camillo B, Rende F, Ciminale V, Toffolo GM, Cobelli C. Retrovirus HTLV-1 gene circuit: a potential oscillator for eukaryotes. **Pac Symp Biocomput**, 2010: 421-32
12. Sambo F, Di Camillo B, Falda M, Toffolo G, Badaloni S. CNET: an algorithm for the inference of gene regulatory interactions from gene expression time series. In: Proceedings of the **14th Workshop on Intelligent Data Analysis in medicine and Pharmacology IDAMAP09**, 2009; 23-28
13. Sambo F., Di Camillo B, Toffolo G. CNET: an algorithm for Reverse Engineering of Causal Gene Networks. In: Bioinformatics Methods for Biomedical Complex Systems Applications. **8th Workshop on Network Tools and Applications in Biology NETTAB 2008**, May 19-21, Varenna, Italy, 2008; 134-136
14. Di Camillo B. G.Toffolo, C.Cobelli. Function-Based Discovery of Temporal Patterns In High-Throughput Genomic Studies. In proceedings of **Foundations of Systems Biology and Engineering** Stuttgart, 2007; 379-384

Book Chapters

1. Sambo F, Sanavia T, Di Camillo B. Integration of Genetic Variation as External Perturbation to Reverse Engineer Regulatory Networks from Gene Expression Data. In: de la Fuente A. Gene Network Inference: Verification of Methods for Systems Genetics Data. Springer-Verlag Berlin Heidelberg 2013.
2. Di Camillo B , Toffolo G. Reverse Engineering of High-Throughput Genomic and Genetic Data. In: Carson E, Cobelli C. Modeling Methodology for Physiology and Medicine, Elsevier Inc. London 2013.
3. Bellazzi R., Bicciato S., Cobelli C., Di Camillo B., Ferrazzi F., Magni P., Sacchi L., Toffolo G. Microarray data analysis: general concepts, gene selection, classification. In: Cerrutti S., Marchesi C. Advanced Methods of Biomedical Signal Processing. IEEE-EMBS, Pàtron (Italy). 2011.

4. Bellazzi R., Bicciato S., Cobelli C., Di Camillo B., Ferrazzi F., Magni P., Sacchi L., Toffolo G. Microarray data analysis: gene regulatory networks In: Cerrutti S., Marchesi C. Advanced Methods of Biomedical Signal Processing. IEEE-EMBS, Pàtron (Italy). 2011.
5. Di Camillo B., Castiglioni I, Sambo F, Gilardi M C, Toffolo G M. Methods for discovery and integration of genetic and neuroimaging biomarkers. In: Fato M M, Gilardi M C, Schenone A. Neuroinformatica. vol. 30, BOLOGNA: Pàtron (Italy). 2011.
6. Corradin A, Di Camillo B., Toffolo G (2010). Modelli deterministici e modelli stocastici per la molecular systems biology. In: Cavalcanti S.. Biologia Sintetica. vol. 29, p. 67-84, Bologna: Patron (Italy).
7. Di Camillo B., Toffolo G., Cobelli C. (2007). Reverse engineering delle reti di regolazione genica. In: Bellazzi R., Bicciato S., Cavalcanti S., Cobelli C., Toffolo G. Genomica e Proteomica Computazionale. (vol. 26). Bologna: Pàtron (Italy).
8. Toffolo G., Di Camillo B., Cobelli C. (2007). Modelli del turnover e della regolazione proteica. In: Bellazzi R., Bicciato S., Cavalcanti S., Cobelli C., Toffolo G. Genomica e Proteomica Computazionale. (vol. 26). Bologna: Pàtron (Italy).
9. Bellazzi R., Bicciato S., Cobelli C., Di Camillo B., Ferrazzi F., Magni P., Sacchi L., Toffolo G. (2004). Analisi di dati di DNA microarray: fondamenti, selezione di geni, classificazione. In: Cerutti S., Marchesi C., Metodi avanzati di elaborazione di segnali biomedici. (vol. 23). Bologna: Pàtron (Italy).
10. Bellazzi R., Bicciato S., Cobelli C., Di Camillo B., Ferrazzi F., Magni P., Sacchi L., Toffolo G. (2004) Analisi di dati di DNA microarray: reti di regolazione. In: Cerutti S., Marchesi C. Metodi avanzati di elaborazione di segnali biomedici. (vol. 23). Bologna: Pàtron (Italy).