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Research Interests

Phylogenetics: phylodynamics, phylogeography; dynamics of pathogen spread; mathematical modelling; metabolic modelling; bio-ontologies; algorithms.

Professional Experience

- 2025- now **Group Leader**, *Institut de Biologie de l'École Normale Supérieure (IBENS) & Institut Pasteur*, Paris FR group Modelling of Pathogens: Evolution, Adaptation and Spread.
- Studying drivers of viral & bacterial pathogenicity, their evolution & spread, using pathogen genomic data: ZIKV, HIV-1, DENV, Cholera, Sars-CoV-2, Rabies, Ebola
 - Epidemiological parameter inference from pathogen phylogenies (phylodynamics)
 - Spatio-temporal analysis of pathogen spread (phylogeography)
 - Modelling drug resistance emergence and transmission
 - Development of mathematical models, algorithms and tools for analysis of large pathogen genomic data sets
- 2024-2025 **Staff scientist (CR)**, *Institut Pasteur*, G5 group Evolutionary Dynamics of Infectious Diseases.
- 2015-2024 **Research engineer**, *Institut Pasteur*, Bioinformatics&Biostatistics Hub / Evolutionary Bioinformatics unit.
- 2014-2015 **Postdoc**, *IBGC/CNRS UMR 5095/U Bordeaux*.
- Bordeaux FR ○ Constraint-based modelling of mitochondrial metabolism
- 2011-2014 **PhD candidate**, *Inria/U Bordeaux/CNRS project-team MAGNOME*.
- Talence FR ○ Knowledge-based generalization and zoomable visualization of metabolic models
- 2009, 2011 **Intern**, *EMBL-EBI*, Functional Genomics & Computational Systems Neurobiology groups.
- Cambridge UK ○ Semantic search in Array Express Archive; Kinetic Simulation Algorithm Ontology development

Education

- 2011-2014 **PhD in Computer Science**, *University of Bordeaux*, FR (advisor: DJ Sherman).
- 2005-2010 **BSc+MSc in Software Engineering and Math**, *St. Petersburg State University*, RU (honours).

Selected Talks

- 18/6/2024 **Epidemiological birth-death models with partner notification**, *MCEB*, Montpellier, FR.
- 3/5/2023 **Phylodynamics: from mathematical modelling to deep learning**, *phyloseminar.org*, inv. seminar.
- 8/9/2018 **Modelling drug resistance spread in HIV**, *5th ESCS @ ECCB 2018*, Athens GR, *keynote*.
- 28/11/2016 **A modeling workflow in systems biol: overview**, *1st RSG Luxembourg congress*, Belval LU, *keynote*.
- 5/8/2015 **Multi-level representation of metabolic networks**, *Cheminform&Metabol gr.*, *EMBL-EBI*, UK, inv. seminar.

Selected Teaching

- 11 – 12/2022 **Approches comparatives phylogénétiques** module of Master 2 EvoGEM, *Paris FR*, 9h.
- 3/2022 PHINDaccess course: **Evolution & Phylogenetics**, *Institut Pasteur Tunis TN*, 8h (coordinator).
- 10/2019 **Behind Evol. Trees: Math & Algorithms in Phylogenetics**, *I Pasteur Montevideo UY*, 10h (co-organiser).
- 10/2019 **Math & Comput. methods for Phylogenetics & Evol. Epidemiology**, *IPK Havana CU*, 7h (co-organiser).

Selected Tutoring [Total: 3 PhD students, 8 interns, 2 scientists]

- 9/2023 – PhD: **Vincent Garot** (College de France), co-advising w. Drs L Jacob (LCQB) & S Alizon (CdF).
- ... ○ Epidemiological parameter estimation from viral genomes with deep learning

- 11/2020 – PhD: **Andrew Holtz** (I Pasteur/FIRE), *co-advised w. Drs H Bourhy (IP) & G Baele (KU Leuven)*.
 12/2023 ◦ Exploring factors that drive & sustain virus spread over time and geographic space
- 11/2019 – PhD: **Jakub Voznica** (I Pasteur/ENS/CRI), *co-advised with Dr H Morlon (IBENS)*.
 11/2021 ◦ Deep learning from phylogenies to uncover the transmission dynamics of epidemics

Grants and scholarships

- 2025 – ... **FR-US epidemiol.& genomic studies of pathogens** (Richard Lounsbery Foundation ~ 175K\$, PI).
 2025 – ... **IBENS new group starting grant** (Subvention d'Etat ~ 200K€, PI).
 2023 – 2028 **DEELOGENY: Machine learning for improved phylogenomic inference** (ANR PRC, partner).
 2022, 2024 **travel grants for teaching @ 26th & 28th VEME workshops (Panama & Brazil)** (PAHO).
 2023 **HKU-Pasteur Research Pole Fellowship** (scientist in charge of grant for intership of R Xie).
 2021 **travel grant for teaching @ Summer school IFUMI (Montevideo)** (IFUMI).
 2019 – 2020 **The dynamics of HIV-1 epidemics in Cuba** (Campus France, collaborator).
 2019 – 2020 **Outcomes of fetuses/infants exposed to Zika in utero in Vietnam** (INCEPTION, collaborator).
 2011 – 2014 **Inria CORDI-S fellowship for doctoral studies** (Inria CORDI-S, recipient).

Software & Ontologies

- treesimulator** Simulation of transmission trees under MTBD-CT-Sky models: pypi.org/project/treesimulator
BDCT Birth-Death with Contact Tracing model estimation from phylogenies: pypi.org/project/bdct
PyBDEI Birth-Death Exposed-Infectious model parameter estimation from phylogenies: pypi.org/project/pybdei
PhyloDeep Deep-learning parameter estimation and model selection from phylogenies: pypi.org/project/phylodeep
PastML Ancestral scenario reconstruction and visualisation for phylogenies: pastml.pasteur.fr
Mimoza Metabolic model visualization and navigation system: mimoza.bordeaux.inria.fr
MAMO Mathematical Modelling Ontology: co.mbine.org/standards/mamo
KiSAO Kinetic Simulation Algorithm Ontology: co.mbine.org/standards/kisao

Academic activity

Talk/poster selection: MCEB'18,'19,'20, AICoB'20, aSSB'15, Dyn.& Evol. of Human Viruses'25
 Conf./seminar organisation: SARS-CoV-2 session @SMPGD'22, Comp Biol Department seminar @ IP (2022-23)
 Journal reviewer: Systematic Biol, MBE, Viruses, GBE, Wellcome Open Res, PLOS One, etc.
 Funding proposal reviewer: University of Oslo (2018), UKRI Medical Research Council (2021)
 Thesis juries: J Voznica (U Paris Cité'21), P de Boissier (U Aix-Marseille'22), A Holtz (U Paris Cité'23), J Andréoletti (Sorbonne U'25)
 Thesis advisory committee: L Nesterenko (Université Lyon 1, 2022)
 Hiring committees: Bioinformatics & Biostatistics Hub research engineer positions @ Institut Pasteur: preselection for interviews (2016,'17,'19,'23), technical jury member (2017)
 Researcher representative, Comp. Biol. Department council of Institut Pasteur (2020-21, 2025-...)

Languages

Russian (*native*), English (*fluent*), French (*fluent*), Italian (*basics*)

Other

- 2019,2021 In top 3% in **Google Code Jam to I/O for Women'19** (30th out of ~ 1000),'21 (95th out of ~ 6500).

Journal articles [¹co-first authors, ✉(co-)corresponding author(s)]

1. [Zhukova](#)✉, A., & Gascuel, O. (2025). Accounting for contact tracing in epidemiological birth-death models. *PLOS Computational Biology*, 21(5), e1012461. doi: 10.1371/journal.pcbi.1012461
2. Hawkey¹, J., Frézal¹, L., Tran Dien, A., [Zhukova](#), A., Brown, D., Chattaway, M. A., Simon, S., Izumiya, H., Fields, P. I., De Lappe, N., Kaftyreva, L., Xu, X., Isobe, J., Clermont, D., Njamkepo, E., Akeda, Y., Issenhuth-Jeanjean, S., Makarova, M., Wang, Y., Hunt, M., Jenkins, B. M., Ravel, M., Guibert, V., Serre, E., Matveeva, Z., Fabre, L., Cormican, M., Yue, M., Zhu, B., Morita, M., Iqbal, Z., Silva Nodari, C., Pardos de la Gandara, M., & Weill, F.-X. (2024). Genomic perspective on the bacillus causing paratyphoid b fever. *Nat Commun*, 15(1), 10143. doi: 10.1038/s41467-024-54418-4
3. Xie✉, R., Adam, D. C., Hu, S., Cowling, B. J., Gascuel, O., [Zhukova](#)✉, A., & Dhanasekaran✉, V. (2024). Integrating contact tracing data to enhance outbreak phylodynamic inference: a deep learning approach. *Molecular Biology and Evolution*, msae232. doi: 10.1093/molbev/msae232
4. Morel, M., [Zhukova](#), A., Lemoine, F., & Gascuel, O. (2024). Accurate Detection of Convergent Mutations in Large Protein Alignments with ConDor. *Genome Biology and Evolution*, evae040. doi: 10.1093/gbe/evae040
5. Maestri¹, R., Perez-Lamarque¹, B., [Zhukova](#), A., & Morlon, H. (2024). Recent evolutionary origin and localized diversity hotspots of mammalian coronaviruses. *eLife*, 13, RP91745. doi: 10.7554/eLife.91745.1
6. Anjou, C., Lotoux, A., [Zhukova](#), A., Royer, M., Caulat, L. C., Capuzzo, E., Morvan, C., & Martin-Verstraete, I. (2024). The multiplicity of thioredoxin systems meets the specific lifestyles of Clostridia. *PLOS Pathogens*, 20(2), e1012001. doi: 10.1371/journal.ppat.1012001
7. [Zhukova](#)✉, A., Hecht, F., Maday, Y., & Gascuel✉, O. (2023). Fast and Accurate Maximum-Likelihood Estimation of Multi-Type Birth–Death Epidemiological Models from Phylogenetic Trees. *Systematic Biology*, syad059. doi: 10.1093/sysbio/syad059
8. Holtz✉, A., Baele, G., Bourhy, H., & [Zhukova](#)✉, A. (2023). Integrating full and partial genome sequences to decipher the global spread of canine rabies virus. *Nature Communications*, 14(1), 4247. doi: 10.1038/s41467-023-39847-x
9. [Zhukova](#)✉, A., Dunn, D., Gascuel✉, O., & the UK HIV Drug Resistance Database & the Collaborative HIV Anti-HIV Drug Resistance Network. (2023). Modeling Drug Resistance Emergence and Transmission in HIV-1 in the UK. *Viruses*, 15(6), 1244. doi: 10.3390/v15061244
10. Voznica✉, J., [Zhukova](#)✉, A., Boskova, V., Saulnier, E., Lemoine, F., Moslonka-Lefebvre, M., & Gascuel✉, O. (2022). Deep learning from phylogenies to uncover the epidemiological dynamics of outbreaks. *Nature Communications*, 13(1), 3896. doi: 10.1038/s41467-022-31511-0
11. Shaikh, B., Smith, L. P., Vasilescu, D., Marupilla, G., Wilson, M., Agmon, E., Agnew, H., Andrews, S. S., Anwar, A., Beber, M. E., Bergmann, F. T., Brooks, D., Brusch, L., Calzone, L., Choi, K., Cooper, J., Detloff, J., Drawert, B., Dumontier, M., Ermentrout, G. B., Faeder, J. R., Freiburger, A. P., Fröhlich, F., Funahashi, A., Garny, A., Gennari, J. H., Gleeson, P., Goelzer, A., Haiman, Z., Hasenauer, J., Hellerstein, J. L., Hermjakob, H., Hoops, S., Ison, J. C., Jahn, D., Jakubowski, H. V., Jordan, R., Kalaš, M., König, M., Liebermeister, W., Sheriff, R. S. M., Mandal, S., McDougal, R., Medley, J. K., Mendes, P., Müller, R., Myers, C. J., Naldi, A., Nguyen, T. V. N., Nickerson, D. P., Olivier, B. G., Patoliya, D., Paulevé, L., Petzold, L. R., Priya, A., Rampadarath, A. K., Rohwer, J. M., Saglam, A. S., Singh, D., Sinha, A., Snoep, J., Sorby, H., Spangler, R., Starruß, J., Thomas, P. J., van Niekerk, D., Weindl, D., Zhang, F., [Zhukova](#), A., Goldberg, A. P., Schaff, J. C., Blinov, M. L., Sauro, H. M., Moraru, I. I., & Karr, J. R. (2022). BioSimulators: a central registry of simulation engines and services for recommending specific tools. *Nucleic Acids Research*, 50(W1), W108-W114. (gkac331) doi: 10.1093/nar/gkac331

12. Seabra¹, S. G., Libin¹, P. J. K., Theys¹, K., [Zhukova](#), A., Potter, B. I., Nebenzahl-Guimaraes, H., Gorbalenya, A. E., Sidorov, I. A., Pimentel, V., Pingarilho, M., de Vasconcelos, A. T. R., Dellicour, S., Khouri, R., Gascuel, O., Vandamme, A.-M., Baele, G., Cuyppers, L., & Abecasis, A. B. (2022). Genome-wide diversity of Zika virus: Exploring spatio-temporal dynamics to guide a new nomenclature proposal. *Virus Evolution*, 8(1), veac029. doi: 10.1093/ve/veac029
13. Fillâtre, P., Dufour, M.-J., Behillil, S., Vatan, R., Reusse, P., Gabelle, A., Velmans, N., Montagne, C., Du Coudret, S. G., Droumaguet, E., Merour, V., Enouf, V., Buzele, R., Valence, M., Guillotel, E., Gagniere, B., Baidaliuk, A., Zhukova, A., Tourdjman, M., Thibault, V., Grolhier, C., Pronier, C., Lescure, F.-X., Simon-Loriere, E., Costagliola, D., Van Der Werf, S., Tattévin, P., & Massart, N. (2021, October). A new SARS-CoV-2 variant poorly detected by RT-PCR on nasopharyngeal samples, with high lethality: an observational study. *Clinical Microbiology and Infection*. Retrieved 2021-10-11, from <https://linkinghub.elsevier.com/retrieve/pii/S1198743X21005656> (Publisher: Elsevier) doi: 10.1016/J.CMI.2021.09.035
14. Bennedbaek, M., [Zhukova](#), A., Tang, M.-H. E., Bennet, J., Munderi, P., Ruxrungtham, K., Gisslen, M., Worobey, M., Lundgren, J. D., & Marvig, R. L. (2021). Phylogenetic Analysis of HIV-1 Shows Frequent Cross-Country Transmission and Local Population Expansions. *Virus Evolution*, 7(2), veab055. doi: 10.1093/ve/veab055
15. Grant, R., Nguyen, T. T. T., Dao, M. H., Pham, H. T. T., Piorkowski, G., Pham, T. D. T., Cao, T. M., Huynh, L. T. K., Nguyen, Q. H., Vien, L. D. K., Lemoine, F., [Zhukova](#), A., Hoang, D. T. N., Nguyen, H. T., Tran, N. T., Le, L. B., Ngo, M. N. Q., Tran, T. C., Le, N. N. T., Nguyen, M. N., Pham, H. T., Hoang, T. T. D., Dang, T. V., Vu, A. T., Nguyen, Q. N. T., de Lamballerie, X., Pham, Q. D., Luong, Q. C., & Fontanet, A. (2021). Maternal and neonatal outcomes related to Zika virus in pregnant women in Southern Vietnam: An epidemiological and virological prospective analysis. *The Lancet Regional Health - Western Pacific*, 11, 100163. doi: 10.1016/j.lanwpc.2021.100163
16. [Zhukova](#) , A., Voznica, J., Felipe, M. D., To, T.-H., Pérez, L., Martínez, Y., Pintos, Y., Méndez, M., Gascuel , O., & Kouri , V. (2021, 8). Cuban history of CRF19 recombinant subtype of HIV-1. *PLOS Pathogens*, 17(8), e1009786. doi: 10.1371/JOURNAL.PPAT.1009786
17. Oprea¹, M., Njamkepo¹, E., Cristea¹, D., [Zhukova](#)¹, A., Clark, C. G., Kravetz, A. N., Monakhova, E., Ciontea, A. S., Cojocar, R., Rauzier, J., Damian, M., Gascuel, O., Marie-Laure, Q., & Weill, F.-X. (2020). The seventh pandemic of cholera in Europe revisited by microbial genomics. *Nature Communications*, 11(1), 5347. doi: 10.1038/s41467-020-19185-y
18. Keating, S. M., Waltemath, D., König, M., Zhang, F., Dräger, A., Chaouiya, C., Bergmann, F. T., Finney, A., Gillespie, C. S., Helikar, T., Hoops, S., Malik-Sheriff, R. S., Moodie, S. L., Moraru, I. I., Myers, C. J., Naldi, A., Olivier, B. G., Sahle, S., Schaff, J. C., Smith, L. P., Swat, M. J., Thieffry, D., Watanabe, L., Wilkinson, D. J., Blinov, M. L., Begley, K., Faeder, J. R., Gómez, H. F., Hamm, T. M., Inagaki, Y., Liebermeister, W., Lister, A. L., Lucio, D., Mjolsness, E., Proctor, C. J., Raman, K., Rodriguez, N., Shaffer, C. A., Shapiro, B. E., Stelling, J., Swainston, N., Tanimura, N., Wagner, J., Meier-Schellersheim, M., Sauro, H. M., Palsson, B., Bolouri, H., Kitano, H., Funahashi, A., Hermjakob, H., Doyle, J. C., Hucka, M., & [SBML Level 3 Community members](#). (2020). Sbml level 3: an extensible format for the exchange and reuse of biological models. *Molecular Systems Biology*, 16(8), e9110. doi: 10.15252/msb.20199110
19. Ishikawa¹, S. A., [Zhukova](#)¹, A., Iwasaki, W., & Gascuel, O. (2019). A fast likelihood method to reconstruct and visualize ancestral scenarios. *Molecular biology and evolution*, 36(9), 2069–2085. doi: 10.1093/molbev/msz131
20. [Zhukova](#), A., Fernandes, L. G., Hugon, P., Pappas, C. J., Sismeiro, O., Coppée, J.-Y., Becavin, C., Malabat, C., Eshghi, A., Zhang, J.-J., Yang, F. X., Picardeau, M., Coppée, J.-Y., Becavin, C., Malabat, C., Eshghi, A., Zhang, J.-J., Yang, F. X., Picardeau, M., & Others. (2017). Genome-wide transcriptional start site mapping and sRNA identification in the pathogen *Leptospira interrogans*. *Frontiers in cellular and infection microbiology*, 7, 10. doi: 10.3389/fcimb.2017.00010

21. Waltemath, D., Karr, J. R., Bergmann, F. T., Chelliah, V., Hucka, M., Krantz, M., Liebermeister, W., Mendes, P., Myers, C. J., Pir, P., Alaybeyoglu, B., Aranganathan, N. K., Baghalian, K., Bittig, A. T., Burke, P. E. P., Cantarelli, M., Chew, Y. H., Costa, R. S., Cursons, J., Czauderna, T., Goldberg, A. P., Gomez, H. F., Hahn, J., Hameri, T., Gardiol, D. F. H., Kazakiewicz, D., Kiselev, I., Knight-Schrijver, V., Knupfer, C., Konig, M., Lee, D., Lloret-Villas, A., Mandrik, N., Medley, J. K., Moreau, B., Naderi-Meshkin, H., Palaniappan, S. K., Priego-Espinosa, D., Scharm, M., Sharma, M., Smallbone, K., Stanford, N. J., Song, J.-H., Theile, T., Tokic, M., Tomar, N., Toure, V., Uhlendorf, J., Varusai, T. M., Watanabe, L. H., Wendland, F., Wolfien, M., Yurkovich, J. T., Zhu, Y., Zardilis, A., [Zhukova](#), A., & Schreiber, F. (2016). Toward Community Standards and Software for Whole-Cell Modeling. *IEEE Transactions on Biomedical Engineering*, 63(10), 2007–2014. doi: 10.1109/TBME.2016.2560762
22. Loira, N., [Zhukova](#), A., & Sherman, D. J. (2015). Pantograph: A template-based method for genome-scale metabolic model reconstruction. *Journal of bioinformatics and computational biology*, 13(02), 1550006. doi: 10.1142/S0219720015500067
23. [Zhukova](#), A., & Sherman, D. J. (2015). MIMOZA: web-based semantic zooming and navigation in metabolic networks. *BMC Systems Biology*, 9(1), 10. doi: 10.1186/s12918-015-0151-5
24. [Zhukova](#), A., & Sherman, D. J. (2014a). Knowledge-based generalization of metabolic models. *J Comp Biol*, 21(7), 534–47. doi: 10.1089/cmb.2013.0143
25. [Zhukova](#), A., & Sherman, D. J. (2014b). Knowledge-based generalization of metabolic networks: a practical study. *Journal of Bioinformatics and Computational Biology*, 12(2), 1441001. doi: 10.1142/S0219720014410017
26. [Zhukova](#), A., Adams, R., Laibe, C., & Le Novère, N. (2012). LibKiSAO: a Java Library for Querying KiSAO. *BMC Research Notes*, 5(1), 520+. doi: 10.1186/1756-0500-5-520
27. Courtot¹, M., Juty¹, N., Knüpfer¹, C., Waltemath¹, D., [Zhukova](#)¹, A., Dräger, A., Dumontier, M., Finney, A., Golebiewski, M., Hastings, J., Hoops, S., Keating, S., Kell, D. B., Kerrien, S., Lawson, J., Lister, A., Lu, J., Machne, R., Mendes, P., Pocock, M., Rodriguez, N., Villeger, A., Wilkinson, D. J., Wimalaratne, S., Laibe, C., Hucka, M., & Le Novère, N. (2011). Controlled vocabularies and semantics in systems biology. *Molecular systems biology*, 7(1), 543. doi: 10.1038/msb.2011.77
28. Malone, J., Holloway, E., Adamusiak, T., Kapushesky, M., Zheng, J., Kolesnikov, N., [Zhukova](#), A., Brazma, A., & Parkinson, H. (2010). Modeling sample variables with an Experimental Factor Ontology. *Bioinformatics*, 26(8), 1112–1118. doi: 10.1093/bioinformatics/btq099

Review articles [¹ co-first authors]

29. Blassel¹, L., [Zhukova](#)¹, A., Villabona-Arenas, C. J., Atkins, K. E., Hué, S., & Gascuel, O. (2021). Drug resistance mutations in HIV: new bioinformatics approaches and challenges. *Current Opinion in Virology*, 51, 56–64. doi: 10.1016/j.coviro.2021.09.009
30. [Zhukova](#), A., Blassel, L., Lemoine, F., Morel, M., Voznica, J., & Gascuel, O. (2020). Origin, evolution and global spread of SARS-CoV-2. *Comptes Rendus. Biologies*, 0(0), 1–20. doi: 10.5802/crbol.29
31. [Zhukova](#), A., Cutino-Moguel, T., Gascuel, O., & Pillay, D. (2017). The Role of Phylogenetics as a Tool to Predict the Spread of Resistance. *The Journal of Infectious Diseases*, 216(suppl_9), S820–S823. doi: 10.1093/infdis/jix411

Conference proceeding articles

32. [Zhukova](#), A., & Mazat, J.-P. (2015). The mitochondrion metabolic model iAS253 revisited. *advances in Systems and Synthetic Biology*, 179–188.
33. [Zhukova](#), A., & Mazin, M. (2010). Actor extension of Java language in MPS Environment. *Sci Tech J Inf Technol Mech Opt*, 10(2), 72–77.

Book chapters

34. [Zhukova](#), A., Gascuel, O., Duchene, S., Ayres, D., Lemey, P., & Baele, G. (2020). Efficiently Analysing Large Viral Data Sets in Computational Phylogenomics. In C. Scornavacca, F. Delsuc, & N. Galtier (Eds.), *Phylogenetics in the genomic era* (pp. 5.3:1–5.3:43). No commercial publisher — Authors open access book.