DAVID S. CAMPO

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SUMMARY

- Computational biologist with 18 years of experience in viral evolution, molecular epidemiology, health data science, machine learning and bioinformatics.
- 14 awards and frequent recipient of intramural funding, 47 peer-reviewed papers (15 as first author), 38 oral presentations at international conferences (13 as first author) and 19 poster/abstracts (5 as first author).

EDUCATION

- La Trobe University. Ph.D. Genetics. Melbourne, 2003- 2007.

Thesis: "High resolution genomic analysis of Hepatitis C Virus 1b: Use of theoretical tools in selection of vaccine candidates" Supervised by John R. Mitchell, Ph.D. (La Trobe University) and David Anderson, Ph.D. (Burnet Institute) where I extracted meaningful patterns of HCV genetic structure, evolution and covariation.

- Universidad Nacional de Colombia. B.Sc. Biology. Bogota, 1996-2002.

Thesis: "Genetic structure and evolutionary history of 14 Amerindian tribes of the Amazonian and Orinoquian regions of Colombia based on seven loci Y-chromosome STR haplotypes: A comparison with the linguistic affiliation", supervised by Juan José Yunis, MD, where I clarified the recent history of Colombian tribes and identified a remarkable correlation between genetic and linguistic evolution.

PROFESSIONAL EXPERIENCE

- Centers for Disease Control and Prevention
  - Dates: 2007 – Present.
  - Location: Atlanta, Georgia, USA.
  - Computational biologist at the Molecular epidemiology and Bioinformatics Laboratory, Division of Viral Hepatitis.
  - Permanent, Full time, 40 hours per week.
  - Duties:
    - Molecular epidemiology of viral Hepatitis.
    - Analysis of sequence data of viral outbreaks.
    - Research and development of bioinformatics algorithms
    - Design and constant improvement of the GHOST platform (Global Hepatitis Outbreak and Surveillance Technology)

- Quality control of Next-Generation Sequencing data
- Drug resistance research
- Liver cancer research

SKILLS

• Analytical: bioinformatics, computational biology, population genetics, phylogenetic analysis, data mining, machine learning, multivariate analysis, graph theory, Bayesian networks, processing of Next-Generation sequencing Data, Agent-based simulations, disruption of networks.

• Computational skills: Python, Matlab, High Performance Computing

• Laboratory techniques: DNA extraction, DNA sequencing, PCR, DNA electrophoresis, Phage Display Peptide Libraries, immune assays (ELISA).

• Languages: English (proficient) and Spanish (proficient).

AWARDS

• My thesis "Genetic structure and evolutionary history of 14 Amerindian tribes of the Amazonian and Orinoquian regions of Colombia based on seven loci Y-chromosome STR haplotypes: A comparison with the linguistic affiliation" received the following awards:

(i)   Mention of *summa cum laude* for the degree of Biology at the "Universidad Nacional de Colombia", year 2002.
(ii)   First place in the "12th National contest: best graduation work of the Universidad Nacional de Colombia", in the area of basic sciences, 2002.
(iii) First place in the "13th Aventis - National Academy of Medicine" in the area of experimental and basic sciences, 2002.
(iv)   First place in the "7th National contest Otto de Greiff: best graduation works", in the area of natural sciences, 2003.

• Recipient of the "La Trobe University Postgraduate Research Scholarship", year 2003-2006, Australia.

• Nominated for the Charles C. Shepard Science Award, year 2009, in the "Laboratory and Methods" Category. First author of the paper "Coordinated evolution of the Hepatitis C Virus".

• Our poster "Seamless Scaling of a Desktop MATLAB Application to an Experimental TeraGrid Resource" a research in collaboration with The Cornell Center for Advanced Computing, received an HPC Innovation Excellence Award from the International Data Corporation (IDC) during SC11 (Seattle, November 12-15, 2011).

• Our poster "Changes in the population of intra-host HCV variants during the first 48 hours of interferon therapy are associated with outcome of treatment at week 12" presented at

the 63rd annual meeting of the American Association of Liver Diseases (AASLD) on November 9-13 of 2012 in Boston obtained the AASLD presidential poster of distinction.

- Nominated for the Charles C. Shepard Science Award, year 2013, in the "Laboratory and Methods" Category. Second author of the paper "Convergence and Coevolution of the Hepatitis B Virus Lamivudine Resistance".

- Member of "The Indiana Injection Drug Use-Associated HIV/HCV Outbreak Response Team", which was selected as the winner of the 2015 CDC/ATSDR Honor Award for Excellence in Emergency Response – Domestic.

- Member of the "Indiana Injection Drug Use Associated with HIV/HCV Outbreak Response Team", which was the recipient of the "NCHHSTP Excellence in emergency response award-DHAP 2016". For Exemplary leadership preventing HIV and HCV infections associated with injection drug use.

- Winner of the Charles C. Shepard Science Award, year 2016, in the "Laboratory and Methods" Category. First author of the paper "Accurate genetic detection of hepatitis C virus transmissions in outbreak settings". This award is presented to the best manuscript on original research published by a CDC or ATSDR scientist in a reputable, peer-reviewed journal.

- Member of the "Molecular Epidemiology & Bioinformatics Team (DVH)", which was the recipient of the "NCHHSTP Excellence in Laboratory Research Award 2018", for developing a novel web-based technology for outbreak investigations and molecular surveillance.

- Winner of the Charles C. Shepard Science Award, year 2019, in the "Data Methods and Study Design Category" Category. First author of the paper "Entropy of Mitochondrial DNA circulating in blood is associated with Hepatocellular Carcinoma". This award is presented to the best manuscript on original research published by a CDC or ATSDR scientist in a reputable, peer-reviewed journal.

LEADERSHIP AND TEACHING EXPERIENCE

- Global Hepatitis Outbreak and Surveillance Technology (GHOST) (2014-present): Supervised Inna Rytsareva (Ph.D.) and Seth Sims (M.Sc.) on the creation of a web-based framework for the molecular detection of Hepatitis C outbreaks. GHOST enables Public Health Labs (PHL) to conduct molecular surveillance by automating the entire data processing in a high-performance computing environment, starting from the upload of raw NGS reads and finishing with visualization of transmission networks. My role in GHOST included the following tasks:
  - Project design.
  - To write and manage intramural grant proposals.
  - To write the main paper describing the underlying method ("Accurate genetic detection of hepatitis C virus transmissions in outbreak settings"), where I was the 1st author, and participate in the writing of three other papers, where I was a co-author.

- Coordination of teams from CDC (NCHHSTP Informatics Office), PHLs (New York State Lab), industry (Northrop Grumman) and universities (Georgia Institute of Technology).
- Design and implementation of computationally efficient algorithms.
- Hired and managed a highly productive team of contractors to develop cloud-based high-performance computing infrastructure.

- I have successfully mentored and/or supervised 10 fellow researchers during their time at CDC (Seth Sims PhD, Amanda Sue M.Sc., Francisco Criscuolo M.Sc., Walker Gussler M.Sc., Duc Hoang Ph.D., Inna Rytsareva Ph.D., Nana Li Ph.D., Hajung Roh Ph.D., Irina Astrakhantseva Ph.D. and June Zhang Ph.D.). Fortunately, most of these collaborations produced presentations at international conferences and/or published papers.

- Conferences: I was part of the program committee of the "Workshop on Computational Advances in Molecular Epidemiology of the IEEE International Conference on Bioinformatics and Biomedicine, November 12-15, Atlanta, GA.", a collaboration with Georgia State University and the University of Connecticut.

- Workshops: I taught epidemiologists on how to use GHOST (Global Hepatitis Outbreak and Surveillance Technology) during three annual workshops (30/11/2016–02/12/2016; 1/11/2017-3/11/2017; 5/11/2018-8/11/2018).

GRANTS

AS CDC is a government institution, all our funding was directly approved from congress. However, in multiple opportunities, I was awarded intramural funding for certain projects:
- 2016. I was awarded 100000 USD for conducting the project "Increased Mitochondrial Genetic Diversity in Persons Infected With Hepatitis C Virus".
- 2015. In an effort to modernize CDC's infrastructure and ability to conduct genomic surveillance, CDC awarded our team with funds to establish the GHOST project (see the leadership section), which received approximately 6 million USD over a period of 8 years.
- 2014. I was awarded 10000 USD for conducting a pilot project on "Cloud-based genomic surveillance".

PATENTS

I am one of the inventors in two patents:

(1) Method of diagnosing cancer using mitochondrial DNA heterogeneity.
Filing Date: 02/13/2018. Please see more details on
https://www.freepatentsonline.com/y2020/0058398.html

(2) Polyvalent vaccines and methods for making them.
Filing Date: 11/14/2022. Please see more details on
https://www.freepatentsonline.com/y2025/0032606.html

PAPERS

I have participated in 47 papers, being the first author of 15 of them. Links to these papers can be found at my "Google scholar" profile:
http://scholar.google.com/citations?user=SicUYoIAAAAJ&hl=en&oi=ao

- Mosa, A. **Campo, DS.** Khudyakov, Y. AbouHaidar, M. Gehring, A. Zahoor, A. Ball, J. Urbanowicz, R. Feld, J. 2023. Polyvalent immunization elicits a synergistic broadly neutralizing immune response to hypervariable region 1 variants of hepatitis C virus. Pro. Natl. Acad. Sci. Vol 120, Issue 24, e2220294120.

- **Campo, DS.** Mosa, A. Khudyakov, Y. 2023. A Novel Information-Theory-Based Genetic Distance That Approximates Phenotypic Differences. Journal of Computational Biology. Vol 30, Issue 4, pages: 420–431.

- Talundzic, E. Scott, S. Owino, S. **Campo, DS.** Lucchi, N. Udhayakumar, V. Moore, J. Peterson, D. 2022. Polymorphic Molecular Signatures in Variable Regions of the Plasmodium falciparum var2csa DBL3x Domain Are Associated with Virulence in Placental Malaria. Pathogens. 11(5):520. doi: 10.3390/pathogens11050520.

- **Campo, DS.** Gussler, JW. Sue, A. Skums, P. Khudyakov, Y. 2020. Accurate Spatiotemporal Mapping of Drug Overdose Deaths by Machine Learning of Drug-related Web-searches. PLoS ONE. 15(12): e0243622. https://doi.org/10.1371/journal.pone.0243622

- **Campo, DS.** Khudyakov, Y. 2020. Machine learning can accelerate discovery and application of cyber-molecular cancer diagnostics. Journal of medical artificial intelligence 3 (7).

- **Campo, DS.** Nayak, V. Srinivasamoorthy, G. Khudyakov, Y. 2019. Entropy of Mitochondrial DNA circulating in blood is associated with Hepatocellular Carcinoma. BMC Medical Genomics 2019, 12(Suppl 4):74.

- Ramachandran, S. Thai, H. Forbi, JC. Galang, RR. Dimitrova, Z. Xia, GL. Lin, Y. Punkova, L. Pontones, PR. Gentry, J. Blosser, SJ. Lovchik, J. Switzer, W. Teshale, E. Peters, P. Ward, J. Khudyakov, Y. **Hepatitis C Investigation Team.** A large HCV transmission network enabled a fast-growing HIV outbreak in rural Indiana, 2015. EBioMedicine. 2018. 37:374-381. doi: 10.1016/j.ebiom.2018.10.007.

- Tsyvina, V. **Campo, DS.** Sims, S. Zelikovsky, A. Khudyakov, Y. Skums, P. 2018. Fast estimation of genetic relatedness between members of heterogeneous populations of closely related genomic variants. BMC Bioinformatics. 19(Suppl 11):360. doi: 10.1186/s12859-018-2333-9

- Sims, S. Longmire, AG. **Campo, DS.** Ramachandran, S. Medrzycki, M. Ganova-Raeva, L. Lin, Y. Sue, A. Thai, H. Zelikovsky, A. Khudyakov, Y. 2018. Automated quality control for a molecular surveillance system. BMC Bioinformatics. 19(Suppl 11):358. DOI: 10.1186/s12859-018-2329-5

- ***Campo, DS.*** Khudyakov, Y. 2018. Intelligent Network DisRuption Analysis (INDRA): a targeted strategy for efficient interruption of hepatitis C transmissions. Infection, Genetics and Evolution. 63: 204-215. DOI: 10.1016/j.meegid.2018.05.028.

- Longmire, AG. Sims, S. Rytsareva, I. ***Campo, DS.*** Skums, P. Dimitrova, Z. Ramachandran, S. Medrzycki, M. Thai, H. Ganova-Raeva, L. Lin, Y. Punkova, L. Sue, A. Mirabito, M. Wang, S. Tracy, R. Bolet, V. Sukalac, T. Lynberg, C. Khudyakov, Y. 2017. GHOST: Global Hepatitis Outbreak and Surveillance Technology. BMC Genomics. 18(Suppl 10):916. DOI 10.1186/s12864-017-4268-3

- Rytsareva, I. ***Campo, DS.*** Zheng, Y. Sims, S. Tetik, C. Chirag, J. Chockalingam, S. Thankachan, S. Sue, A. Aluru, S. Khudyakov, Y. 2017. Efficient detection of viral transmissions with Next-Generation Sequencing data. BMC Genomics. 18(Suppl 4):372. DOI: 10.1186/s12864-017-3732-4

- ***Campo, DS.*** Zhang, J. Ramachandran, S. Khudyakov, Y. 2017. Transmissibility of intra-host hepatitis C virus variants. BMC Genomics18(Suppl 10):881

- Forbi, JC. Dillon, M. Purdy, MA. Drammeh, BS. Tejada-Strop, A. McGovern, D. Xia, G. Lin, Y. Ganova-Raeva, L. ***Campo, DS.*** Thai, H. Vaughan, G. Haule, D. Kutaga, R. Basavaraju, SV. Kamili, S. Khudyakov, Y. 2017. Molecular epidemiology of hepatitis B virus infection in Tanzania. Journal of General Virology. 98(5):1048-1057.

- ***Campo, DS.*** Roh, HJ. Pearlman, B. Fierer, D. Ramachandran, S. Vaughan, G. Hinds, A. Dimitrova, Z. Skums, P. Khudyakov, Y. 2016. Increased Mitochondrial Genetic Diversity in Persons Infected With Hepatitis C Virus. Cellular and Molecular Gastroenterology and Hepatology. 2(5):676–684. http://dx.doi.org/10.1016/j.jcmgh.2016.05.012

- Skums, P. Artyomenko, A. Glebova, O. ***Campo, DS.*** Dimitrova, Z. Zelikovsky, A. Khudyakov, Y. 2016. Error Correction of NGS Reads from Viral Populations. Computational Methods for Next Generation Sequencing Data Analysis. Pages 329-353. John Wiley & Sons, Inc.

- Skums, P. Artyomenko, A. Glebova, O. Ramachandran, S. ***Campo, DS.*** Dimitrova, Z. Mandoiu, I. Zelikovsky, A. Khudyakov, Y. 2016. Pooling Strategy for Massive Viral Sequencing. Computational Methods for Next Generation Sequencing Data Analysis. Pages 57-83. John Wiley & Sons, Inc.

- ***Campo, DS***. Xia, GL. Dimitrova, Z. Lin, Y. Forbi1, JC. Ganova-Raeva, L. Punkova, L. Ramachandran, S. Thai, H. Skums, P. Sims, S. Rytsareva, I. Vaughan, Roh. HJ, G. Purdy, M. Sue, A. Khudyakov, Y. 2016. Accurate genetic detection of hepatitis C virus transmissions in outbreak settings. Journal of Infectious Diseases. J Infect Dis. 213 (6): 957-965. doi: 10.1093/infdis/jiv542.

- Forbi JC, Layden JE, Phillips RO, Mora N, Xia GL, ***Campo, DS,*** Purdy MA, Dimitrova Z, Owusu D, Punkova L, Skums P, Owusu-Ofori S, Sarfo FS, Vaughan G, Roh H, Opare-Sem OK, Cooper RS, Khudyakov YE. 2015. Next-Generation Sequencing Reveals Frequent Opportunities for Exposure to Hepatitis C Virus in Ghana. PLoS One. 10(12):e0145530. doi: 10.1371/journal.pone.0145530.

- Gargis AS, Kalman L, Bick DP, da Silva C, Dimmock DP, Funke BH, Gowrisankar S, Hegde MR, Kulkarni S, Mason CE, Nagarajan R, Voelkerding KV, Worthey EA, Aziz N, Barnes J, Bennett SF, Bisht H, Church DM, Dimitrova Z, Gargis SR, Hafez N, Hambuch T, Hyland FC, Luna RA, MacCannell D, Mann T, McCluskey MR, McDaniel TK, Ganova-Raeva LM, Rehm HL, Reid J, *Campo, DS,* Resnick RB, Ridge PG, Salit ML, Skums P, Wong LJ, Zehnbauer B, Zook JM, Lubin IM. Good laboratory practice for clinical next-generation sequencing informatics pipelines. 2015. Nature Biotechnology. 2015 Jul;33(7):689-93. doi: 10.1038/nbt.3237.

- Ganova-Raeva, L. Punkova, L. *Campo, DS*. Dimitrova, Z. Skums, P. Vu, Dat, DT. Dalton, H. Khudyakov, Y. 2015. Cryptic hepatitis B and E virus infections among cases of apparent acute nonA-E hepatitis. Journal of Infectious Diseases. DOI: 10.1093/infdis/jiv315

- Skums, P. Artyomenko, A. Glebova, O. Ramachandran, S. Mandoiu, I. *Campo, DS*. Dimitrova, Z. Zelikovsky, A. Khudyakov, Y. 2015. Computational Framework for Next-Generation Sequencing of Heterogeneous Viral Populations using Combinatorial Pooling. Bioinformatics. 31(5):682-90. doi: 10.1093/bioinformatics/btu726.

- Ramachandran, S. Purdy, M. Xia, GL. *Campo, DS*. Dimitrova, Z. Teshale, E. Teo, CG. Khudyakov, Y. 2014. Recent Population Expansions of Hepatitis B Virus in the United States. Journal of Virology. 88(24): 13971–13980. doi:10.1128/JVI.01594-14

- *Campo, DS*. Dimitrova, Z. Yamasaki, L. Skums, P. Lau, D. Vaughan, G. Forbi, J. Teo, CG, Khudyakov, Y. 2014. Next-generation sequencing reveals large connected networks of intra-host HCV variants. BMC Genomics 15 (Suppl 5), S4.

- Forbi, J. *Campo, DS*. Purdy, D. Dimitrova, Z. Skums, P. Xia, G. Punkova, L. Ganova-Raeva, L. Vaughan, L. Ben-Ayed, Y. Switzer, W. Khudyakov, Y. 2014. Intra-host diversity and evolution of hepatitis C virus endemic to Côte d'Ivoire. Journal of Medical Virology. Volume 86, Issue 5, pages 765–771. doi: 10.1002/jmv.23897

- *Campo, DS*. Skums, P. Dimitrova, Z. Vaughan, G. Forbi, J. Teo, CG. Khudyakov, Y. Lau, D. 2014. Drug-resistance of a viral population and its individual intra-host variants during the first 48 hours of therapy. Clinical Pharmacology and Therapy. **95** 6, 627–635. doi:10.1038/clpt.2014.20.

- Skums, P. Glebova, O. Zelikovsky, A. Dimitrova, Z. *Campo, DS*. Ganova-Raeva, L. Khudyakov, Y. Alignment of DNA Mass-Spectral Profiles Using Network Flows. 2013. Bioinformatics research and applications. In: Lecture Notes in Computer Science, Volume 7875. Cai, Z. Eulenstein, O. Janies, D. Schwartz, D. (Eds.) Springer, Charlotte, NC. pp. 149-160.

- Yunis, JJ. Acevedo, L. *Campo, DS*. Yunis, E. Geno-geographic origin of Y-specific STR haplotypes of a sample of Caucasian-Mestizo and African descent male individuals from Colombia. Biomédica. 2013;33(3).

- Ganova-Raeva, L. Dimitrova, Z. *Campo, DS*. Lin, Y. Ramachandran, S. Xia, G. Honisch, C. Cantor, C. Khudyakov, Y. 2013. Detection of hepatitis C virus transmission using

mass spectrometry. Journal of Infectious Diseases. 207(6):999-1006.doi: 10.1093/infdis/jis938.

- Ganova-Raeva, L. Dimitrova, Z. *Campo, DS*. Khudyakov, Y. Application of Mass Spectrometry to Molecular Surveillance of Hepatitis B and C Viral Infections. 2012. Antiviral Therapy. 17:1477-1482 doi: 10.3851/IMP2466

- *Campo, DS*. Dimitrova, Z. Lara, J. Purdy, M. Thai, H. Ramachandran, S. Ganova-Raeva, L. Zhai, X. Forbi, J. Teo, C. Khudyakov, Y. 2011. Coordinated evolution of the Hepatitis B Virus Polymerase. In Silico Biology 11(5): 175–182. doi 10.3233/ISB-2012-0452

- Dimitrova, Z. *Campo, DS*. Ramachandran, S. Vaughan, G. Ganova-Raeva, L. Lin, y. Forbi, J. Xia, G. Skums, P. Honisch, C. Pearlman, B. Khudyakov, Y. 2012. Evaluation of Viral Heterogeneity Using Next-Generation Sequencing, End-point Limiting-dilution and Mass Spectrometry. In Silico Biol. 11(5):183-92. doi: 10.3233/ISB-2012-0453.

- Astrakhantseva, I. *Campo, DS*. Khudyakov, Y. Araujo, A. Teo, C. Kamili, S. 2012. Differences in variability of hypervariable region 1 of hepatitis C virus (HCV) between acute and chronic stages of HCV infection. In Silico Biology. 11(5):163-73. doi: 10.3233/ISB-2012-0451.

- Skums, P. *Campo, DS*. Dimitrova, Z. Lau, D. Khudyakov, Y. 2011. Modeling differential interferon resistance of HCV quasispecies. In Silico Biology. 11(5):263-9. doi: 10.3233/ISB-2012-0460.

- Thai, H. *Campo, DS*. Lara, J. Dimitrova, Z. Ramachandran, S. Xia, G. Ganova-Raeva, L. Teo, CG. Lok, A. Khudyakov, Y. 2012. Convergence and Coevolution of the Hepatitis B Virus Lamivudine Resistance. Nature communications. 3:789. doi:10.1038/ncomms1794

- Forbi, J. Purdy, M. *Campo, DS*. Vaughan, G. Dimitrova, Z. Ganova-Raeva, L. Xia, G. Khudyakov, Y. Epidemic history of hepatitis C virus infection in two remote communities in Nigeria, West Africa. 2012. Journal of General Virology. 93, 1410–1421.

- *Campo, DS*. Dimitrova, Z. Yokosawa, J. Hoang, D. Perez, N. Ramachandran, S. Khudyakov, Y. 2012. HCV antigenic convergence. Scientific reports. 2, 267; DOI:10.1038/srep00267

- Skums, P. Dimitrova, Z. *Campo, DS*. Vaughan, D. Rossi, L. Forbi, J. Yokosawa, J. Khudyakov, Y. Efficient Error Correction of High-throughput Viral Sequencing. 2011. BMC bioinformatics. 2012, 13(Suppl 10):S6.

- Ramachandran, S. Zhai, X. Thai, H. *Campo, DS*. Xia, G. Ganova-Raeva, L. Drobeniuc, J. Khudyakov, Y. 2011. Evaluation of intra-host variants of the entire hepatitis B virus genome. PLoS ONE 6(9): e25232. doi:10.1371/journal.pone.0025232

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- Forbi, J. Vaughan, G. Purdy, M. *Campo, DS*. Xia, G. Ganova-Raeva, L. Ramachandran, L. Thai, H. Khudyakov, Y. 2010. Epidemic History and Evolutionary Dynamics of Hepatitis B Virus Infection in Two Remote Communities in Rural Nigeria. PLoS ONE 5(7): e11615. doi:10.1371/journal.pone.0011615.

- *Campo, DS*., Dimitrova, Z., Mitchell, R., Lara, J. & Khudyakov, Y. 2008. Coordinated evolution of the hepatitis C virus. Proc Natl Acad Sci USA. 105(28):9685-90.

- *Campo, DS*. 2008. Analysis of coordinated substitutions in proteins In: Medicinal Protein Engineering. Khudyakov, Y (Ed). CRC Press. Boca Raton, FL, pp 107-122.

- *Campo, D*S., Dimitrova, Z. & Khudyakov, Y. 2008. Physicochemical Correlation between Amino Acid Sites in Short Sequences under Selective Pressure. In Lecture Notes in Computer Science, Volume 4983. Bioinformatics research and applications. Mandoiu, I., Sunderraman, R., & Zelikovsky, A. (Eds). Springer, Atlanta, GA, pp. 146-158.

- Westbrooks, K. Astrovskaya, I. *Campo, DS*. Khudyakov, Y. Berman, P. Zelikovsky, A. 2008. HCV Quasispecies Assembly Using Network Flows. In Lecture Notes in Computer Science, Volume 4983. Bioinformatics research and applications. Mandoiu, I., Sunderraman, R., & Zelikovsky, A. (Eds). Springer, Atlanta, GA, pp. 159-170.

- Mitchell, RJ. Reddy, M. *Campo, DS*. Infantino, T. Kaps, M. Crawford, M. 2006 Genetic diversity within a caste population of India as measured by Y-chromosome haplogroups and haplotypes: Subcastes of the Golla of Andhra Pradesh. American Journal of Physical Anthropology. 30(3):385-93.

- Yunis, J. Acevedo, L. E., *Campo, DS*, and Yunis, E. J. 2005. Population data of Y-STR minimal haplotypes in a sample of Caucasian-Mestizo and African descent individuals of Colombia. Forensic Sci. Int. 151(2-3): 307-313.

ORAL PRESENTATIONS

I have participated in 38 oral presentations, being the first author of 13 of them.

- **Campo, DS.** Khudyakov, Y. Mixed Infection: A novel genetic marker for surveillance of high-risk populations. Oral presentation. 12th Workshop on Computational Advances in Molecular Epidemiology (CAME2025) at the 13th International Conference on Computational Advances in Bio and Medical Sciences (ICCABS). January 12-14, 2025, Atlanta, GA, USA.
- **Campo, DS.** Khudyakov, Y. Evaluation of methods for estimating information entropy from limited sequence data Oral presentation. 12th Workshop on Computational Advances in Molecular Epidemiology (CAME2025) at the 13th International Conference on Computational Advances in Bio and Medical Sciences (ICCABS). January 12-14, 2025, Atlanta, GA, USA.
- **Campo, DS.** Khudyakov, Y. HAPLOQ: A simple strategy for correcting sequencing errors on viral amplicons. Oral presentation. 13th Workshop on Computational Advances for Next Generation Sequencing (CANGS2025) at the 13th International Conference on

Computational Advances in Bio and Medical Sciences (ICCABS). January 12-14, 2025, Atlanta, GA, USA.

- **Campo, DS.** Khudyakov, Y. Convex hulls in hamming space: a data structure with several applications. Oral presentation. 8th Workshop on Computational Advances in Molecular Epidemiology (CAME2019) at the 10th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB), Niagara Falls, September 7th, 2019.

- Tsyvina, V. *Campo, DS.* Sims, S. Zelikovsky, A. Khudyakov, Y. Skums, P. 2017. Efficient filtering algorithm for detection of genetic similarity between large genomic datasets. Oral presentation. IEEE 7th International Conference on Computational Advances in Bio and Medical Sciences (ICCABS). October 19-21, 2017, Orlando, FL, USA.

- Longmire, AG. Sims, S. Rytsareva, I. *Campo, DS.* Dimitrova, Z. Ganova-Raeva, L. Ramachandran, S. Medrzycki, M. Thai, H. Lin, Y. Punkova, LT. Sue, A. Skums, P. Mirabito, M. Wang, S. Tracy, R. Sukalac, T. Lynberg, C. Bolet , V. Khudyakov, Y. 2016. GHOST: Global Health Outbreak and Surveillance Technology. Oral presentation. Workshop on Computational Advances in Molecular Epidemiology (CAME2016) of the IEEE 6th International Conference on Computational Advances in Bio and Medical Sciences (ICCABS). October 13-15, Atlanta, GA, USA.

- *Campo, DS*. Zhang, J. Ramachandran, S. Khudyakov, Y. 2017. Transmissibility of Intra-Host Hepatitis C Virus Variants. Oral presentation. Workshop on Computational Advances in Molecular Epidemiology (CAME2016) of the IEEE 6th International Conference on Computational Advances in Bio and Medical Sciences (ICCABS). October 13-15, Atlanta, GA, USA.

- Rytsareva, I. *Campo, DS.* Zheng, Y. Sims, S. Tetik, C. Chirag, J. Chockalingam, S. Thankachan, S. Sue, A. Aluru, S. Khudyakov, Y. 2015. Efficient Detection of Viral Transmission with Threshold-based methods. IEEE 5th International Conference on Computational Advances in Bio and Medical Sciences (ICCABS), 2015. p1-6. doi: 10.1109/ICCABS.2015.7344723

- Skums, P. Glebova, O. *Campo, DS.* Li, N. Dimitrova, Z. Sims, S. Bunimovich, L. Zelikovsky, A. Khudyakov, Y. 2015. Algorithms for Detection of Viral Transmissions using Analysis of Intra-Host Viral Populations. IEEE 5th International Conference on Computational Advances in Bio and Medical Sciences (ICCABS), 2015.

- *Campo, DS*. Dimitrova, Z. Xia, G. Skums, P. Ganova-Raeva, L. Khudyakov, Y. 2014. New Computational Methods for Assessing the Genetic Relatedness of Close Viral Variants. Oral presentation. Workshop on Computational Advances in Molecular Epidemiology (CAME2014) of the IEEE 4th International Conference on Computational Advances in Bio and Medical Sciences (ICCABS). Miami, FL. June 2-4.

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- **Campo, DS**. Dimitrova, Z. Skums, P. Khudyakov, Y. 2013. Mutational Robustness of Hepatitis C Virus Intra-host Variants. Oral presentation. Workshop on Computational Advances in Molecular Epidemiology (CAME2013) of the IEEE 3rd International Conference on Computational Advances in Bio and Medical Sciences (ICCABS). New Orleans, LA. June 12-14.

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POSTERS AND ABSTRACTS

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