Lukas Forer

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Date and place of birth:	27.06.1985 in Bruneck, Italy
Academic titles:	Ph.D.

Education:

1999-2004:	Matura at Gewerbeoberschule Bruneck, Italy
2004-2010:	Study of Computer Science at the University of Innsbruck (MSc.)
2010-2014:	Study of Computer Science at the University of Innsbruck (Ph.D.)

Awards:

Aug. 2010:	Amazon Research Grant
Sep. 2010:	Scientific price of the Austrian Society for Human Genetics
Feb. 2012:	Aktion D. Swarovski & Co 2011, Research Funding
Apr. 2013	Amazon Research Grant
May 2015	Best Paper Award, 38th International Convention on Information and Communication Technology, Electronics and Microelectronics (MIPRO)

Employments:

2006-2008:	Scientific Software Developer at the European Academy of Bozen/Bolzano (EURAC), Italy
2008-2009:	Scientific Software Developer at the Research Laboratory of the Department of Urology, Innsbruck Medical University
2009-2010:	Project member at the Division of Genetic Epidemiology, Innsbruck Medical University
2010-2014:	Scientific Assistant at the Division of Genetic Epidemiology, Innsbruck Medical University
Since 2014	Postdoc at the Division of Genetic Epidemiology, Innsbruck Medical University

Publications

1   2007   Fuchsberger C, Miksch S, <u>Forer L</u>, Pattaro C: *Analyzing Populations with Visual and Analytical Methods to Identify Family Clustered Diseases*. In: **Proc. of the 12th World Congress on Health (Medical) Informatics** (Medinfo'2007). Brisbane, Australia, pp. P317 (1-2).

2   2008   Fuchsberger C, <u>Forer L</u>, Pattaro C, Hicks A, Pramstaller P, Miksch S: *Visual Analytical Methods to Identify Family Clustered Diseases*. In: **Proc. 21st IEEE International Symposium on Computer-Based Medical Systems** (CBMS '08), pp. 602-604.

3   2008   Fuchsberger C, Falchi M, <u>Forer L,</u> Pramstaller P: *PedVizApi: a Java API for the interactive, visual analysis of extended pedigrees*. **Bioinformatics**, 2008; Vol. 24(2), pp. 279- 281.

4   2010   <u>Forer L</u>, Schönherr S, Weissensteiner H, Haider F, Kluckner T, Gieger C, Wichmann HE, Specht G, Kronenberg F, Kloss-Brandstätter A[*]: *CONAN: copy number variation analysis software for genome-wide association studies*. **BMC Bioinformatics** 2010; 11(1):318

5   2011   Schönherr S*, <u>Forer L</u>*, Weissensteiner H, Kronenberg F, Specht G, Kloss-Brandstätter A: *A feedback guided interface for elastic computing*. In: **Proceedings of the 23nd Workshop Grundlagen von Datenbanken (GvDB 2011)**, Obergurgl, Austria, 2011. CEUR-WS.org, Vol. 733, online urn:nbn:de:0074-733-4.

6   2011   Jacquemont S, Reymond A, Zufferey F, Harewood L, Walters RG, Kutalik Z, Martinet D, Shen Y, Valsesia A, Beckmann ND, Thorleifsson G, Belfiore M, Bouquillon S, Campion D, de Leeuw N, de Vries BB, Esko T, Fernandez BA, Fernández-Aranda F, Fernández-Real JM, Gratacòs M, Guilmatre A, Hoyer J, Jarvelin MR, Frank Kooy R, Kurg A, Le Caignec C, Männik K, Platt OS, Sanlaville D, Van Haelst MM, Villatoro Gomez S, Walha F, Wu BL, Yu Y, Aboura A, Addor MC, Alembik Y, Antonarakis SE, Arveiler B, Barth M, Bednarek N, Béna F, Bergmann S, Beri M, Bernardini L, Blaumeiser B, Bonneau D, Bottani A, Boute O, Brunner HG, Cailley D, Callier P, Chiesa J, Chrast J, Coin L, Coutton C, Cuisset JM, Cuvellier JC, David A, de Freminville B, Delobel B, Delrue MA, Demeer B, Descamps D, Didelot G, Dieterich K, Disciglio V, Doco-Fenzy M, Drunat S, Duban-Bedu B, Dubourg C, El-Sayed Moustafa JS, Elliott P, Faas BH, Faivre L, Faudet A, Fellmann F, Ferrarini A, Fisher R, Flori E, <u>Forer L</u>, Gaillard D, Gerard M, Gieger C, Gimelli S, Gimelli G, Grabe HJ, Guichet A, Guillin O, Hartikainen AL, Heron D, Hippolyte L, Holder M, Homuth G, Isidor B, Jaillard S, Jaros Z, Jiménez-Murcia S, Joly Helas G, Jonveaux P, Kaksonen S, Keren B, Kloss-Brandstätter A, Knoers NV, Koolen DA, Kroisel PM, Kronenberg F, Labalme A, Landais E, Lapi E, Layet V, Legallic S, Leheup B, Leube B, Lewis S, Lucas J, Macdermot KD, Magnusson P, Marshall C, Mathieu-Dramard M, McCarthy MI, Meitinger T, Antonietta Mencarelli M, Merla G, Moerman A, Mooser V, Morice-Picard F, Mucciolo M, Nauck M, Coumba Ndiaye N, Nordgren A, Pasquier L, Petit F, Pfundt R, Plessis G, Rajcan-Separovic E, Paolo Ramelli G, Rauch A, Ravazzolo R, Reis A, Renieri A, Richart C, Ried JS, Rieubland C, Roberts W, Roetzer KM, Rooryck C, Rossi M, Saemundsen E, Satre V, Schurmann C, Sigurdsson E, Stavropoulos DJ, Stefansson H, Tengström C, Thorsteinsdóttir U, Tinahones FJ, Touraine R, Vallée L, van Binsbergen E, Van der Aa N, Vincent-Delorme C, Visvikis-Siest S, Vollenweider P, Völzke H, Vulto-van Silfhout AT, Waeber G, Wallgren-Pettersson C, Witwicki RM, Zwolinksi S,

Andrieux J, Estivill X, Gusella JF, Gustafsson O, Metspalu A, Scherer SW, Stefansson K, Blakemore AI, Beckmann JS, Froguel P: *Mirror extreme BMI phenotypes associated with gene dosage at the chromosome 16p11.2 locus*. **Nature**, 2011, doi: 10.1038/nature10406.

7   2012   Schönherr S*, <u>Forer L</u>*, Weißensteiner H, Kronenberg F, Specht G, and Kloss-Brandstätter *A: Cloudgene: a graphical execution platform for MapReduce programs on private and public clouds*. **BMC Bioinformatics**, 13(1):200, Jan. 2012

8   2012   Lamina, C., <u>Forer, L</u>., Schönherr, S., Kollerits, B., Ried, J. S., Gieger, C., Peters, A., et al. (2012): Evaluation of gene-obesity interaction effects on cholesterol levels: a genetic predisposition score on HDL-cholesterol is modified by obesity. **Atherosclerosis**, *225*(2), 363-9. doi:10.1016/j.atherosclerosis.2012.09.016

9   2013   Weissensteiner H, Haun M, Schönherr S, Neuner M, <u>Forer L</u>, Specht G, Kloss-Brandstätter A, Kronenberg F, and Coassin. S: *SNPflow: A Lightweight Application for the Processing, Storing and Automatic Quality Checking of Genotyping Assays*. **PloS one,** 8(3):e59508, Jan. 2013

10   2014   Summerer M, Horst J, Erhart G, Weißensteiner H, Schönherr S, Pacher D, <u>Forer L</u>, Horst D, Manhart A, Horst B, Sanguansermsri T, Kloss-Brandstätter A: *Large-scale mitochondrial DNA analysis in Southeast Asia reveals evolutionary effects of cultural isolation in the multi-ethnic population of Myanmar.* **BMC Evolutionary Biology** 2014 (1), 17

11   2014   <u>Forer L</u>, Lipic T, Schönherr S, Weißensteiner H, Davidovic D, Kronenberg F, Afgan E: *Delivering Bioinformatics MapReduce Application in the Cloud* **Proceedings of 37th International ICT Convention MIPRO**, 2014, Croatia

12   2015   Titze S, Schmid M, Köttgen A, Busch M, Floege J, Wanner C, Kronenberg F, Eckardt K, Prokosch H, Bärthlein B, others (2015). *Disease burden and risk profile in referred patients with moderate chronic kidney disease: composition of the German Chronic Kidney Disease (GCKD) cohort*. **Nephrology Dialysis Transplantation**, 30(3), 441-451

13   2015   Jing J, Kielstein JT, Schultheiss UT, Sitter T, Titze SI, Schaeffner ES, McAdams-DeMarco M, Kronenberg F, Eckardt K, Köttgen A, others (2015). *Prevalence and correlates of gout in a large cohort of patients with chronic kidney disease: the German Chronic Kidney Disease (GCKD) study*. **Nephrology Dialysis Transplantation**, 30(4), 613-621.

14   2015   <u>Forer L</u>, Afgan E, Weißensteiner H, Davidovic D, Specht G, Kronenberg F, Schonherr S (2015). *Cloudflow - A framework for MapReduce pipeline development in Biomedical Research*. **Proceedings in 38th International Convention on Information and Communication Technology, Electronics and Microelectronics** (MIPRO), 172-177. **(Best Paper Award)**

15   2015   Raschenberger J, Kollerits B, Titze S, Köttgen A, Bärthlein B, Ekici AB, <u>Forer L</u>, Schönherr S, Weissensteiner H, Haun M, others (2015). *Association of relative telomere length with cardiovascular disease in a large chronic kidney disease cohort: The GCKD study*. **Atherosclerosis**, 242(2), 529-534.

16   2015   Kloss-Brandstätter A, Weissensteiner H, Erhart G, Schäfer G, <u>Forer L</u>, Schönherr S, Pacher D, Seifarth C, Stöckl A, Fendt L, others (2015). *Validation*

of Next-Generation Sequencing of Entire Mitochondrial Genomes and the Diversity of Mitochondrial DNA Mutations in Oral Squamous Cell Carcinoma. **PloS one**, 10(8), e0135643.

17 2015 Spjuth O, Bongcam-Rudloff E, Hermandez GC, <u>Forer L</u>, Giovacchini M, Guimera RV, Kallio A, Korpelainen E, Kandula MM, Krachunov M, others (2015). *Experiences with workflows for automating data-intensive bioinformatics*. **Biology direct**, 10(1), 1-12.

18 2015 Raschenberger J, Kollerits B, Titze S, Köttgen A, Bärthlein B, Ekici AB, <u>Forer L</u>, Schönherr S, Weissensteiner H, Haun M, others (2015). *Do telomeres have a higher plasticity than thought? Results from the German Chronic Kidney Disease (GCKD) study as a high-risk population*. **Experimental gerontology**, 72(), 162-166.

19 2016 Weissensteiner H, Pacher D, Kloss-Brandstätter A, <u>Forer L</u>, Specht G, Bandelt HJ, Kronenberg F, Salas A, Schönherr S (2016). *HaploGrep 2: mitochondrial haplogroup classification in the era of high-throughput sequencing*. **Nucleic Acids Res.** 2016 Apr 15. pii: gkw233.

20 2016 Weissensteiner H*, <u>Forer L</u>*, Fuchsberger C, Schöpf B, Kloss-Brandstätter A, Specht G, Kronenberg F, Schönherr S (2016). *mtDNA-Server: next-generation sequencing data analysis of human mitochondrial DNA in the cloud*. **Nucleic Acids Res**. 2016 Apr 15. pii: gkw247.

21 2016 <u>Forer L</u>, Afgan E, Weißensteiner H, Davidovic D, Specht G, Kronenberg F, Schonherr S (2016). *Cloudflow - enabling faster biomedical pipelines with MapReduce and Spark*. **Scalable Computing - Practice and Experience** 17(2), 103–114. DOI: 10.12694/scpe.v17i2.1159.

22 2016 McCarthy S, Das S, Kretzschmar W, Delaneau O, Wood AR, Teumer A, Kang HM, Fuchsberger C, Danecek P, Sharp K, Luo Y, Sidore C, Kwong A, Timpson N, Koskinen S, Vrieze S, Scott LJ, Zhang H, Mahajan A, Veldink J, Peters U, Pato C, van Duijn CM, Gillies CE, Gandin I, Mezzavilla M, Gilly A, Cocca M, Traglia M, Angius A, Barrett JC, Boomsma D, Branham K, Breen G, Brummett CM, Busonero F, Campbell H, Chan A, Chen S, Chew E, Collins FS, Corbin LJ, Smith GD, Dedoussis G, Dorr M, Farmaki AE, Ferrucci L, <u>Forer L</u>, Fraser RM, Gabriel S, Levy S, Groop L, Harrison T, Hattersley A, Holmen OL, Hveem K, Kretzler M, Lee JC, McGue M, Meitinger T, Melzer D, Min JL, Mohlke KL, Vincent JB, Nauck M, Nickerson D, Palotie A, Pato M, Pirastu N, McInnis M, Richards JB, Sala C, Salomaa V, Schlessinger D, Schoenherr S, Slagboom PE, Small K, Spector T, Stambolian D, Tuke M, Tuomilehto J, Van den Berg LH, Van Rheenen W, Volker U, Wijmenga C, Toniolo D, Zeggini E, Gasparini P, Sampson MG, Wilson JF, Frayling T, de Bakker PI, Swertz MA, McCarroll S, Kooperberg C, Dekker A, Altshuler D, Willer C, Iacono W, Ripatti S, Soranzo N, Walter K, Swaroop A, Cucca F, Anderson CA, Myers RM, Boehnke M, McCarthy MI, Durbin R, Abecasis G, Marchini J (2016). *A reference panel of 64,976 haplotypes for genotype imputation.* **Nature Genetics**. DOI: 10.1038/ng.3643

Book Chapters

1 2010 <u>Forer L</u>, Schönherr S, Weißensteiner H, Specht G, Kronenberg F, Brandstätter A. *Cloud Computing - Bringing computational power to medical genetics*. In Zlatko Trajanoski, editor, **Computational Medicine: Tools and Challenges**,

pages 27–36. Springer, 2012.

Presentations and Posters

1   2010   **10. Jahrestagung der ÖGH in Wien,** 24.09.2010, Wien, Österreich

2   2011   **European Society of Human Genetics Conference 2011**, 2011-05-27 – 2011-05-31, Amsterdam, Nederland

3   2011   **23. Workshop Grundlagen von Datenbanken**, 2011-06-1 – 2011-06-03,Obergurgl, Austria

4   2011   **12th Annual Bioinformatics Open Source Conference,** 2011-07-14 - 2012-07-17,Wien, Austria

5   2011   **11. Jahrestagung der ÖGH in Salzburg**, 30.09.2011, Salzburg, Austria

6   2012   **13th Annual Bioinformatics Open Source Conference,** 2012-07-13 – 2012-07-14, Long Beach, USA

7   2012   **imzML Workshop: Improved Data Sharing and Data Analysis,** 2012-09-23 - 2012-09-27, Rauischholzhausen, Germany

8   2013   **Workshop of Genetic Epidemiology 2013,** 2013-04-10 – 2013-04-12, Grainau, Germany

9   2013   **Hadoop and NGS Data Processing Hackathon III,** 2013-06-04 - 2013-06-05, Pula, Italy

10   2014   **Hadoop and NGS Data Processing Hackathon IV,** 2014-04-01 - 2014-04-02, Sofia, Bulgaria

11   2014   **Workshop of Genetic Epidemiology 2014**, 2014-05-07 – 2014-05-09, Grainau, Germany

12   2014   **37th International ICT Convention MIPRO,** 2014-05-29, Opatija, Croatia

13   2015   **Workshop on e-Infrastructures for Massively Parallel Sequencing**, 2015-01-19 – 2015-01-20, Uppsala, Sweden

14   2015   **3th Bioinformatics Workshop in Galaxy Training Network: Bioinformatics Methods in Genomics**, 2015-03-02 – 2015-03-03, Zagreb, Croatia

15   2015   **38th International ICT Convention MIPRO,** 2015-05, Opatija, Croatia