# David Schryer

Programmer — Data analyst — Technical editor/writer

**summary**

**Systems biologist/programmer with a chemical engineering background.**

I seek a position in a visionary company within a great team. Most people would characterize me as an excellent communicator (founder of ScientificScribe) with an eye for detail who enjoys tackling difficult technical problems. I enjoy creating software and would like an opportunity to work within a professional team.

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**employment**

**University of Tartu, Researcher**
**2012 — 2014.**

Analysis of label-free, dynamic SILAC, and static SILAC MS/MS proteomics data.
Custom analysis of sequencing data, including analysis of ribosome profiling data.
Instruction of PhD students in Python data analysis and visualization techniques.

**Scientific Scribe OÜ, Founder**
**2012.**

Technical editing of grant proposals, academic manuscripts, and PhD dissertations.
Typesetting and layout of complex documents in LaTeX.

**Tallinn University of Technology, Institute of Cybernetics, Researcher**
**2008 – 2012.**

Development of tools to build and simulate isotopomer and isotopologue models.
Application of isotopomer modeling to study the recycling dynamics of phosphorylated metabolites in heart.
Flux Balance Analysis (FBA) of genome scale metabolic models.

**TFTAK, Systems biology developer**
**2006 – 2008.**

Developed computational tools for systems biology analysis.
Installed and improved the fermentation systems and laboratory infrastructure.
Introduced Python to an MS Excel based analysis team.

**Tallinn University of Technology, Department of Chemical Engineering**
**2004 – 2006.**

Ran a pilot plant for the industrial extraction of protein from rapeseed.
Wrote an English language curriculum document for department accreditation.

**EBS high school, Science teacher**
**2005 – 2006.**

Developed and gave courses in Chemistry, Physics, and Computer Science.
Wrote an English language curriculum document for internal use at EBS.

**University of Toronto, Research assistant**

**2000 – 2004.**

Upgrade and repair of an X-ray photoelectron spectrometer (XPS).

Maintenance of a custom mass spectrometer and associated UHV systems.

Designed and built a multi-annulus flow apparatus used to measure the transport properties of solid oxide fuel cell membranes at 1000°C.

Studied the kinetics of water exchange with cellulose using isotope tracers.

Developed a multimedia fate & transport model to study persistent organic pollutants.

**Tallinn University of Technology, Doctor of philosophy**

**Ph.D. in Technical Physics**

Graduation April 2012.

Dissertation — *Metabolic Flux Analysis of Compartmentalized Systems using Dynamic Isotopologue Modeling*

Awards: (A) Archimedes Foundation Grant for PhD studies – $5904 per annum (B) DoRa travel awards for two Biophysical Society meetings – Below cost

**University of Toronto, Master of Applied Science**

**M.A.Sc. in Chemical Engineering**

Graduation June 2005.

Dissertation — *On the determination of sub-second water–cellulose sorption kinetics using mass spectrometry*

Awards: A) Ontario Graduate Scholarship in Science and Technology (OGSST) – $15000 per annum (B) University of Toronto Fellowship – $1200 (received twice)

**University of Toronto, Bachelor of Applied Science**

**B.A.Sc. in Chemical Engineering**

Graduation June 2000.

Dissertation — *Measuring the ion mobility of oxygen through solid oxide membranes using transient* [18] *O exchange and* SIMS *depth profiling*

Awards: (A) Best Plant Design Project 2000 (B) Undergraduate Achievement Scholarship – $1500 (received twice)

**Experienced programmer in:**

Python (package development, unit testing, reusable code)

**Visualization and analysis of data using:**

Python (matplotlib, pandas, NumPy, SciPy, BioPython, statsmodels)

**Development of complex documents, course material, and presentations:**

LaTeX, reST, Sphinx, Django, Beamer, IPython notebook.

**Practices safe computation with version control and unit testing:**

hg, git, svn, bzr, nosetests

**Avid supporter of FOSS with an emphasis on sharing my code:**

Bitbucket (schryer), GitHub (schryer).

**Basic proficiency in:**

C, C++, Fortran, COBOL, Pascal, Java.

**Basic front-end and advanced back-end web development using:**

GAE, OpenShift, dotCloud, Python

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## publications

Kannan K, Kanabar P, Schryer DW, Florin T, Oh E, Bahroos N, Tenson T, Weissman JS, Mankin AS: *The general mode of translation inhibition by macrolide antibiotics.* Proc Natl Acad Sci U S A. 2014 Nov 11;111(45):15958-63

Schryer DW, Peterson P, Illaste A, Vendelin M: *Sensitivity analysis of flux determination in heart by $H_2^{18}O$ -provided labeling using a dynamic isotopologue model of energy transfer pathways.* PLoS Computational Biology 2012, 8(12):e1002795

Schryer DW, Peterson P, Illaste A, Vendelin M: *Mathematical model of oxygen labeling to study heart energy transfer.* Biophysical Journal, 2012, 102(3):141a

Schryer DW, Vendelin M, Peterson P: *Symbolic flux analysis for genome-scale metabolic networks.* BMC Systems Biology 2011, 5:81.

Illaste A, Kalda M, Schryer DW, Sepp M: *Life of mice - development of cardiac energetics.* The Journal of Physiology 2010, 588(Pt 23):4617–4619.

Illaste A, Schryer DW, Birkedal R, Peterson P, Vendelin M: *Determination of regional diffusion coefficients of fluorescent ATP in rat cardiomyocytes.* Biophysical Journal 2010, 98(3):749a.

Schryer DW, Peterson P, Paalme T, Vendelin M: *Bidirectionality and compartmentation of metabolic fluxes are revealed in the dynamics of isotopomer networks.* International Journal of Molecular Sciences 2009, 10(4):1697–1718.

Schryer DW, Peterson P, Paalme T, Vendelin M: *Isotopomeric $^{13}C$ labeling of amino acids reveal compartmentation in Saccharomyces uvarum.* Biophysical Journal 2009, 96(3):308a.

Schryer DW, Bhavsar S, Diamond ML: *A preliminary model of the fate of geosmin & MIB2 in Lake Ontario.* In The Canadian Association on Water Quality Annual Meeting 2001.

Schryer DW, Diamond ML, Liu Q, Stern G, McCarry B: *Multimedia Urban Model: Validation and uncertainty analysis using a dynamic Monte Carlo method.* In 22nd Annual SETAC meeting 2001.

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## contact

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