BIOGRAPHICAL SKETCH

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NAME: Damir Sudar

eRA COMMONS USER NAME (credential, e.g., agency login): dsudar

POSITION TITLE: Staff Scientist

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Delft University of Technology, The Netherlands	B.S.	11/1984	Applied Physics
Delft University of Technology, The Netherlands	Ir. (M.S. equivalent)	11/1988	Applied Physics
University of California, San Francisco	Postdoctoral	10/1990	Molecular Cytogenetics

Please refer to the Biographical Sketch sample in order to complete sections A, B, C, and D of the Biographical Sketch.

A. Personal Statement

I am a staff scientist in LBNL's Life Sciences Division with broad expertise in light microscopy techniques, image analysis, and data analysis and an image data scientist with Quantitative Imaging Systems, LLC. I have led LBNL's Integrated Bioimaging Initiative which worked to integrate imaging modalities over multiple spatial, temporal, and functional/structural scales. I have an Associate Scientist appointment at OHSU where I work on developing and optimizing image data management and image analysis software capabilities, assistance with imaging and data analysis, and reporting and management.

B. Positions and Honors

Positions and Employment

1988 Software Consultant, TNO Institute of Applied Physics, Delft, The Netherlands
1990-1991 Staff Scientist, Lawrence Livermore National Laboratory, Livermore, CA
1991-1994 Image Analysis Specialist, Div. of Mol. Cytometry, University of California, San Francisco, CA
1994-1998 Biophysicist Staff Scientist, Lawrence Berkeley National Laboratory, Berkeley, CA
1998-present Consultant – Image Analysis Applications, Quantitative Imaging Sys, LLC, Pittsburgh, PA
1998-1999 Image Analysis Specialist, Cellomics, Inc. Pittsburgh, PA
1999-2000 Director of Computations, Resolution Sciences Corp., San Francisco and Corte Madera, CA
2000-present Biophysicist Staff Scientist, Life Sciences Division, Lawrence Berkeley Natl Lab, Berkeley, CA
2001-2014 Deputy Division Director, Life Sciences Division, LBNL, Berkeley, CA
2012-present Associate Scientist, Oregon Health and Science University, Portland, OR

Other Experience and Professional Memberships

1994-present Member International Society for Analytical Cytology (ISAC)
1998 Program Committee - ISAC XIXth Congress
2000-present Member American Society for Cell Biology (ASCB)
2002 Co-Chair Dept. of Energy Genomes to Life Imaging workshop
2003 Grant Review, DOE Medical Sciences
2003-2010 Editorial Board, Cancer Genomics and Proteomics
2006 Ad-hoc member NIH BioData Management and Analysis Study Section

Honors/Awards/Patents

1986	KIVI Student Travel Award
1988	International Society for Analytical Cytology Travel Award
1992	Gordon Conference Invited Speaker, Molecular Cytogenetics
1999	Specimen illumination apparatus with optical cavity for dark field illumination, USA, 5982534
2004	Wide Field Imaging System for Microarrays, USA, 7499166
2008	AACR Team Science Award

C. Contribution to Science

1. My early work was primarily focused on development of microscopy automation and image analysis methods in the field of metaphase-based molecular cytogenetics. With our advances in Fluorescence In-Situ Hybridization (FISH) technology including our development of Comparative Genomic Hybridization (CGH) we needed rapid, quantitative, and accurate technologies to acquire and analyze images. I (co-)developed most of the microscopy automation, imaging, and image analysis approaches described in these studies:

a. Kallioniemi A., Kallioniemi O.-P., Sudar D., Rutovitz D., Gray J.W., Waldman F., and Pinkel D. Comparative Genomic Hybridization for Molecular Cytogenetic Analysis of Solid Tumors. Science 258:818-821, 1992
b. Piper J., Poggensee M., Hill W., Jensen R., Ji L., Poole I., Stark M., and Sudar D., An Automatic Fluorescence Metaphase Finder Speeds Scoring of Translocations in FISH Painted Chromosomes. Cytometry, 16:7-16, 1994
c. Piper J., Rutovitz D., Sudar D., Kallioniemi A., Kallioniemi O.-P., Waldman F., Gray J.W., and Pinkel D., Computer Image Analysis of Comparative Genomic Hybridization. Cytometry, 19:10-26, 1995
d. Mascio L.N., Verbeek P.W., Kuo W.-L., Sudar D., and Gray J.W. Semi-Automated DNA Probe Mapping Using Digital Imaging Microscopy. I. System development. Cytometry, 19:51-59, 1995

2. With our development of array-based CGH and the need for very sensitive wide-field imaging of entire DNA micro-arrays, we designed a special purpose imaging system and associated software. Again my role was primarily in the optical and software design of the systems and the image analysis software for accurate quantitative analysis of the imaging data as reported in this study and patents:

a. Pinkel D, Segraves R, Sudar D, Clark S, Poole I, Kowbel D, Collins C, Kuo W-L, Chen C, Zhai Y, Dairkee S, Ljung B-M, Gray JW, and Albertson DG. High resolution analysis of DNA copy number variation using comparative genomic hybridization to microarrays. Nature Genetics, 20:207-211, 1998
b. Hamilton G, Brown N, Oseroff V, Huey B, Segraves R, Sudar D, Kumler J, Albertson D, Pinkel D, A large field CCD system for quantitative imaging of microarrays, Nucleic Acids Research, 34(8) e58, 2006
c. Specimen illumination apparatus with optical cavity for dark field illumination, USA, 5982534, 1999
d. Wide Field Imaging System for Microarrays, USA, 7499166, 2004

3. Understanding transcription regulation underlying animal development in complex organisms has been one of the great challenges in the post-genomics era. Our Berkeley Drosophila Transcription Network Project (BDTNP) was an inter-disciplinary study combining in-vivo and in-vitro biochemical binding assays, computational predictions, testing in transgenic constructs, and my component was the development of methods to quantitatively analyze gene expression in entire 3D embryos at cellular resolution. I led a team of imaging and computer scientists to develop 2-photon based confocal imaging, automated image segmentation, multi-sample registration, visualization, and database software. This work was reported below and is continuing in studies of the post-gastrula stages:

a. Luengo Hendriks CL, Keränen SVE, Fowlkes CC, Simirenko L, Weber GH, DePace AH, Henriquez C, Kaszuba DW, Hamann B, Eisen MB, Malik J, Sudar D, Biggin MD, Knowles DW, 3D morphology and gene expression in the Drosophila blastoderm at cellular resolution I: data acquisition pipeline, Genome Biology, 7: R123, 2006
b. Keränen SVE, Fowlkes CC, Luengo Hendriks CL, Sudar D, Knowles DW, Malik J, Biggin MD, 3D morphology and gene expression in the Drosophila blastoderm at cellular resolution II: dynamics, Genome Biology, 7: R124, 2006
c. Rübel O, Weber GH, Fowlkes CC, Luengo Hendriks CL, Shah N, Biggin MD, Hagen H, Knowles DW, Malik J, Sudar D, Hamann B, PointCloudXplore: Visual Analysis of 3D Gene Expression Data Using Physical Views and Parallel Coordinates, EuroVIS 2006, Eurographics/IEEE-VGTC Symposium on Visualization, 2006

d. http://bdtnp.lbl.gov/Fly-Net/ - an online resource of 3D expression patterns in Drosophila pregastrula embryos driven by 37 transcription factors for 95 genes derived from over 2500 high-resolution 3D embryo images.

4. Across many areas of biology research quantitative image analysis is critical to turn the vast information content in scientific images into useable data that can be turned into knowledge. Over the years I have been active in many aspects of this important and complex field of research including in microscopic image acquisition where image data and metadata is carefully maintained, accurate image segmentation and quantitative feature extraction, and development of useful hardware and software systems while employed at Cellomics working on the Arrayscan high-content screening systems and at Resolution Sciences Corp on tissue-block 3D imaging. Some of my contributions are:

a. Dean P., Mascio L., Ow D., Sudar D. and Mullikin J. Proposed Standard for Image Cytometry Data Files. Cytometry, 11:561-569, 1990
b. Ortiz de Solorzano C, Garcia Rodriguez E, Jones, AL, Sudar D, Pinkel D, Gray JW, and Lockett SJ. Segmentation of confocal microscope images of cell nuclei in thick tissue sections. Journal of Microscopy 193(3):212-226, 1999
c. Knowles D, Sudar D, Bator-Kelly C, Bissell MJ, Lelievre SA, Automated local bright feature image analysis of nuclear protein distribution identifies changes in tissue phenotype, PNAS, 103(12):4445-4450, 2006
d. Spidlen J, Moore W, Parks D, et al. Data File Standard for Flow Cytometry, Version FCS 3.1, Cytometry part A, 77A (1): 97-100, 2010

Complete List of Published Work in MyBibliography:
http://www.ncbi.nlm.nih.gov/sites/myncbi/damir.sudar.1/bibliography/48055471/public/?sort=date&direction=ascending

C. Research Support

Ongoing Research Support

U54 HG008100 Gray (PI) 09/01/14-08/31/20
Extrinsic Perturbations of Cell Physiology and Associated Regulatory Networks
The overall goal of this study is to produce high quality data measuring phenotypes, protein and phospho-proteomics, and RNA expression in up to 30 cell lines grown on diverse microenvironments (ME) and develop quantitative cellular network signatures to populate the LINCS community data matrix.
Role: Co-Investigator

Completed Research Support

DE-AC03-76SF00098 Sudar (PI) 10/01/12-09/30/14
Berkeley Lab LDRD / Department of Energy
Development of Protein Localization Atlases at Multiple Scales in Eukaryotes
The purpose of this LDRD project at Lawrence Berkeley National Laboratory is to develop efficient gene product tagging, automated image acquisition using multiple modalities, visualization-supported image and image-derived data analysis tools, and to integrate these into a high-throughput pipeline to build protein localization atlases, starting with the fruit fly *Drosophila*.
Role: PI

W81XWH-07-1-0663-BC061995 Gray (PI) 09/17/07 – 09/16/12
USAMRMC
Early Detection of Metastasis-Prone Breast Cancers.
The goal of this multi-institutional project is to develop anatomic and histologic molecular imaging strategies to detect metastasis prone breast cancers before they have metastasized.
Role: Image Acquisition and Analysis Scientist

DE-AC02-05CH11231 Karpen (PI) 10/01/08 - 09/30/14
Department of Energy - Low Dose Scientific Focus Area
Four inter-connected SFA research components coordinately investigate low dose responses through complementary studies using both in vivo mouse models of differing radiosensitivity and comparative culture

systems for mammary-derived mouse and human cells. Component 1 focuses on non-linear and adaptive response mechanisms in mammary cell culture models. Component 2 investigates mammary tissue radiation response phenotypes predicted by transcriptome responses. Component 3 uses systems genetics and organotypic culture to understand differences in susceptibility to low-dose radiation-induced mammary tumors. The Integration Hub provides support for advanced technologies and integrative data analysis applied across all components.
Role: Integration Hub Lead