Stanford



David Dill

Donald E. Knuth Professor in the School of Engineering, Emeritus

Computer Science

CONTACT INFORMATION

- **Administrator**

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Bio

BIO

Dill has interests in the theory and application of formal verification techniques to system designs, which encompass hardware, protocols, and software and in computational systems biology. He has also done research in asynchronous circuit verification and synthesis, and in verification methods for hard real-time systems.

He retired in 2017 and is no longer taking new students. He is collaborating with researchers at Stanford and elsewhere.

ACADEMIC APPOINTMENTS

- Emeritus Faculty, Acad Council, Computer Science
- Member, Bio-X

HONORS AND AWARDS

- Member, National Academy of Engineering (2013)
- Fellow, American Academy of Arts and Sciences (2013)
- Fellow, IEEE
- Fellow, ACM
- Pioneer Award, Electronic Frontier Foundation
- CAV Award for developing the Reluplex algorithm, for verifying real-world deep neural networks., International Conference on Computer-Aided Verification (2024)
- CAV Award for pioneering contributions satisfiability modulo theories (SMT)., International Conference on Computer-Aided Verification (2021)
- Alonzo Church Award for outstanding contributions to logic., ACM SIGLOG, EATCS, EACSL, and KGS (2016)
- CAV Award for fundamental contributions to the theory of real-time systems verification., International Conference on Computer-Aided Verification (2008)

PROGRAM AFFILIATIONS

- Symbolic Systems Program

PROFESSIONAL EDUCATION

- PhD, Carnegie Mellon (1987)

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

Secure and reliable blockchain technology at Facebook.

Teaching

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biomedical Data Science (PhD Program)

Publications

PUBLICATIONS

- **Reasoning About Vectors: Satisfiability Modulo a Theory of Sequences** *JOURNAL OF AUTOMATED REASONING*
  Sheng, Y., Notzli, A., Reynolds, A., Zohar, Y., Dill, D., Grieskamp, W., Park, J., Qadeer, S., Barrett, C., Tinelli, C.
  2023; 67 (3)
- **Reasoning About Vectors Using an SMT Theory of Sequences**
  Sheng, Y., Notzli, A., Reynolds, A., Zohar, Y., Dill, D., Grieskamp, W., Park, J., Qadeer, S., Barrett, C., Tinelli, C.
  edited by Blanchette, J., Kovacs, L., Pattinson, D.
  SPRINGER INTERNATIONAL PUBLISHING AG.2022: 125-143
- **Reluplex: a calculus for reasoning about deep neural networks** *FORMAL METHODS IN SYSTEM DESIGN*
  Katz, G., Barrett, C., Dill, D. L., Julian, K., Kochenderfer, M. J.
  2021
- **Aquila_stLFR: diploid genome assembly based structural variant calling package for stLFR linked-reads.** *Bioinformatics advances*
  Liu, Y. H., Grubbs, G. L., Zhang, L., Fang, X., Dill, D. L., Sidow, A., Zhou, X.
  2021; 1 (1): vbab007
- **Aquila enables reference-assisted diploid personal genome assembly and comprehensive variant detection based on linked reads.** *Nature communications*
  Zhou, X., Zhang, L., Weng, Z., Dill, D. L., Sidow, A.
  2021; 12 (1): 1077
- **The m6A RNA demethylase FTO is a HIF-independent synthetic lethal partner with the VHL tumor suppressor.** *Proceedings of the National Academy of Sciences of the United States of America*
  Xiao, Y. n., Thakkar, K. N., Zhao, H. n., Broughton, J. n., Li, Y. n., Seoane, J. A., Diep, A. N., Metzner, T. J., von Eyben, R. n., Dill, D. L., Brooks, J. D., Curtis, C. n., Leppert, et al
  2020
- **The Move Prover**
  Zhong, J., Cheang, K., Qadeer, S., Grieskamp, W., Blackshear, S., Park, J., Zohar, Y., Barrett, C., Dill, D. L.
  edited by Lahiri, S. K., Wang, C.
  SPRINGER INTERNATIONAL PUBLISHING AG.2020: 137-150
- **Mebendazole for Differentiation Therapy of Acute Myeloid Leukemia Identified by a Lineage Maturation Index.** *Scientific reports*
  Li, Y. n., Thomas, D. n., Deutzmann, A. n., Majeti, R. n., Felsher, D. W., Dill, D. L.
  2019; 9 (1): 16775
- **The Marabou Framework for Verification and Analysis of Deep Neural Networks**
  Katz, G., Huang, D. A., Ibeling, D., Julian, K., Lazarus, C., Lim, R., Shah, P., Thakoor, S., Wu, H., Zeljic, A., Dill, D. L., Kochenderfer, M. J., Barrett, et al

edited by Dillig, Tasiran, S.
SPRINGER INTERNATIONAL PUBLISHING AG.2019: 443–52

- **IDH1 Mutant AML Is Susceptible to Targeting De Novo Lipid Synthesis Independent of 2-Hydroxyglutarate and Has a Distinct Metabolic Profile from IDH2 Mutant AML**
  Thomas, D., Nakauchi, Y., Wu, M., Zheng, M., Sinha, S., Dill, D., Peltz, G., Majeti, R.
  AMER SOC HEMATOLOGY.2018

- **Systematic discovery of mutation-specific synthetic lethals by mining pan-cancer human primary tumor data.** *Nature communications*
  Sinha, S., Thomas, D., Chan, S., Gao, Y., Brunen, D., Torabi, D., Reinisch, A., Hernandez, D., Chan, A., Rankin, E. B., Bernards, R., Majeti, R., Dill, et al
  2017; 8: 15580-?

- **Systematic discovery of mutation-specific synthetic lethals by mining pan-cancer human primary tumor data.** *Nature communications*
  Sinha, S., Thomas, D., Chan, S., Gao, Y., Brunen, D., Torabi, D., Reinisch, A., Hernandez, D., Chan, A., Rankin, E. B., Bernards, R., Majeti, R., Dill, et al
  2017; 8: 15580-?

- **A geographically-diverse collection of 418 human gut microbiome pathway genome databases** *SCIENTIFIC DATA*
  Hahn, A. S., Altman, T., Konwar, K. M., Hanson, N. W., Kim, D., Relman, D. A., Dill, D. L., Hallam, S. J.
  2017; 4

- **Our Elections Are Not Secure** *SCIENTIFIC AMERICAN*
  Dill, D. L.
  2017; 316 (3): 12

- **Towards Proving the Adversarial Robustness of Deep Neural Networks** *ELECTRONIC PROCEEDINGS IN THEORETICAL COMPUTER SCIENCE*
  Katz, G., Barrett, C., Dill, D. L., Julian, K., Kochenderfer, M. J.
  2017: 19–26

- **Reluplex: An Efficient SMT Solver for Verifying Deep Neural Networks**
  Katz, G., Barrett, C., Dill, D. L., Julian, K., Kochenderfer, M. J.
  edited by Majumdar, R., Kuncak
  SPRINGER INTERNATIONAL PUBLISHING AG.2017: 97–117

- **Isocitrate Dehydrogenase 1 Mutant Cancers Are Metabolically Vulnerable to Inhibition of Acetyl CoA Carboxylase Via a 2-Hydroxyglutarate Independent Mechanism**
  Thomas, D., Sinha, S., Chan, S. M., Wu, M., Torabi, D., Peltz, G., Gao, Y., Dill, D. L., Majeti, R.
  AMER SOC HEMATOLOGY.2016

- **Cell cycle progression in Caulobacter requires a nucleoid-associated protein with high AT sequence recognition** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Ricci, D. P., Melfi, M. D., Lasker, K., Dill, D. L., McAdams, H. H., Shapiro, L.
  2016; 113 (40): E5952-E5961

- **A Pharmacogenetic Discovery: Cystamine Protects Against Haloperidol-Induced Toxicity and Ischemic Brain Injury** *GENETICS*
  Zhang, H., Zheng, M., Wu, M., Xu, D., Nishimura, T., Nishimura, Y., Giffard, R., Xiong, X., Xu, L. J., Clark, J. D., Sahbaie, P., Dill, D. L., Peltz, et al
  2016; 203 (1): 599-?

- **The multiple PDZ domain protein Mpdz/MUPP1 regulates opioid tolerance and opioid-induced hyperalgesia** *BMC GENOMICS*
  Donaldson, R., Sun, Y., Liang, D., Zheng, M., Sahbaie, P., Dill, D. L., Peltz, G., Buck, K. J., Clark, J. D.
  2016; 17

- **CauloBrowser: A systems biology resource for Caulobacter crescentus.** *Nucleic acids research*
  Lasker, K., Schrader, J. M., Men, Y., Marshik, T., Dill, D. L., McAdams, H. H., Shapiro, L.
  2016; 44 (D1): D640-5

- **CauloBrowser: A systems biology resource for Caulobacter crescentus.** *Nucleic acids research*
  Lasker, K., Schrader, J. M., Men, Y., Marshik, T., Dill, D. L., McAdams, H. H., Shapiro, L.
  2016; 44 (D1): D640-5

- **Deciphering Cancer Biology using Boolean Methods**
  Sinha, S., Dill, D. L., IEEE
  IEEE.2016: 150–54

- **Boolean Implication Mining for Synthetic Lethal Interactions in AML Identifies Acetyl-CoA Carboxylase As a Synthetic Lethal Partner of the IDH1 mutation**
  Sinha, S., Thomas, D., Chan, S. M., Gao, Y., Jansen, R., Majeti, R., Dill, D. L.
  AMER SOC HEMATOLOGY.2015

- **Discovery of differentiation therapeutics using a systems biology approach**
  Li, Y., Seita, J., Felsher, D., Dill, D.
  AMER ASSOC CANCER RESEARCH.2015

- **A systems biology approach for the discovery of differentiation therapeutics**
  Li, Y., Seita, J., Felsher, D., Dill, D. L.
  AMER ASSOC CANCER RESEARCH.2015

- **Deciphering the cancer methylome with Boolean implications to find novel drivers of aberrant DNA methylation and actionable drug targets**
  Sinha, S., Thomas, D., Majeti, R., Dill, D. L.
  AMER ASSOC CANCER RESEARCH.2015

- **Towards in vivo estimation of reaction kinetics using high-throughput metabolomics data: a maximum likelihood approach** *BMC SYSTEMS BIOLOGY*
  Zhang, W., Kolte, R., Dill, D. L.
  2015; 9

- **The role of Abcb5 alleles in susceptibility to haloperidol-induced toxicity in mice and humans.** *PLoS medicine*
  Zheng, M., Zhang, H., Dill, D. L., Clark, J. D., Tu, S., Yablonovitch, A. L., Tan, M. H., Zhang, R., Rujescu, D., Wu, M., Tessarollo, L., Vieira, W., Gottesman, et al
  2015; 12 (2)

- **The role of abcb5 alleles in susceptibility to haloperidol-induced toxicity in mice and humans.** *PLoS medicine*
  Zheng, M., Zhang, H., Dill, D. L., Clark, J. D., Tu, S., Yablonovitch, A. L., Tan, M. H., Zhang, R., Rujescu, D., Wu, M., Tessarollo, L., Vieira, W., Gottesman, et al
  2015; 12 (2): e1001782

- **Mutant WT1 is associated with DNA hypermethylation of PRC2 targets in AML and responds to EZH2 inhibition.** *Blood*
  Sinha, S., Thomas, D., Yu, L., Gentles, A. J., Jung, N., Corces-Zimmerman, M. R., Chan, S. M., Reinisch, A., Feinberg, A. P., Dill, D. L., Majeti, R.
  2015; 125 (2): 316-326

- **The global regulatory architecture of transcription during the Caulobacter cell cycle.** *PLoS genetics*
  Zhou, B., Schrader, J. M., Kalogeraki, V. S., Abeliuk, E., Dinh, C. B., Pham, J. Q., Cui, Z. Z., Dill, D. L., McAdams, H. H., Shapiro, L.
  2015; 11 (1)

- **The Global Regulatory Architecture of Transcription during the Caulobacter Cell Cycle.** *PLoS genetics*
  Zhou, B., Schrader, J. M., Kalogeraki, V. S., Abeliuk, E., Dinh, C. B., Pham, J. Q., Cui, Z. Z., Dill, D. L., McAdams, H. H., Shapiro, L.
  2015; 11 (1)

- **Towards in vivo estimation of reaction kinetics using high-throughput metabolomics data: a maximum likelihood approach.** *BMC systems biology*
  Zhang, W., Kolte, R., Dill, D. L.
  2015; 9: 66-?

- **Leukemia Cell Differentiation upon Targeted Therapy Revealed By a Systems Biology Approach**
  Li, Y., Seita, J., Felsher, D. W., Dill, D.
  AMER SOC HEMATOLOGY.2014

- **MYC through miR-17-92 Suppresses Specific Target Genes to Maintain Survival, Autonomous Proliferation, and a Neoplastic State.** *Cancer cell*
  Li, Y., Choi, P. S., Casey, S. C., Dill, D. L., Felsher, D. W.

2014; 26 (2): 262-272

- **Automated identification of stratifying signatures in cellular subpopulations** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Bruggner, R. V., Bodenmiller, B., Dill, D. L., Tibshirani, R. J., Nolan, G. P.
  2014; 111 (26): E2770-E2777
- **Automated identification of stratifying signatures in cellular subpopulations.** *Proceedings of the National Academy of Sciences of the United States of America*
  Bruggner, R. V., Bodenmiller, B., Dill, D. L., Tibshirani, R. J., Nolan, G. P.
  2014; 111 (26): E2770-7
- **Mining TCGA data using Boolean implications.** *PloS one*
  Sinha, S., Tsang, E. K., Zeng, H., Meister, M., Dill, D. L.
  2014; 9 (7)
- **Mining TCGA Data Using Boolean Implications.** *PloS one*
  Sinha, S., Tsang, E. K., Zeng, H., Meister, M., Dill, D. L.
  2014; 9 (7)
- **Liquid chromatography/mass spectrometry methods for measuring dipeptide abundance in non-small-cell lung cancer.** *Rapid communications in mass spectrometry : RCM*
  Wu, M., Xu, Y., Fitch, W. L., Zheng, M., Merritt, R. E., Shrager, J. B., Zhang, W., Dill, D. L., Peltz, G., Hoang, C. D.
  2013; 27 (18): 2091-2098
- **Identification of drug targets by chemogenomic and metabolomic profiling in yeast** *PHARMACOGENETICS AND GENOMICS*
  Wu, M., Zheng, M., Zhang, W., Suresh, S., Schlecht, U., Fitch, W. L., Aronova, S., Baumann, S., Davis, R., St Onge, R., Dill, D. L., Peltz, G.
  2012; 22 (12): 877-886
- **Computational genetic discoveries that could improve perioperative medicine** *CURRENT OPINION IN ANESTHESIOLOGY*
  Zheng, M., Dill, D., Clark, J. D., Peltz, G.
  2012; 25 (4): 428-433
- **Gene Expression Commons: An Open Platform for Absolute Gene Expression Profiling** *PLOS ONE*
  Seita, J., Sahoo, D., Rossi, D. J., Bhattacharya, D., Serwold, T., Inlay, M. A., Ehrlich, L. I., Fathman, J. W., Dill, D. L., Weissman, I. L.
  2012; 7 (7)
- **Cd14 SNPs regulate the innate immune response** *MOLECULAR IMMUNOLOGY*
  Liu, H., Hu, Y., Zheng, M., Suhoski, M. M., Engleman, E. G., Dill, D. L., Hudnall, M., Wang, J., Spolski, R., Leonard, W. J., Peltz, G.
  2012; 51 (2): 112-127
- **A better prognosis for genetic association studies in mice** *TRENDS IN GENETICS*
  Zheng, M., Dill, D., Peltz, G.
  2012; 28 (2): 62-69
- **Cd14 SNPs regulate the innate immune response** *Molecular Immunology*
  Lu, H., Hu, Y., Zheng, M., Engleman, E., Dill, D., Hudnall, M.
  2012; 2 (51): 112–127
- **Gene Expression Commons: an open platform for absolute gene expression profiliing** *PLoS One*
  Seita, J., Sahoo, D., Rossi, D., Bhattacharya, D., Serwold, T., Inlay, M., Dill, D.
  2012; 7
- **A better prognosis for genetic association studies in mice** *Trends in Genetics*
  Zheng, M., Dill, D., Peltz, G.
  2012; 2 (28): 62–69
- **Identification of drug targets by chemogenomic and metabolomic profiling in yeast.** *Pharmacogenetic Genomics*
  Wu, M., Zheng, M., Zhang, W., Suresh, S., Schlecht, U., Fitch, W. L., Dill, D.
  2012

- **Identification of drug targets by chemogenomic and metabolomic profiling in yeast.** *Pharmacogenetic Genomics*
  Wu, M., Zheng, M., Zhang, W., Suresh, S., Schlecht, U., Fitch, W. L., Dill, D.
  2012
- **Next-Generation Computational Genetic Analysis: Multiple Complement Alleles Control Survival after Candida albicans Infection** *INFECTION AND IMMUNITY*
  Peltz, G., Zaas, A. K., Zheng, M., Solis, N. V., Zhang, M. X., Liu, H., Hu, Y., Boxx, G. M., Phan, Q. T., Dill, D., Filler, S. G.
  2011; 79 (11): 4472-4479
- **Are Cells Asynchronous Circuits? (Invited Talk)** *12th International Conference on Verification, Model Checking, and Abstract Interpretation*
  Dill, D. L.
  SPRINGER-VERLAG BERLIN.2011: 1–1
- **Next-generation computational genetic analysis: Multiple complement alleles control survival after candida albicans infection** *Infection and Immunity*
  Peltz, G., Zaas, A., K., Zheng, M., Solis, N., V., Zhang, M., X., Liu, H., H., Dill, D.
  2011; 11 (79): 4472–4479
- **The Role of Interleukin-1 in Wound Biology. Part II: In Vivo and Human Translational Studies** *ANESTHESIA AND ANALGESIA*
  Hu, Y., Liang, D., Li, X., Liu, H., Zhang, X., Zheng, M., Dill, D., Shi, X., Qiao, Y., Yeomans, D., Carvalho, B., Angst, M. S., Clark, et al
  2010; 111 (6): 1534-1542
- **The Role of Interleukin-1 in Wound Biology. Part I: Murine In Silico and In Vitro Experimental Analysis** *ANESTHESIA AND ANALGESIA*
  Hu, Y., Liang, D., Li, X., Liu, H., Zhang, X., Zheng, M., Dill, D., Shi, X., Qiao, Y., Yeomans, D., Carvalho, B., Angst, M. S., Clark, et al
  2010; 111 (6): 1525-1533
- **Towards Program Optimization through Automated Analysis of Numerical Precision.** *Proceedings of the ... CGO : International Symposium on Code Generation and Optimization. International Symposium on Code Generation and Optimization*
  Linderman, M. D., Ho, M., Dill, D. L., Meng, T. H., Nolan, G. P.
  2010; 2010: 230-237
- **MiDReG: A method of mining developmentally regulated genes using Boolean implications** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Sahoo, D., Seita, J., Bhattacharya, D., Inlay, M. A., Weissman, I. L., Plevritis, S. K., Dill, D. L.
  2010; 107 (13): 5732-5737
- **Timing Robustness in the Budding and Fission Yeast Cell Cycles** *PLOS ONE*
  Mangla, K., Dill, D. L., Horowitz, M. A.
  2010; 5 (2)
- **The role of interleukin-1 in wound biology. part i: murine in silico and in vitro experimental analysis** *Anesthesia & Analgesia*
  Hu, Y., Liang, D., Li, X., Liu, H., Zhang, X., Zheng, M., Dill, D.
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- **Timing robustness in the budding and fission yeast cell cycles** *PLoS ONE*
  Mangla, K., Dill, D. L., Horowitz, M. A.
  2010; 2 (5): e8906
- **The role of interleukin-1 in wound biology. part ii: in vivo and human translational studies** *Anesthesia & nalgesia*
  Hu, Y., Liang, D., Li, X., Liu, H., Zhang, X., Zheng, M., Dill, D.
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- **Gene expression changes induced by genistein in the prostate cancer cell line lncap** *Open Prostate Cancer J*
  Bhamre, S., Sahoo, D., Tibshirani, R., Dill, D., L., Brooks, J., D
  2010; 3: 86–98
- **Ly6d marks the earliest stage of B-cell specification and identifies the branchpoint between B-cell and T-cell development** *GENES & DEVELOPMENT*
  Inlay, M. A., Bhattacharya, D., Sahoo, D., Serwold, T., Seita, J., Karsunky, H., Plevritis, S. K., Dill, D. L., Weissman, I. L.
  2009; 23 (20): 2376-2381

- **Identification of the branchopoint between B and T cell development through MiDReG**
  Inlay, M. A., Bhattacharya, D., Sahoo, D., Seita, J., Karsunky, H., Serwold, T., Plevritis, S., Dill, D., Weissman, I. L.
  AMER ASSOC IMMUNOLOGISTS.2009

- **Temporal Changes in Gene Expression Induced by Sulforaphane in Human Prostate Cancer Cells** *PROSTATE*
  Bhamre, S., Sahoo, D., Tibshirani, R., Dill, D. L., Brooks, J. D.
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  Inlay, Matthew, A., Bhattacharya, D., Sahoo, D., Serwold, T., Seita, J., Karsunky, H., Dill, D.
  2009; 20 (23): 2376–2381

- **EXE: Automatically Generating Inputs of Death** *13th ACM Conference on Computer and Communications Security*
  Cadar, C., Ganesh, V., Pawlowski, P. M., Dill, D. L., Engler, D. R.
  ASSOC COMPUTING MACHINERY.2008

- **Point/Counterpoint The U. S. Should Ban Paperless Electronic Voting Machines** *COMMUNICATIONS OF THE ACM*
  Dill, D. L.
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- **Architecture and inherent robustness of a bacterial cell-cycle control system** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Shen, X., Collier, J., Dill, D., Shapiro, L., Horowitz, M., McAdams, H. H.
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- **Genomic and proteomic analysis reveals a threshold level of MYC required for tumor maintenance** *CANCER RESEARCH*
  Shachaf, C. M., Gentles, A. J., Elchuri, S., Sahoo, D., Soen, Y., Sharpe, O., Perez, O. D., Chang, M., Mitchel, D., Robinson, W. H., Dill, D., Nolan, G. P., Plevritis, et al
  2008; 68 (13): 5132-5142

- **Combined Analysis of Murine and Human Microarrays and ChIP Analysis Reveals Genes Associated with the Ability of MYC To Maintain Tumorigenesis** *PLOS GENETICS*
  Wu, C., Sahoo, D., Arvanitis, C., Bradon, N., Dill, D. L., Felsher, D. W.
  2008; 4 (6)

- **Boolean implication networks derived from large scale, whole genome microarray datasets** *GENOME BIOLOGY*
  Sahoo, D., Dill, D. L., Gentles, A. J., Tibshirani, R., Plevritis, S. K.
  2008; 9 (10)

- **Boolean implication networks derived from large scale, whole genome microarray datasets** *Genome Biology*
  Sahoo, D., Dill, D., L., Gentles, A., J., Tibshirani, R., Plevritis, S., K.
  2008; 10 (9): R157

- **Architecture and inherent robustness of a bacterial cell-cycle control system** *Proceedings of the National Academy of Sciences*
  Shen, X., Collier, J., Dill, D., L., Shapiro, L., Horowitz, M., McAdams, H., H.
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- **EXE: automatically generating inputs of death.** *ACM Transactions on Information and System Security*
  Cadar, C., Ganesh, V., Pawlowski, Peter, M., Dill, David, L., Engler, Dawson, R.
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- **Combined analysis of murine and human microarrays and chip analysis reveals genes associated with the ability of myc to maintain tumorigenesis.** *PLoS Genetics*
  Wu, C., H., Sahoo, D., Arvanitis, C., Bradon, N., Dill, D., L., Felsher, D., W.
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  Shachaf, C., M., Gentles, A., J., Elchuri, S., Sahoo, D., Soen, Y., Sharpe, O., Dill, D.
  2008; 13 (68): 5132
- **Automatic Formal Verification of Block Cipher Implementations** *8th International Conference on Formal Methods in Computer-Aided Design*
  Smith, E. W., Dill, D. L.
  IEEE.2008: 45–51
- **A retrospective on Mur phi** *Symposium on 25 Years of Model Checking (25MC)*
  Dill, D. L.
  SPRINGER-VERLAG BERLIN.2008: 77–88
- **Extracting binary signals from microarray time-course data** *NUCLEIC ACIDS RESEARCH*
  Sahoo, D., Dill, D. L., Tibshirani, R., Plevritis, S. K.
  2007; 35 (11): 3705-3712
- **A decision procedure for bit-vectors and arrays** *19th International Conference on Computer Aided Verification*
  Ganesh, V., Dill, D. L.
  SPRINGER-VERLAG BERLIN.2007: 519–531
- **A retrospective on murφ** *In 25 years of Model Checking, volume 4925 of Lecture Notes in Computer Science*
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- **Extracting boolean signals from microarray time course data.** *Nucleic Acids Research*
  Sahoo, D., Dill, David, L., Tibshirani, R., Plevritis, Sylvia, K.
  2007; 11 (35): 3705–3712
- **The Pathalyzer: A tool for analysis of signal transduction pathways** *Joint Annual Workshop on Systems Biology and on Regulatory Genomics*
  Dill, D. L., Knapp, M. A., Gage, P., Talcott, C., Laderoute, K., Lincoln, P.
  SPRINGER-VERLAG BERLIN.2007: 11–22
- **A refinement method for validity checking of quantified first-order formulas in hardware verification** *6th International Conference on Formal Methods in Computer Aided Design*
  Abu-Haimed, H., Dill, D. L., Berezin, S.
  IEEE COMPUTER SOC.2006: 145–152
- **Multiple representations of biological processes.** *Transactions on Computational Systems Biology*
  Talcott, C., Dill, David, L.
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- **Multiple representations of biological processes** *4th International Conference on Computational Methods in Systems Biology*
  Talcott, C., Dill, D. L.
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- **A Practical Approach to Partial Functions in CVC Lite** *ELECTRONIC NOTES IN THEORETICAL COMPUTER SCIENCE*
  Berezin, S., Barrett, C., Shikanian, I., Chechik, M., Gurfinkel, A., Dill, D. L.
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- **The pathway logic assistant**
  Talcott, C., Dill, David, L.
  2005
- **Evaluation of voting systems.** *Commun. ACM*
  Vora, P., L., Adida, B., Bucholz, R., Chaum, D., Dill, D., L., Jefferson, D.
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