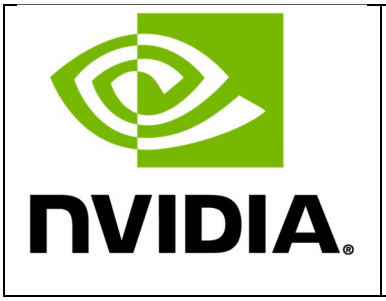

NVIDIA Deep Learning Tutorial

Hosted by IEEE-IPDPS 2017

Tuesday, May 30, 2017 @ 7:00 PM
Meyer Suite on Lobby Level
Buena Vista Palace Hotel Orlando
Welcoming All IPDPS 2017 Attendees

IPDPS 2017
NVIDIA Deep Learning Tutorial

Julie Bernauer, NVIDIA
Senior Solutions Architect for Machine Learning and Deep Learning

Tuesday, May 30, 2017 @ 7:00 PM
Meyer Suite on Lobby Level
Buena Vista Palace Hotel Orlando

IPDPS 2017 Attendees will have all day Tuesday to sign-up to attend.

See NVIDIA representative at the NVIDIA Exhibit Table in Foyer.

ABSTRACT:
As AI becomes ubiquitous, it is critically important to understand the technology and how it is integrated in a variety of applications. This tutorial details the inter-workings of machine learning and neural networks, and how they apply in practice leveraging GPUs in both on premise and cloud environments. Multiple application examples will be presented along with a discussion on how they are developed. Learn how hardware and software stacks enable not only quick prototyping, but also efficient large-scale production deployments. The tutorial will conclude with a discussion about hands-on deep learning training opportunities as well as free academic teaching materials and GPU cloud platforms for university faculty."

BRIEF BIO:
Julie Bernauer is Senior Solutions Architect for Machine Learning and Deep Learning at NVIDIA Corporation. She joined NVIDIA in 2015 after fifteen years in academia as an expert in machine learning for computational structural biology. She obtained her PhD from Université Paris-Sud in Structural Genomics studying Voronoi models for modelling protein complexes. After a post-doc at Stanford University with Pr. Michael Levitt, Nobel Prize in Chemistry 2013, she joined Inria, the French National Institute for Computer Science. While Senior Research Scientist at Inria, Adjunct Associate Professor of Computer Science at École Polytechnique and Visiting Research Scientist at SLAC, her work focused on computational methods for structural bioinformatics, specifically scoring functions for macromolecule docking using machine learning, and statistical potentials for molecular simulations.