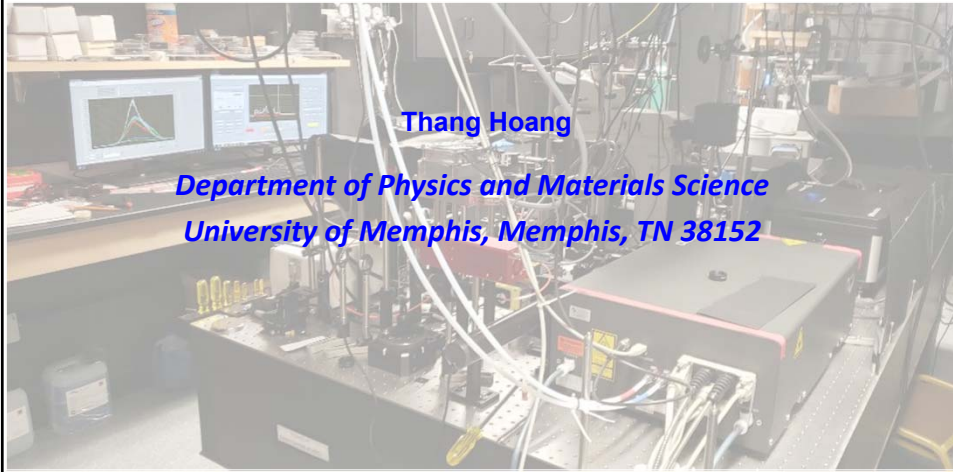


Development of fully automated software systems for data acquisition and real-time data analysis



Thang Hoang

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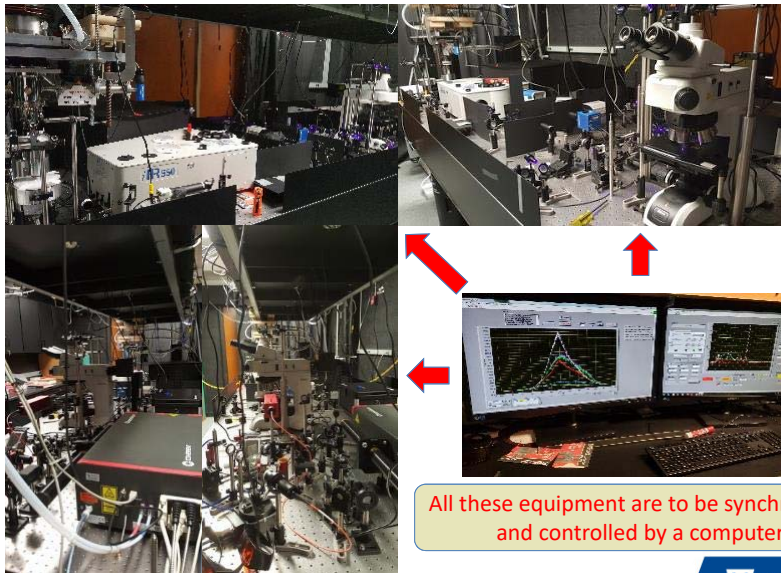
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Nanophotonics Laboratory MN 107



All these equipment are to be synchronized and controlled by a computer

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Goals of this project

Fully automated software systems for data acquisition and real time data analysis

Computer

- Multiple equipment control.
- Large data sets.
- Real time data plot and analysis.
- Can be adapted to various experiments.

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National Instrument© Labview programming environment

Available through the University of Memphis Citrix system

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Multiple equipment control

The screenshot displays the GenScan Acquisition Thru software interface. The central window shows a spectral plot with 'Counts' on the y-axis (ranging from -500 to 2750) and 'Wavelength (nm) (Wavenumber (cm-1))' on the x-axis (ranging from 634 to 678). The plot shows several peaks, with a prominent one around 650 nm. To the left of the plot are various control panels for system status, settings (integration time, number of axes, etc.), and hardware parameters (cell type, micro ID, etc.). To the right, there are buttons for 'Move stages', 'Mapping', and 'Wavelength' control. At the bottom, there are buttons for 'ACQUIRE', 'ACQUIRE RANGE', and 'STOP'. A yellow box at the bottom of the screenshot contains the text: 'Acquiring data and performing data analysis simultaneously'.

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Nanoparticle tracking in real time

The screenshot displays the biosome-image-processing-7/85_Lvl software interface. The main window is divided into several panels. On the left, there are image windows showing the original grayscale image and the processed image with particles highlighted in red. The central panel shows a 'Signal Imposed' image with a blue signal overlay. On the right, there is a 'Histogram Graph' showing a distribution of particle sizes. Below the histogram, there are tables of 'Extract result' and 'Cleared result' data. The 'Extract result' table has columns for 'ID', 'Diameter', 'Minimum Value', 'Maximum Value', and '# Shifts'. The 'Cleared result' table has columns for 'ID', 'Diameter', 'Minimum Value', 'Maximum Value', and '# Shifts'. The software version is 6.04/M_04/01/2019 Thru.

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NIH Grant Proposal

A module of the software has been used to produce data for an NIH grant proposal:
"Single exosome mapping for early cancer detection using plasmonic nanoparticles"
 (In collaboration with Prof. Xiaohua Huang, Chemistry)

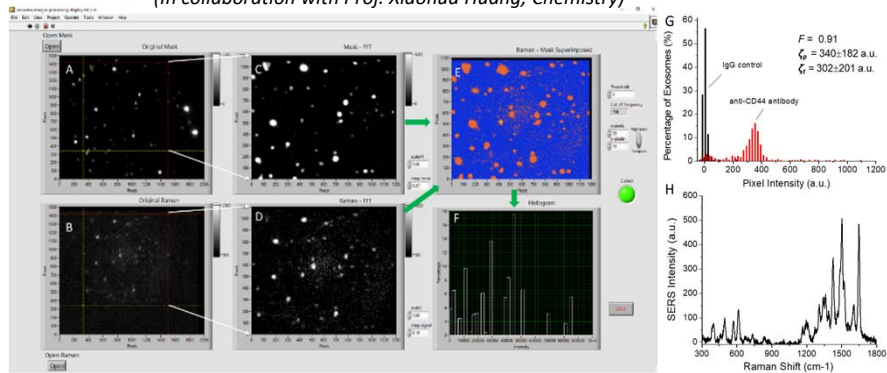
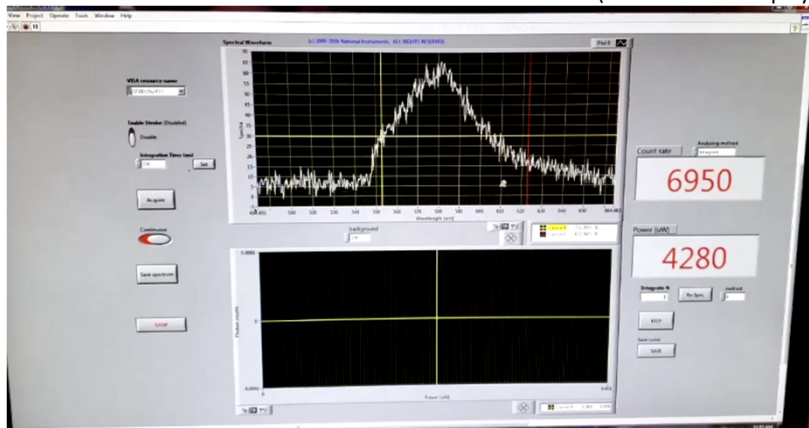


Fig.7 (A) Illustration of major steps in SEDIA. The example is analysis of HER2 expression on SKBR3 exosomes. (B) SERS spectrum of HER2-targeted SKBR3 exosomes using the same microscopic system. (C) Population density histogram of HER2 expression on SKBR3 exosomes compared with the control without using primary antibody. The results show that 80% SKBR3 exosomes are HER2-positive.

NIH review score: 25
 NIH pay-line score for year 2020: 25 → Expect to be funded

Plasmonic nanolasers

(Click on video to play)

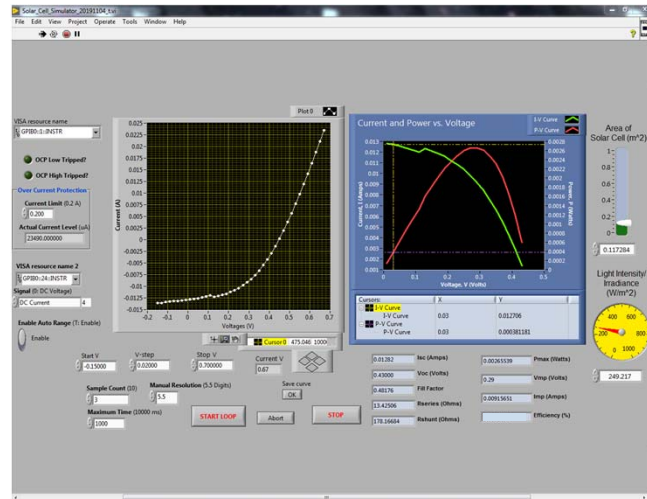


Random lasing using plasmonic nanostar

- Manuscript to be submitted.
- Work will be presented at the American Physical Society, Denver, 3/2020

Education

Integrate Labview programming into PHYS 4320 and PHYS 6320 (Electronics)



Photovoltaic study: students perform measurements on Solar cells and analysis in real time using their own codes

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- Collaborators
 - University of Memphis: Xiao Shen (Physics), Xiaohua Huang (Chemistry)
 - University of Nebraska-Lincoln: Prof. Christos Argyropoulos



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