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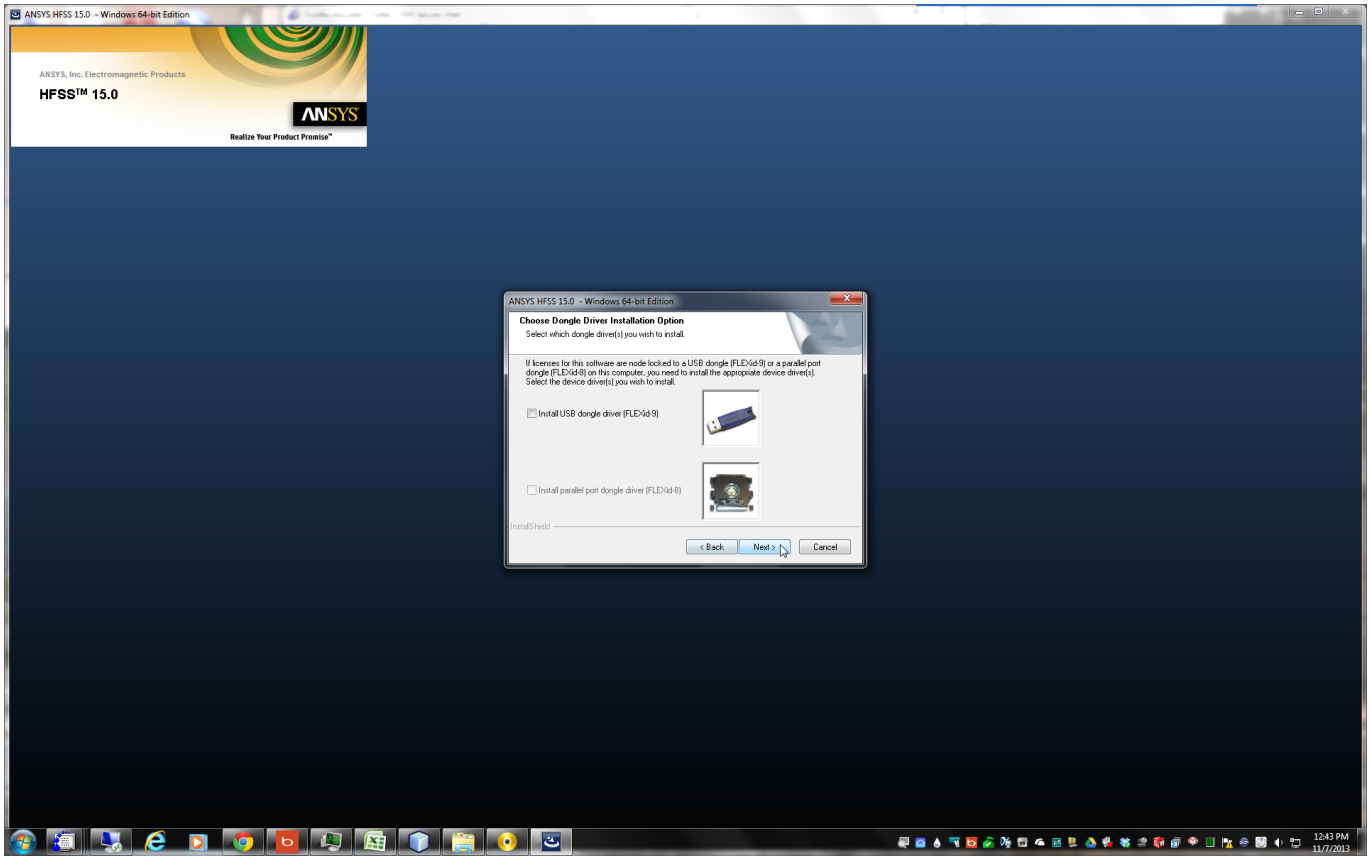

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In this regard, I would like to mention the following resources and tools available to the readers of this forum. [NetMiner]{} {#part-iv-for-the-results-of-the-modified-algorithm-of-the-neometric-predictor-netminer-jvx.unnumbered} ========== ========== ========== In this part we present the results of our modified algorithm, [NetMiner]{}. From Figure \[fig-w-rho-z1\] we can see that the hyperparameter-nudged performance of [NetMiner]{} is generally similar to that of [RooFit]{} and [SARAH]{}. Figure \[fig-pp-w-rho-z1\] shows the precision-recall curve of [NetMiner]{}. Figure \[fig-robust-improvement\] shows the robustness improvement of [NetMiner]{} (on x-axis) over [RooFit]{} and [SARAH]{}. ![The comparison of precision-recall curves of different methods (for $w = rho = z = 1$).[]{data-label="fig-pp-w-rho-z1"}](./pp_w_rho_z1.pdf){width="0.35\linewidth"} ![The comparison of robustness improvement over the other methods (on x-axis) for different settings of w, rho and z (in percentage).[]{data-label="fig-robust-improvement"}](./robust_improvement.pdf){width="0.5\linewidth"} Conclusion {#part-v-conclusion.unnumbered} ========== This part of the paper describes our novel work on deep learning based identification of protein-ligand binding sites, i.e. the sites of the protein molecule that bind to a small molecule ligand. The existing methods suffer from a lack of generalizability and high false positive rates. Our approach addresses these issues by using convolutional neural networks and a newly proposed scoring function to enhance the prediction accuracy. The experiments show that the proposed method has a better performance compared with other state-of-the-art methods. Further, we also find f3e1b3768c