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## LASER SPECTROSCOPY OF ALKOXY AND ALKYLTHIO RADICALS

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The alkoxy (RO; R=$CH_3$, $C_2H_5$, i-$C_3H_7$) and alkylthio (RS) radicals are significant reaction intermediates in gas-phase atmospheric and combustion processes. Laser-induced fluorescence (LIF), in association with a supersonic jet expansion, has been employed to probe the spectroscopy of these radicals. RO radicals were generated *in situ* in the supersonic expansion by excimer laser (KrF @ 248 nm) photolysis of RONO, while RS molecular fragments were produced from similar photodissociation of $R_2S_2$. Both Nd:YAG-pumped and excimer-pumped tunable dye laser systems have been used to record rotationally-resolved laser excitation spectra of the jet-cooled RO and RS radicals. Dispersed fluorescence spectra of $CH_3O$ and $CH_3S$ were obtained by exciting the molecules at the wavelength of a strong rotational transition within a specific vibronic band. Rotational and vibrational frequencies have been assigned and least-squares fits performed to obtain molecular parameters for the free radicals in both upper and lower electronic states.

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## LASERS AND LIPOSOMES: A SUCCESSFUL MARRIAGE FOR DYE RELEASE AND DRUG DELIVERY

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Liposomes are vesicles composed of phospholipid bilayers distributed in an aqueous environment. Liposomes have structural similarities to membranes of biological cells and lipid vesicles. We have prepared liposomes with dyes either encapsulated in the internal volume (e.g. sulforhodamine) or intercalated in the bilayer membrane (e.g. methylene blue). One of the main aims of these investigations has been to release efficiently the internal contents of the liposomes by pulsed laser excitation. A single 8 ns wide pulse at 532 nm caused significant release of liposome contents, being dependent on liposome size, internal dye concentration, and pulse energy density. Time-correlated single photon counting measurements performed provided insight into the distribution of dye molecules in the interior of the liposome and the bilayer. This technique of laser-mediated release of dyes from liposomes can be used for targeted release of drugs and for localized photothermal release of dye-drug complexes leading to destruction of tumor tissue.

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## QUANTIFYING SOFTWARE USING BOUNDARY VALUE ANALYSIS.

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Recently, there has been a great deal of interest in defining appropriate ways to measure software to provide feedback to developers that can be used in the design process to avoid unnecessary complexity and thus defective software. Software metrics are used to characterize the essential features of software quantitatively, so that classification, comparison, and mathematical analysis can be applied. After a number of useful metrics is identified, it is then important to measure software in an algorithmic and objective fashion, so that the values of the selected metrics are consistent among different software products, and are independent of the measurer. A software metric is defined by a rule by which a given software related product can be quantified.

Boundary Value Analysis (BVA) estimates the amount of "black box" or specification-based testing necessary to verify software. It is a well-defined number that may be computed for software that is coded or that is specified in sufficient detail to determine all interfaces to other modules, whether the interface is by arguments to the module or by access to global variables. Thus the BVA metric can be computed in any stage beyond the specifications in the software life cycle.

The BVA metric is based on the number and type of input parameters to program subunits. As such, it is one measure of program modularity. It is calculated using a count of the number of test cases needed to separate the domain of all possible test cases into regions where the selection of a test case chosen from any one of these regions is essentially as likely to produce a software fault as any other test case chosen from the same region.

The BVA metric is different from conventional software metrics such as Halstead and McCabe analyses in that it uses data structures to measure the complexity of software : traditional metrics ignore data organization. With the growth of object-oriented technologies it is important to be able to measure software in terms of its component objects, or data structures.

The BVA metric was developed at Howard University as a first generation, academic research tool. The results of the BVA analysis provides details on data complexity that offers new insights into software behavior.

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## ANALYSIS OF CONNECTIVIE TISSUE PROTEIN mRNA CONTENT OF VARIOUS TUMORS AND TRANSFORMED CELL LINES.

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Connective tissue matrix proteins comprise the structural network of tissues and organs. The role of these proteins is to stabilize and form a net to partition and support tissues. It is known that transformed cells and tumors have the ability to spread to distal organs - metastasize. The goal of this project was to determine whether the process of transformation compromises the integrity of this fibrillar network by influencing the synthesis of connective tissue proteins. Comparisons of paired sets of tissue or cells (i.e. normal cells versus transformed or tumor cells from the same organ system) for the presence or absence of various connective tissue proteins were made. Several cell types were utilized. Northern blot analyses were employed using standardized concentrations of mRNA and $^{32}P$- radiolabed cDNA of several connective tissue (extracellular matrix) proteins as probes. In this manner it was determined whether the various connective tissue proteins were present. Comparisons of transcriptional levels of the various connective tissue proteins were made. The preliminary studies for this project show that there is differential expression of beta actin and osteonectin between transformed cell lines and specific types of cancer.

Research Faculty Mentor: Agnes A. Day, Ph.D.