The Washington D.C. Branch and George Mason University Student Chapter of ASM are pleased to invite you to:

The Third Joint Meeting
At George Mason University

April 14th 6-9 PM

Branch Lecturer:
Jeffrey G. Gardner, Ph.D.

UMBC
http://gardlab.umbc.edu/

Title TBD

- Student Oral and Poster Presentations
- Student Awards presentations
- Refreshments and networking

Please join us at 105 Innovation Hall
George Mason University
Fairfax, VA 22030

Campus and Parking Map:
http://info.gmu.edu/Maps/FairfaxMap14_Parking.pdf

For more information contact:
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There is no registration for this event. All are welcome.

IN SILICO ANALYSIS OF DNA METHYLTRANSFERASES ENZYMES REVEALS AN ATYPICAL DIVERSIFICATION AMONG EUBACTERIA TAXA.

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Methylation is the most typical epigenetic mark, which is involved in gene regulation, cell memory, silencing and other relevant processes. These functions are accomplished by methylases, a family of enzymes which is widespread in both eukaryote and prokaryote. Although there are many reports about the roles of these enzymes in Archea, there is few information and reports about the role of these in Eubacteria taxa.

The aim of this study was to contribute to the *in silico* characterization of these group of enzymes in Eubacteria under a structural bioinformatics approach and phylogenetic analysis. Firstly, Eubacteria's orthologous proteins were inferred by individual Eubacteria – phylum BLASTP searches against human DNMT3a (NP_783328.1) as a template. Nonetheless, the phylogenetic reconstruction based on the conserved S-adenosil domain, revealed two major cluster, some phyla similar to Human DNMT3a and other not. In this sense, these findings show a lack of congruence within the species tree of Eubacteria.

Furthermore, *Ab initio* modelling was performed in order to obtain some probable structures of the Eubacteria´s methyltransferases. All the structures showed typical sandwich conformation for methylases family. Using Prosite tool from ExPASy the aminoacids of active site were identified, and showed considerable differences in the pattern of sequences among the two main groups found in the phylogeny analysis; although all of them conserve a cysteine residue in the catalytic domain. According to our discoveries, the current diversification of methylases presents in Eubacteria could have had multiple distinct origins through the Eubacteria phyla suggesting different sceneries as possible explanations of sources, which have implications in the role in structural and enzymatic functions.