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# Gene Expression Omnibus: Ncbi Gene Expression and Hybridization Array Data Repository

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#### Introduction

The Gene Expression Omnibus (GEO) project was initiated in response to the growing demand for a public repository for highthroughput gene expression data. GEO provides a flexible and open design that facilitates submission, storage and retrieval of heterogeneous data sets from high-throughput gene expression and genomic hybridization experiments. GEO is not intended to replace in house gene expression databases that benefit from coherent data sets, and which are constructed to facilitate a particular analytic method, but rather complement these by acting as a tertiary, central data distribution hub. The three central data entities of GEO are platforms, samples and series, and were designed with gene expression and genomic hybridization experiments in mind. These techniques have been used to measure the molecular abundance of mRNA and genomic DNA either in absolute or relative terms. Mainly contributing to this popularity is the highly parallel nature of these techniques and the concomitant conservation of time and resources brought about by the large number of simultaneous (or near-simultaneous) molecular sampling events performed under very similar conditions. Over the last several years, there has been an international effort to catalog the minimal set of information which is necessary in order for microarray experiments to be properly interpreted and to be comparable with one another. The codification and publication of this set of guidelines will be invaluable as a guide for high-throughput gene expression and genomic hybridization data producers and data repositories. An instance of a sample describes the derivation of the set of molecules that are being probed and utilize platforms to generate molecular abundance data. Each sample has one, and only one, parent platform which must be previously defined. For example, a sample data table may contain columns indicating the final, relevant abundance value of the corresponding spot defined in its platform, as well as any other GEO-defined (e.g. raw signal, background signal) and submitterdefined columns. Sample accession numbers have a 'GSM' prefix [1].

## Higher Power Usually Reveals Nuclear Atypia

Nevoid melanoma may resemble benign compound or intradermal nevi by their silhouette and profile on low power. Higher power usually reveals nuclear atypia, confluence of cells, incomplete maturation and dermal mitotic activity. However, to some extent all of these features maybe seen in benign compound or intradermal nevi and no single criteria can be used to differentiate nevoid melanoma from a benign nevus. The distinction can be particularly problematic in nevi that show mitotic activity and we have noted a recent trend in diagnosis of melanocytic neoplasms with dermal mitosis as nevoid melanoma despite the presence of normal maturation in the dermis and lack of significant nuclear atypia. Therefore in this study we evaluated 10 nevoid melanomas, 4 of which resulted in metastasis and 10 mitotically active nevi with fluorescence in situ hybridization targeting key chromosomal loci previously shown to effectively discriminate been malignant and benign melanocytic neoplasms. All 10 nevoid melanomas showed copy number abnormalities by fluorescence in situ hybridization in either chromosome 6 or 11 while none of the 10 mitotically active nevi did. The results demonstrate that fluorescence in situ hybridization targeting key chromosomal loci on chromosomes 6 and 11 can be effective in discriminating nevoid melanomas from mitotically active nevi. Additionally, our study presents further evidence that dermal mitoses alone without other diagnostic features such as nuclear atypia and lack of maturation does not constitute sufficient evidence alone for a diagnosis of melanoma [2].

When reticulation events occur, the evolutionary history of a set of existing species can be represented by a hybridization network instead of an evolutionary tree. When studying the evolutionary history of a set of existing species, one can obtain a phylogenetic tree of the set of species with high confidence by looking at a segment of sequences or a set of genes. When looking at another segment of sequences, a different phylogenetic tree can be obtained with high confidence too. This

Vol.5 No.8:109

indicates that reticulation events may occur. Thus, we have the following problem: given two rooted phylogenetic trees on a set of species that correctly represent the tree-like evolution of different parts of their genomes, what is the hybridization network with the smallest number of reticulation events to explain the evolution of the set of species under consideration [3].

Adverse reactions to polyacrylamide gel occur as swellings or nodules, and controversy exists whether these are due to bacterial infection or an autoimmune reaction to the filler. Biopsies from culture-negative long-lasting nodules after injection with different types of polyacrylamide gel were examined with a combination of Gram stain and fluorescence in situ hybridization. Bacteria were detected in biopsies from seven of eight patients. They inhabited gel and intervening tissue and tended to lie in aggregates [4].

The correlations between the amount of precipitation at a locality in western Kansas and the phenotype of oriole that occurs there are high (about 0.90). This suggests that precipitation per se is a factor that determines the distributional limits of these birds relative to each other. There are no recent changes, however, in the average climatic conditions in western Kansas. Perhaps the orioles present at a site in any given season are a reflection of the conditions there the previous season or two. The analyses of size variation among samples collected in the 1970's show an east-west cline that is more-or-less congruent with that found for plumage features; at any given site, the variability in size is positively correlated with the variability in plumage. Specimens of Northern ("Baltimore" and "Bullock's") orioles collected at six sites in western Kansas in 1976 and 1978 are compared with specimens collected at the same sites in the mid-1960's. No changes in the location or size

of the step-cline ("hybrid zone") between the two taxa are indicated by comparisons of the plumage features of the male specimens; the distribution of phenotypes of birds from sites where both Baltimore and Bullock's orioles occur is not bimodal, and, therefore, there is no indication of selection against intermediate birds. Female Bullock's-like orioles, however, are found farther east along the Cimarron River in southwestern Kansas than they were in the 1960's [5]. The correlations between the amount of precipitation at a locality in western Kansas and the phenotype of oriole that occurs there are high (about 0.90). This suggests that precipitation per se is a factor that determines the distributional limits of these birds relative to each other. There are no recent changes, however, in the average climatic conditions in western Kansas. Perhaps the orioles present at a site in any given season are a reflection of the conditions there the previous season or two.

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