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**What is the goal of DGEA? (Weekly Checklist Objective Question)**

-The main goal of Differential Gene Expression Analysis (DGEA) is to identify genes that show significant changes in expression levels between different conditions or groups.

-It can find genes that behave differently in two or more biological states.

-This helps researchers understand which genes are active, suppressed, or altered in different conditions.

-This can identify potential biomarkers for early diagnosis of diseases and can support drug discovery.

**Biological Pathways:**

-Organized series of molecular interactions within a cell that lead to a specific outcome.

-It is like a cellular assembly line: each molecule performs a step that leads to the next.

-Each step can result in turning genes on or off.

-Help respond to stimuli and maintain homeostasis.

-Disruptions in these pathways can lead to diseases.

-Comparing pathways in healthy vs. diseased cells reveals therapeutic targets (a specific biological molecule that plays a role in a disease and can be modulated by drugs or therapy).

**Overrepresented Biological Pathways:**

-Means more genes from that pathway appear in your data set than would be expected by random chance.

-If you compare your list of significant genes to known pathways and many genes match up, it is considered overrepresented.

-This suggests that pathway is biologically relevant to the condition you are studying.

-Significance measured by statistical tests like the hypergeometric test and Fisher’s exact tests.

-Narrows down thousands of genes into meaningful biological insights.

**Pathway Enrichment Analysis:**

-Used to uncover which biological pathways are statistically overrepresented in a list of genes.

-Method to uncover biological significance behind gene expression changes.

-Helps researchers interpret large gene lists by grouping them into known biological pathways.

-Reveals functions that may be driving a disease.

-Highlights biological processes that are active or disrupted.

**Enrichr Database:**

-Web-based tool for gene set enrichment analysis.

-Compares your list of genes found in a study to annotated gene sets from curated databases.

-Tells you which biological processes are overrepresented in your gene list.

-Allows you to view relationships between genes and biological terms.

-You can submit a human or mouse gene list.

-Includes 30+ gene set libraries including Gene Ontology (GO).

-Identifies key biological themes in your data.

-Suggests regulatory mechanisms or disease links.

-Can visualize results with interactive charts.

**Enrichr Analysis Video Notes – How are Top Genes Utilized to Identify Information Through Various Pathway Analyses?**

-Firstly, you input your list of top ranked genes based on statistical thresholds.

-Database compares input gene list against curated set libraries.

-Uses statistical methods to identify overlaps between input and annotated sets.

-Results include:

-Enriched pathways ranked by significance.

-Associated biological terms.

-Interactive visualizations (bar charts, network graphs, etc.)

-Predicted gene association, connecting genes to terms across multiple libraries

-Researchers can use this information to reveal disease mechanisms.

-Key regulators can be identified including transcription factors, or microRNA.

-Suggests therapeutic targets or biomarkers.

-Supports hypotheses for future research.

-Can export data for publication, or for future experiments.