MCATalyst MCAT Lab Techniques Cheat Sheet

Note: the corresponding Anki Deck (found here) will have a bit more information (and pictures) not listed here

Chemical Separation Techniques

Chromatography- for separation of molecules based on chemical characteristics

Name	Setup	Results	Other Important Info
Gas Chromatography	Nonpolar Mobile Phase Polar Stationary Phase	Order of elution: most nonpolar to most polar	Used to separate gases of different polarities
Liquid Chromatography	Nonpolar Mobile Phase Polar Stationary Phase	Order of elution: most nonpolar to most polar	Used to separate liquids of different polarities
Normal-Phase High-Performance Liquid Chromatography (HPLC)	Nonpolar Mobile Phase Polar Stationary Phase	Order of elution: most nonpolar to most polar	Liquid Chromatography w/ a higher resolution: • "Finer" stationary phase (more surface area for interactions) • Higher pressure
Reverse-Phase HPLC	Polar Mobile Phase Nonpolar Stationary Phase	Order of elution: most polar to most nonpolar	*Only* polarity chromatography to have Polar Mobile and Nonpolar Stationary Phase, so results flip
Thin-Layer Chromatography	Nonpolar Mobile Phase Polar Stationary Phase	Order of elution: Most nonpolar travel furthest (highest R_f), most polar travel least (lowest R_f)	Nonpolar liquids travel up TLC paper with mobile phase, polar liquids stay near the bottom $R_f = \frac{\text{Compound Travel Distance}}{\text{Mobile Phase Travel Distance}}$
Flash Chromatography	Nonpolar Mobile Phase Polar Stationary Phase	Order of elution: Most nonpolar travel furthest (highest R_f), most polar travel least (lowest R_f)	TLC just in bulk.
Size-Exclusion (Gel Filtration) Chromatography	Liquid compounds are poured over gel beads	Order of elution: largest to smallest molecules	Molecules are poured over gel beads, which only allow smaller molecules through and cause them to travel along longer paths than large molecules that can travel around the beads (in shorter paths).
Cation-Exchange Chromatography	Charged compounds poured over negatively charged beads	Most negatively charged molecules elute first, positive elute last	Can also be used to separate cations (not anions) of different strengths
Anion-Exchange Chromatography	Charged compounds poured over positively charged beads	Most positively charged molecules elute first, negative elute last	Can also be used to separate cations (not anions) of different strengths
Affinity Chromatography	Protein solution is poured over beads with specific ligands attached	Proteins that can interact with the ligands will stick to the beads, proteins that don't will be poured off/removed	To liberate the protein from the bead, free-ligand (not attached to a bead) is added to displace the protein from the bead-bound ligand.

Distillations- for separation of molecules based on boiling point (BP)

Ways to increase BP (in decreasing priority order):

Having stronger intermolecular interactions (Ionic > Hydrogen Bond > Dipole-Dipole (Polar) > van der Waals)

Having a larger surface area (larger molecules with less branching and more saturation have higher BP)

Having a higher mass (when comparing two very similar molecules)

Name	Results	Other Important Info
Simple Distillation	Molecules with the lowest BP elute first, highest BP elute last	Used for molecules w/ very different (>25^{o}C) BPs
Fractional Distillation	Molecules with the lowest BP elute first, highest BP elute last	Used for molecules w/ similar (<25^{o}C) BPs
Vacuum Distillation	Molecules with the lowest BP elute first, highest BP elute last	Used for molecules w/ very high BPs that risk decomposition (hundreds of ^{o}C), vacuum decreases ambient pressure making BP lower and more safe

Extractions- for separation of molecules based on solubility differences

Name	Setup	Results	Other Important Info
Liquid Extraction	Compounds separate into aqueous (hydrophilic) phase or organic (hydrophobic)	Polar compounds are dissolved and removed via the aqueous phase Nonpolar compounds are dissolved and removed via the organic phase	**Common aqueous/water miscible solvents**: water, alcohols, diluted acids or bases, or very polar molecules **Common organic solvents**: Diethyl ether, DCM, hexanes, other nonpolar molecules **Distribution Coefficient**- if a compound is partially soluble in both phases, this is simply the ratio of compound dissolved in the organic layer to compound dissolved in aqueous layer
Acid/Base Extraction	Compounds separate into aqueous (hydrophilic) phase or organic (hydrophobic)	Compounds are ionized one at a time and removed in the aqueous phase, all non-ionized compounds retain in the organic phase	Typical order of steps (all compounds begin in the organic phase): 1. Add weak base to deprotonate stronger acids, ionizing them and making them soluble in the aqueous phase 2. Add strong base to deprotonate weaker acids (so they can be removed in the aqueous phase) 3. Repeat steps 1 and 2 if needed but add acids instead to remove basic molecules. 4. Non-ionizable molecules will remain in the organic phase.

Chemical Structure Techniques

Name	Goal	Data	Other Important Notes
H-NMR	Determine the structure of a molecule utilizing the organization and properties of Hydrogens	**PPM (Chemical Shift) values**: Alkane H's = 0-5 Alkene H's = 5-7 Aromatic H's (Benzene) = 6-8 Aldehyde H's = 9-10 Carboxylic Acid H's = 10-13	**Neighboring Hydrogens (NH)**: The Hydrogens on an adjacent carbon **Splitting**: # of neighboring H's + 1, represented by the # of peaks at a certain chemical shift (singlet/1 peak = no NHs, doublet/2 peaks = 1 NH, triplet = 2 NHs, etc.) **Chemical Shift:** If H's are near other electronegative atoms, their peaks will appear shifted "downfield" or to the left. If H's are only near C's and H's, they will be shifted "upfield" or to the right. **Integration**: The "area under the curve", or area of each set of peaks, which identifies how many of those specific types of H's there are.
C-NMR	Determine the structure of a molecule utilizing the organization and properties of Carbons	**PPM (Chemical Shift) values**: Alkane C's = 0-70 Alkene C's = 90-120 Aromatic C's = 110-160 Carbonyl C's = 160-200	None. Not nearly as important as H-NMR.
IR	Identifies the presence of certain functional groups due to vibrations caused by dipole moments	**Functional Group Wavenumber Peaks to know**: Carbonyls = Sharp, 1700-1750 Alcohols = Broad, 3200-3600 Primary Amine = Two Sharp, 3300-3400 Secondary Amine = One Sharp, 3300-3400 Triple Bonds (CC or CN) = Sharp, 2100-2300	**X-Axis**: Wavenumber (the inverse of wavelength) **Y-Axis**: Transmittance (basically the inverse of Absorbance, how much light passes through a molecule at a certain wavelength/wavenumber of light) **Signal Shapes**: • Sharp- pointed peaks instead of round • Broad- rounded peaks instead of pointed
UV-Vis	Identifies the degree of conjugation (alternating pi bonds, basically) in a molecule	More conjugation = Absorbs larger wavelengths of light (lower Energy light) Less conjugation = Absorbs smaller wavelengths of light (higher Energy light)	When conjugated (pi) electrons absorb light: • It is called a **π → π* excitation** (* = excited) • Pi electrons absorb light and are promoted from the **HOMO to the LUMO** • The color of light that is **absorbed is perceived as the opposite color** (absorbing Green means Red is perceived)

Mass Spectrometry	Identifies the mass and presence of Cl or Br in a molecule	**What each peak tells us:** Base Peak = Highest abundance M+ Peak = Mass of molecule M+1 Peak = # of Carbons M+2 = Presence of Cl or Br	• Mass to Charge ratio (m/z) is just the mass of the molecule/fragment • The Base Peak *can* be the same as the M+ peak, but it not always is. • **M+ Peak** is the highest peak in the last grouping of peaks on the far right. • **M+2 Ratios**: If the ratio of M+ to M+2 Peak is roughly 1:1, Br is present. If the ratio is 3:1, Cl is present. If there is no M+2 peak, no Cl or Br is present. • **Heavier mass molecules will "deflect" *less* than lighter mass molecules** (which deflect more)
X-Ray Crystallography	Determines the 3D structure of molecules, especially proteins and DNA	None for the MCAT.	X-Rays are shone onto the molecule, where the different angles of diffraction light takes through the different parts of the molecule can be calculated and turned into a 3D image.

Acid-Base Lab Techniques/Technology

Name	Goal	Other Important Notes
Litmus Paper	Determines the relative acidity or basicity of a compound	Acids turn the paper red, Bases turn the paper blue.
Titrations	Determine the pK_A or concentration of an unknown Acid or Base by adding a Strong Base or Acid (respectively) and measuring the pH of the solution as neutralization occurs	**Titrant**: the Strong Acid or Base of a known concentration being added to the unknown Base or Acid **Titrand**: The Acid or Base of an unknown concentration or pK_A **Indicators**: molecules that will change color as pH changes, goal is to pick an indicator with a pK_A close to the pH of the Equivalence Point. **Half-Equivalence Point**: The pK_A of the unknown Acid or Base = the pH at the Half-Equivalence point, where there are equal concentrations of acid and conjugate base ([Acid] = [Conjugate Base]). Vice versa if Titrand is a Base. **Equivalence Point**: There are equal amounts of H^+ donated by the acid as OH^- donated by the base. Indicator will change color here. • Strong Acid + Weak (Unknown) Base = Eq Point is below pH of 7 • Strong Base + Weak (Unknown) Acid = Eq Point is above pH of 7 • Strong Acid + Strong Base = Eq Point is *at* (equal to) pH of 7 **Number of Equivalence Points** = Number of H's (for acids) or OH's (for bases) to donate

Biological and Biochemical Lab Techniques

Goal of Lab Technique:

Identification: Simply determining whether or not the molecule is present
Qualitative: Identifies the mass, structure, or characteristics of a molecule
Quantitative: Identifies the actual amount or concentration of a molecule

Nucleic Acid Lab Techniques and Technology

Name	Goal	Results	Other Important Notes
Agarose Gel Electrophoresis	**Qualitative**: Identify **mass** of **DNA** strands	**Lightest** strands travel **furthest down** the gel, **heaviest** travel the **least** and stay near the **top**	**The Ladder**: Many strands of DNA of *known* weights are loaded into a well so the strands of unknown weight can be compared to and measured **Agarose:** Gel with large pores to compensate for large DNA molecules (instead of Polyacrylamide, used for smaller proteins) Larger proteins can be used in agarose but that is rare (the results are interpreted the same).
Northern Blotting	**Identification**: Identifies the presence of specific **RNA** strands	**Thicker band**: higher amounts the desired RNA are present **Thinner band**: lower amounts of the desired RNA are present **No band**: the desired RNA is not present	***Not* Quantitative**- we cannot calculate the amount/concentration, simply whether or not the RNA is there and if there's relatively more or less than another sample.
Southern Blotting	**Identification**: Identifies the presence of specific **DNA** strands	**Thicker band**: higher amounts the desired DNA are present **Thinner band**: lower amounts of the desired DNA are present **No band**: the desired DNA is not present	***Not* Quantitative**- we cannot calculate the amount/concentration, simply whether or not the DNA is there and if there's relatively more or less than another sample.
PCR	**Identification**: Identifies the presence of desired **DNA** strands by amplifying the number of copies	**Number of Copies = $x2^N$** N = number of rounds of PCR x = number of copies at the start of PCR	**Steps (Mnemonic: Don't Ask Emily):** 1. **Denaturation-** Hydrogen bonds are split via high heat 2. **Annealing-** Cooling to allow primers to bind to target sequences 3. **Extension (or Synthesis)-** Taq polymerase (a DNA Polymerase) added to extend/synthesize new strands
qPCR (Quantitative PCR)	**Quantitative:** Measures amount/concentration of genes being expressed	**Number of Copies = $x2^N$** N = number of rounds of PCR x = number of copies at the start of qPCR	**Same steps as normal PCR,** but utilizes a fluorescent dye that will increase in fluorescence (which can be measured) as the number of strands increases.

RT-PCR (Reverse Transcriptase PCR)	**Identification:** Can identify if a specific mRNA is present. **Qualitative:** Determines when or if a gene is being expressed (and therefore it's functioning)	**Thicker band**: higher amounts the desired mRNA are present **Thinner band**: lower amounts of the desired mRNA are present **No band**: the desired mRNA is not present	**For identification and qualitative purposes,** not quantitative. **How it works**: Reverse Transcriptase is added, converting desired mRNA into cDNA (which will eventually be double stranded, but missing UTRs such as introns). cDNA can then be run through PCR. **Reverse Transcriptase:** Reads mRNA and forms DNA. Sometimes used **Quantitatively** via **qRT-PCR.**
cDNA Libraries	**Identification:** Can identify if a specific mRNA is present. **Qualitative:** Can determine which genes are active in a certain tissue, and therefore their function.	Collection of cDNA is created utilizing Reverse Transcriptase of the genes present in a certain tissue at that time.	Allows us to understand **what genes are active and present in a cell at different times** and in different tissues.
FISH	**Identification:** Identifies whether a specific DNA or RNA sequence is present.	DNA or RNA sequences of interest, when present, will bind to a probe.	**How it works:** Probe carrying a single-stranded complementary sequence (fluorescently labeled) to desired DNA or RNA binds to those sequences via hybridization (complementary strands binding).
Sanger Sequencing	**Qualitative:** Identifies the sequence of a specific strand of DNA.	Resulting Gel Electrophoresis is read from **bottom up (5' to 3' direction)** to determine the sequence of the DNA.	**ddNTPs:** Di-Deoxy Nucleoside Triphosphates, missing the 3' hydroxyl required for polymerizing/extending DNA strands. **How it works:** ddNTPs for each base are added during replication of a desired strand, causing the stoppage of polymerization at random points. These strands of different lengths are added to Gel Electrophoresis, where the sequence can be understood by reading the gel bottom up (5' to 3' direction).
In Vitro Mutagenesis	**Qualitative**: Identifies the functioning of a gene.	Random mutations are introduced into a gene to see how the functioning of the gene changes.	None.
RFLP	**Identification:** Identifies mutations or polymorphisms	If DNA fragments, cut by restriction enzymes, are different lengths than expected, mutations or polymorphisms are present.	Often used for **genetic fingerprinting or paternity testing** to compare DNA sequences to each other.

Protein Lab Techniques and Technology

Name	Goal	Results	Other Important Notes
Native PAGE	**Qualitative:** Separates proteins on the basis of either size, shape, or charge	**For size comparisons**: lightest proteins travel the furthest down the gel, heaviest stay near the top. **For charge comparisons**: cationic proteins → negative terminal (cathode, high pH), anionic proteins → positive terminal (anode, low pH)	**Does not use a reducing agent or SDS**, so proteins remain intact, folded, and with their natural charge. **Gel Used**: Polyacrylamide (PA) is used for proteins in gel electrophoresis because it has smaller pores, which are more accurate for proteins (DNA is significantly larger than proteins so we use agarose for DNA). • Smaller Nucleic Acids can be used in PAGE but that is much more rare (the results are interpreted the same). **Reasons Used**: When we want to understand the properties of a protein in its natural, unaltered structure, and potentially still study the functioning of the protein after PAGE analysis. Smaller DNA/RNA *can* be used in PAGE, but it's uncommon and results are not interpreted any differently.

Non-reducing SDS Page	**Qualitative**: Separates proteins (and their subunits) on the basis of their weight. In quaternary structure, only non-covalent interactions are disrupted.	For example, a tripeptide (3 subunits): **If there are only non-covalent quaternary interactions:** All 3 subunits will separate and run as individual, smaller weight proteins **If there are any quaternary disulfide bonds:** The 3 subunits will still remain intact and will run as one larger weight protein.	**SDS**: Sodium Dodecyl Sulfate, added to proteins to coat them with a *uniform negative charge* and breaks all *quaternary non-covalent interactions*. Does not break quaternary covalent interactions (disulfide bonds).
			Non-reducing: No reducing agent was added, so all quaternary covalent interactions (disulfide bonds) will remain intact.
			Homo-: Prefix stating that the subunits of a protein are identical and therefore have the same mass.
			Hetero-: Prefix stating that the subunits of a protein are different and therefore have different masses.
			Example:
			• Protein A (heterotrimer, subunits with weights of 10 kDa, 20kDa, and 30kDa with both covalent and non-covalent quaternary interactions)
			  • Will not separate (quaternary covalent interactions remain intact) and will run as a single 60kDa protein.
			• Protein B (Heterodimer, subunits with weights of 20 kDa and 40 kDa with only non-covalent quaternary interactions)
			  • Subunits will separate and run as a 20 kDa protein and a 40 kDa protein as two distinct bands.
			• Protein C (Homodimer, subunits both weigh 30kDa with only non-covalent quaternary interactions)
			  • Subunits will separate and run as 30 kDa proteins as one (lighter in weight) band.

Reducing SDS PAGE	**Qualitative**: Separates proteins (and their subunits) on the basis of their weight, breaking all quaternary interactions and separating all subunits into individual proteins.	**Heavier subunits**: do not migrate as far, stay near the top. **Lighter subunits**: migrate further down the gel towards the bottom.	**SDS** will still coat the proteins with a uniform negative charge as well as disrupt non-covalent quaternary interactions. **Reducing Agent** that's added will disrupt any quaternary covalent (disulfide bonds) interactions. **Since every quaternary interaction is broken,** all proteins will run as their respective subunits. **Homomers** (identical subunits) will appear as **one individual band** (since the separated subunits all weigh the same). **Heteromers** (different subunits) will appear as **separate/distinct bands** (since the separated subunits all weigh different).
Isoelectric Focusing	**Qualitative**: Separates proteins on the basis of their charge (specifically their isoelectric point, pI)	**Proteins stop migrating at their pI**; **Cationic proteins** → negative terminal (cathode, low pH), **Anionic proteins** → positive terminal (anode, high pH)	Very similar to how Native PAGE separates on the basis of charge, but **IF *only* separates on the basis of charge** and specifically is **used to find the isoelectric point (pI)** of a specific protein or amino acid. **Isoelectric Point (pI):** the pH of which, on average, a protein or amino acid is *uncharged*. **pI of Acidic Amino Acids:** $(pK_{A,\ Carboxyl\ Group} + pK_{A,\ R\text{-}Group}) / 2$ **pI of Basic Amino Acids:** $(pK_{A,\ Amino\ Group} + pK_{A,\ R\text{-}Group}) / 2$
Western Blotting	**Identification:** Identifies whether or not a protein of interest is present.	**If the protein is present**, a **band at the expected weight** (of that protein) will **appear**.	**Utilizes SDS PAGE** to separate the proteins based on weight. **Utilizes Chemiluminescence** to visualize the protein of interest.
ELISA	**Quantitative**: Identifies the concentration of an antigen/antibody (proteins) of interest.	Color changes caused by antibody-antigen interactions (of interest) are measured via their absorbance, **higher absorbance = higher concentration**.	**Indirect ELISA:** Detects specific antibody or antigen concentrations of a sample. **Sandwich ELISA:** Detects specific antigen concentrations of a sample. **How it works:** Both types are similar, an antibody will bind to a target, followed by a labeled secondary antibody binding to that antibody for detection (and concentration measuring).
Radio-immunoassay	**Quantitative:** Identifies the concentration of a protein of interest.	Antibody that binds the protein of interest is added, antigen is stained with iodine, decrease in radioactivity = increased protein concentration.	Very similar to ELISA, but can **also identify more than just proteins,** including **drugs** or **steroid hormones**.

Immuno-precipitation	**Identification and Qualitative:** Purifies a protein of interest from a solution of proteins.	Protein of interest will be **bound to a bead-bound antibody**.	Every other protein that *cannot* bind the antibody will be poured off/removed. Used to study protein-protein interactions.
Immuno-histochemistry	**Qualitative:** Identifies protein expression during specific times within tissues to determine the protein's function.	Dyes or tags reveal the location of protein of interest so it's functioning within the tissue can be determined.	**Similar to FISH** just for a **protein** of interest *instead* of DNA/RNA of interest.
Bradford Quantification	**Quantitative**: Measures the concentration of proteins in a sample.	Higher protein concentration = stronger blue color	**Coomassie Blue** dye is added to the sample and **binds to proteins,** the stronger the blue, the more protein present.
Edman Degradation	**Qualitative**: Identifies the primary sequence of a protein.	**N-term amino acids** are cleaved one at a time and identified to determine sequence.	Has the same goal as Sanger Sequencing, just for proteins instead of DNA.
Ramachandran Plot	**Qualitative**: Determines the secondary structure of a protein.	**Top Left Quadrant**: β-Sheets present **Top Right Quadrant**: Left-Handed α-helices present **Bottom Left Quadrant**: Right-Handed α-Helices present	**Deviations** from these regions *can* demonstrate the secondary structure is **unstable or unfavorable**. **Glycine** is more flexible which causes deviations in locations of alpha helices.

Carbohydrate Lab Techniques

Name	Goal	Results	Other Important Notes
Tollen's Test	Detects **reducing** sugars	**Reducing Sugar Present**: Ag^+ is reduced by the sugar into Ag(s) forming a "silver mirror"	**Reducing Sugar**: A sugar that, in ring structure, contains a hydroxyl group (-OH) on the anomeric carbon (a hemiacetal). **Aldose**: A sugar that contains an aldehyde at the anomeric carbon. **Ketose**: A sugar that contains a ketone at the anomeric carbon. • Tollen's can **indirectly detect reducing ketose (anomeric hemiketal) presence.**
Benedict's Test	Detects **reducing** sugars	**Reducing Sugar Present**: Cu^{2+} is reduced to Cu^+ which precipitates as a red precipitate.	**Color shift** from blue → red means that reducing sugars were present. Benedict's directly detects reducing aldoses and indirectly detects reducing ketoses.
Fehling's Test	Detects **reducing** sugars	**Same as Benedict's**	**Very similar to Benedict's Test**, but uses tartrate instead of citrate and leads to a less stable solution (and is used less often).

Other Biological Lab Techniques

Name	Goal	Results	Other Important Notes
Gram Stains	**Qualitative**: Determines whether or not bacteria is Gram Negative or Positive	**Purple** Color = Gram **Positive** Pink Color = Gram Negative	**Periplasm**: region between the cell wall and membrane that retains the dye. **Gram Positive**: Contain a single **thick** peptidoglycan cell wall that traps the purple stain. Only have **one cell membrane**. **Gram Negative**: Contain a single **thin** peptidoglycan cell wall that *doesn't* trap the purple stain upon washing, so a pink stain is added for visualization. Have an **inner and outer cell membrane**, and contain **endotoxins** (like LPS).
Flow Cytometry	**Quantitative**: Identifies cell size and count	Specific cell proteins are stained for visualization.	Allows for the sorting of different types of cells.

Other Lab Technique Relevant Terms to Know

Term	Definition
Reporter	Any measurable signal (such as color, fluorescence, radioactivity, etc.) that can be used to determine if a molecule is present or an event has occurred, such as gene expression, antibody binding, etc.
Primary Antibody	The antibody that binds directly to the target molecule (commonly an antigen or protein).
Secondary Antibody	An antibody that has a reporter attached that binds to the primary antibody.
Supernatant	The liquid that remains above a pellet/bead after centrifugation.
In Vitro	Anything done outside of a living organism, commonly in a petri dish or test tube. Artificial.
In Vivo	Anything done inside of a living organism, like drug tests. Natural.
RNAi	Natural cellular process where siRNA or miRNA silence gene expression by binding to and causing the degradation of mRNA.
Primer	A short strand of RNA that is added to a strand of DNA that allows the binding of a polymerase for DNA replication.

Study Design

Subject	Terms	Definition	Example
Variables	Independent	A variable that is manipulated to see its effect on the dependent variable.	When studying an antidepressant: **Independent**: the dosage of the drug **Dependent**: the level of depressive symptoms after drug treatment **Confounding**: Sleep quality, which can influence how well the drug works, distorting the results. **Mediating**: Serotonin levels, since the drug causes an increase in serotonin which leads to a decrease in depressive symptoms. **Moderating**: Genetic predispositions, since certain people may be more or less likely to respond well to the treatment or serotonin level changes.
	Dependent	A variable that is measured in response to the changing independent variable, the outcome/effect we are studying.	
	Confounding	An external variable that distorts the relationship between the independent and dependent variables.	
	Mediating	A variable that helps explain the relationship between the independent and dependent variables.	
	Moderating	A variable that either changes the strength or direction of the relationship between the independent and dependent variables.	
Groups	Control Group	The group that *doesn't* receive a treatment for comparison purposes.	When testing whether a new drug lowers blood pressure: **The control group** would not be exposed to the drug and BP would be measured. **The experimental group** would receive the drug and have their BP compared to the Control.
	Experimental Group	The group that receives a treatment that is being studied.	
Negative Controls	Negative Control	Any control group where the treatment is withheld in any way.	See the BP experiment described above.
	Vehicular Control	A type of negative control where the procedural steps are kept the same between the control and experimental group, but the negative control group receives an inert treatment.	When determining the efficacy of a vaccine: **The vehicular control group** would receive a shot that contains saline (salt-water). **The experimental group** would receive a shot that contains the vaccine.

	Placebo	A type of negative control where the control group is given an inert treatment designed to control for psychological effects of the treatment.	When determining the efficacy of a painkiller: **The placebo control group** would receive a pill that only contains sugar. **The experimental group** would receive a pill that contains the painkiller.
Positive Controls	Positive Control	A type of control group where an effective treatment is given with an already understood response to ensure proper functioning of the test.	When determining if a drug kills bacteria: **Negative control group** doesn't receive any antibiotics. **Positive control group** receives a previously understood antibiotic to ensure the bacteria can be killed by an effective drug. **Experimental group** receives the new antibiotic to see if the bacteria is resistant or not to it.
Blinds	Single Blind	When only the participants are *unaware* of which group (control vs experimental) they are in to mitigate participant bias.	When determining if a new antidepressant is effective: **Control group** receives a placebo. **Experimental group** receives the antidepressant. **Single Blind** study would mean the participants don't know if they received the placebo or antidepressant. **Double Blind** study would mean neither the participants or observers are aware of which group each participant is in.
	Double Blind	When both the participants *and* the experimenter observers are *unaware* of which group the subjects are in to mitigate both participant and researcher biases.	
Conclusions	Correlation	When two variables change at the same rate, only having a mathematical relationship. Positive correlation: R = 1, Negative correlation: R = -1, no correlation: R = 0.	When studying people at the beach: If both the number of sunburns and amount of ice cream consumed both increase, that is a ***correlation***. If the number of sunburns and time spent under the sun both increase, that is a ***causation***.
	Causation	When the altering of one variable *causes* a proportional change in the other variable.	
Mathematical Study	Potentiation	The factor or degree with which a variable changed, determining how significantly the variable was changed.	If the treatment of drug X causes protein concentrations of Protein A to increase from 0.1M to 0.5M, the **potentiation factor is 5**. If the same treatment causes [Protein B] to increase from 0.001M to 0.2M, the **potentiation factor is 200**. There was a **more significant change in Protein B**, despite having a lower final concentration.
	Mean	The average.	For the following set of numbers: 1, 1, 2, 3, 5, 8, 13 **Mean** = 4.7 **Median** = 3
	Median	The middle number in a list of numbers.	
	Statistical Significance	The odds (P-value) that the results of an experiment are due to chance, rather than the variable causing some actual effect. P-value is most commonly 0.05.	When studying how a drug can lower BP: A p-value of 0.02 (which is less than 0.05) causes the data of the hypothesis to be accepted as "Statistically Significant".
	Confidence Interval	A range of values that we are *confident* the true value lies within, typically within 95% confidence.	You may find that Ozempic causes, on average (the mean), 7 pounds of weight loss. But to account for some error, we'd say that we are 95% confident that the true mean weight loss falls somewhere between 6-8 pounds.
	Error Bars	Graphical representations of the variability or uncertainty of data. If the error bars of two values overlap, the difference between the two is *not* statistically significant (treat them as the same).	If a data point has an error bar that extends from 0.4 to 0.6, and another data point has an error bar that extends from 0.55 to 0.75, their error bars overlap, and therefore we cannot say that they are different values and we treat them as if they were the same result.
Validity	Internal Validity	Whether the results of the study conducted are due to the variables being studied and *not* due to confounding variables.	If a drug that successfully lowers blood pressure is found to have no confounding variables, that means that the drug truly does directly cause the lowering of BP and has **high internal validity**.
	External Validity	Whether the results of the study can be generalized to the population in which it aims to study.	If a drug is only tested on 25-year-old males, it would have ***low*** **external validity** to the entire population of humans.
Errors	Type I Error	False-Positive, where you conclude that there is an effect when there truly isn't.	Claiming that a vitamin improves memory when in reality it does not.
	Type II Error	False-Negative, where you conclude that there is no effect when there truly is one.	Finding that a new cancer drug doesn't properly treat that cancer, when in reality it does.