

Laboratory of Bioinformatics 1

Saul Pierotti

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Course organization

- Lab1 in the first (Lab1a) and second semester are actually separate courses
- In february there is a 1 week intensive course run by professor Allegravia, which is part of Lab1a
 - It is about protein-protein interaction
 - We will have an exam also for this part
- There will be a written test on 09/01/20
- We have to write a report for 10/01/20 or 22/01/20
 - If we submit for the first deadline we will have feedback
- The oral defence will be in the last week of January
 - Probably it will be 29-31/01/20

Introduction

- Hydrogens bond are mainly located at the level of the backbone
- The reference source in the field is the Journal of Bioinformatics
- Functional annotation is the core of this course
- Functional annotation studies the relationship between structure and function
- Functional annotation requires data collection, storage and analysis
- Functional annotation is the activity of attributing structural and functional features to translated protein sequences
- Before starting data analysis, be sure of the quality of your data (!)
- A database must be implemented, curated and mined
- Database curation refers to updating the data and to keeping them compliant with the database standard
- A database release is its content at a given date
- Data mining is the retrieval of information from a database
 - It is done with a browser
- In Hamburg there is an EMBL facility that uses X-rays in a flow cytometer

Random

- Affinity among molecules comes from the electron densities
- The biological unit of a structure can be retrieved from PDBsum

X-ray cristallography

- I can understand that I have a protein crystal by shining light on it and seeing how it diffracts
- Routinely X-ray diffraction is not able to locate hydrogens
- Each crystal has a unit cell

- Electron density is the result of data analysis on diffraction maps
- The main crystallographic techniques are NMR and X-rays
- X-rays are used because they have a wavelength comparable to an atomic bond, and therefore they can resolve with that level of detail
- X-ray sources used for studying protein structure are rotating anode tubes or synchrotrons
- In the rotating anode tube electrons are accelerated towards the anode in a vacuum
 - The anode rotates, so to expose a different portion to the electron beam at each moment and avoid damage
 - X-rays are released when the electrons collide with the anode, as a way to get rid of their kinetic energy
 - Only 1% of the kinetic energy is converted to photons, the rest heats up the anode
- Synchrotron source give an anisotropic beam, which gives semicircles in the diffraction map instead of focused spot
 - They are located in the US, Europe or Japan
 - X-rays are produced by charged particles moving in a magnetic field
- In order to have a diffraction pattern you need to have interference between the diffracted beams
- Bragg diffraction law: $2d \cdot \sin \theta = n\lambda$
 - When the same beam is reflected by 2 planes, the part which is reflected by the lower plane travels for a longer distance
 - The distance is exactly $2d \cdot \sin \theta$, where θ is the angle of incidence and d is the distance between the planes
 - If this distance is equal to n wavelengths, we observe reflection because of interference
 - By knowing all the terms except d , I can derive the minimal distance between the diffraction planes
- A typical diffraction map is organized with 3 coordinates (H, K, L) and an intensity dimension (I)
 - The intensity is proportional to the amplitude, therefore to the amount of constructive interference
 - The 3 coordinates reflect the facts that we are operating in 3 dimensions
 - I can recover the electron densities from the diffraction pattern with the Fourier transform
 - * It is a computation-heavy task
- I cannot recover the phase from the diffraction map
 - In a synchrotron, I can recover the phase of the wave with the anisotropy approach
- Once I have the electron density, I need to fit my molecule in it to determine the conformation
 - This is easier if my electron density has a high resolution
 - I can take advantage of similar proteins with a similar structure to do the fitting
 - This fitting procedure is called refinement, because it reduces noise in the model
- To validate my model, I compute the diffraction pattern of the theoretical protein structure to check if it matches the experimental pattern within a reasonable tolerance

Cryo-electron microscopy

- Cryo-electron microscopy gives us a diffraction pattern using an electron beam
- It is really useful for really big complexes that cannot be crystallized
- Resolution is lower than X-ray diffraction
- It allowed to obtain the structure of entire ribosomes
- It cannot be used with small proteins that cannot withstand the electron bombardment
- It is possible to capture the protein in different conformations, and so understand how it works
 - It was used by Rubinstein to obtain a movie of V-ATPase (!)
- It is really costly, around 6000€/day

Nuclear magnetic resonance

- It does not require the crystal, it is performed in a homogeneous really concentrated protein solution
- The frequencies used are on the radiowave length, so really low energies

- NMR measures contacts among atoms in solution, it measure frequency changes when nuclei come close to each other
- The data produced is a contact map
- The only nuclei considered are mainly O, H, C
- From NMR I get many conformation for each molecule, and if I visualize it in a molecular visualization software I see many superimposed structures
 - The core is usually stable and in agreement with X-ray data, while regions with high temperature factor have many configurations
 - From the many structures I can recover a consensus structure

Time resolved X-ray crystallography

- I use pulsed X-ray instead of a continuous beam
- I can observe the conformational changes of the protein between different pulses

PDB and other DBs and tools

- The PDB file does not contain the electron density, it is an approximation of the structure
- The resolution of an X-ray diffraction is important
 - 5.0Å resolution is reasonably accurate only for the position of the backbone
 - 1.5Å can be generally trusted, also for drug design
- A ligand in PDB is any molecule co-crystallized with the macromolecule considered
- Signal peptides are 10 to 30 residues in length
 - They are usually cleaved and therefore they do not appear in the protein 3d structure
- A PDB file has a unique identifier of 4 letters and numbers
- On PDB I can also find the FASTA file for the protein
 - FASTA contains the covalent structure (i.e the sequence) of the protein
 - FASTA has 60 residues per line
 - It is the sequence derived from the structure, it can be different than the one in uniprot (!)
- Coverage refers to the percentage of protein sequences covered in the protein structure
- PDB files produced using a synchrotron source have 2 spots associated with every atom
- For each ATOM we have the xyz coordinates, the occupancy, and temperature factor
 - Occupancy is how well the atom fits the electron density
 - The temperature factor refers to the mobility of the position
- The PDB file contains the atomic model of a macromolecule
- The CPK colorscheme is a popular set of colors used for the different atoms
- The structure validation window reports the percentile rank of different validation methods
 - Blue is good, red is bad
- DSSP is a program that reads a PDB file and assigns a secondary structure to each PDB coordinate
 - It was made by Sanders, one of the founders of bioinformatics, and Kabsch
- A database can be defined by its statistics
- Data in a DB can be distributed in categories that are relevant for the interpretation of data
- The space group refers to the symmetries of the unit cell
- The Ramachandran plot of a structure can be generated with Procheck (EMBL)
 - It is much more informative than the 3d view generated with 17Rasmol
- Some PDB statistics
 - 158180 macromolecular structures
 - 76380 enzymes
 - 48974 distinct protein sequences
 - Resolution range from < 1Å to > 4.6Å, with a peak around 2Å
 - * Distribution not normal with a long right tail
 - 1702 source organisms

PDBsum

- It is a pictorial database that provides an at-a-glance overview of the contents of each 3D structure deposited in the Protein Data Bank
- It is hosted by EMBL-EBI
- It shows also the Procheck/Procheck NMR Ramachadran plot for the structure
- It shows the biological unit instead of the unit cell

PDB101

- A crystal is composed of the unit cell, that is translationally repeated in the crystal
- The unit cell is composed of asymmetric units, that rotated and translated form the unit cell
- The asymmetric unit is the unique part of the crystal structure
- The biological assembly is the biologically relevant form
- Occupancy of an atom is the fraction of times that atom is in the specified position in the crystal
 - The occupancies for an atom always sum to 1, giving the possible alternate conformations
- The R-value is the fit between the theoretical diffraction pattern of the model and the experimental one
 - 0 is a perfect fit, 0.63 is a the fit of a random diffraction pattern
- R-free is another statistic that avoids the bias introduced in the refinement step

Ramachadran plot

- α carbons in proteins are 3.8Å apart
- The ϕ angle is the dihedral angle between N-C α , ψ is between C α -COOH
- The Ramachadran plot graphs the ϕ angle of a residue against its ψ angle
- Some regions of the plot are really common and allowed, some are not because of steric hindrance
- The Ramachadran plot of a protein is a scatterplot of its dihedral angles superimposed on a color code for the allowed conformational spaces
- Procheck and Procheck NMR calculate Ramachadran plots from PDB files

Protein structural alignment

- Rigid superimposition requires the knowledge of at least 3 non-allineated equivalent residues, while structural alignment requires no previous knowledge of equivalent positions
- The output of a structural alignment is a set of superimposed 3D coordinates, one for each input structure
- A structural alignment implies a corresponding sequence alignment, from which we can calculate sequence identity and similarity
 - Sequence similarity is meaningful only with an underlying structural similarity
 - Sequence identity is a score between 0 and 1 that gives the number of corresponding residues after the alignment
 - Sequence similarity is a score between 0 and 1 that gives the number of similar residues after the alignment
 - Residues are considered similar if they belong to the same chemical class (polar, non polar, cationic, anionic,...)
 - Structure is conserved more than sequence (!)
- Generally, I keep 1 protein fix as a template, and I try to superimpose the other backbone onto it, allowing the introduction of gaps
- There are many different algorithms to do structural alignment
- The reduce representation of a protein contains only the C – C α – N elements of the backbone
 - Structural allignemnt usually only considers the position of the backbone, so it works on the reduced representation of the protein

- After the alignment, it is possible to derive various measures of structural similarity
 - The simplest metric is the root mean squared deviation (RMSD) among atomic coordinates
 - The raw score can be normalized by subtracting the mean and dividing by the standard deviation, so to get the z-score
- One of the most famous structural alignment algorithms is jCE (Java Combinatorial Extension), written by Philippe Bourne, the director of the PDB
 - It is one of the best-performing algorithms
 - It breaks down the proteins in fragments, and it tries to align the structure of these by several methods (RMSD, secondary structure, ...)
 - It forms a series of aligned fragment pairs (AFPs) and filters them, retaining only those that respect a given measure of local similarity
 - It generates an optimal path among AFPs, that yields the final alignment
 - The first AFP that nucleates the alignment can occur at any position
 - The size of AFP and the maximum allowed gap are parameters, usually set to heuristic optimal values
 - An important drawback is that it does not deal well with flexible regions that can have different conformations, since it is based on rigid superimposition
- FATCAT is another algorithm that deals better with flexible regions, but can also give spurious alignments among unrelated regions
- Many algorithms cannot recognize structural similarities that are not sequence order dependent
- Triangle Match deals with sequence order independent relationships
- The length of an alignment is the length of the protein sequence, plus the gaps introduced
- In the PDB, all possible pairwise structural alignments are pre-calculated and stored in xml files
 - The database is updated weekly
- When aligning structures, it is better to use structures taken with the same method

Protein structural classification

- A protein family is the set of proteins that perform the same function in different organism, and therefore share a similar structure
- Protein families were discovered by M. Dayhoff
- Multiple structural alignment allows to define protein families
- We know around 14000 protein families
- Multiple alignments are the result of repeated pairwise alignments
- We are doing multiple alignments in order to build a sequence profile
- A sequence profile is a matrix with residues in the y axis and the position in the alignment in the x axis
 - It is a compressed way to describe a consensus sequence
- A protein family is a set of proteins characterised by structural superimposition
- Protein families are important because they allow us to cluster PDB data
 - They are constructed starting by comparing proteins with the same function
 - It can be then computationally described with structural alignment
 - A protein family is described with an HMM (hidden markov model)
 - Hidden Markov Models are also called Pfam domains
- Proteins in the same family can also be really different in sequence, but their structure is really similar
- We cannot detect sequence similarity when under 30%, but we can detect structure similarity in those cases
 - Under 30% the result of a sequence alignment is not statistically significant
- Pfam categorizes all the entries in the PDB in protein families, clustering for structural similarity
 - The Pfam database was built by performing pairwise comparison of all the PDB entries
 - A protein family is described by a Hidden Markov Model (HMM)
- A superfamily is a set of protein families with different foldings that can perform the same function
- A protein domain coincides with the folded protein for small globular proteins (150 aa)
- When the PDB grew, we realised that multi-domain proteins share domains with small globular proteins

- SCOP categorizes proteins in superfamilies, Pfam families and fold
- The SCOP fold can be all alpha, all beta, alpha+beta, alpha/beta, small proteins
 - Alpha+beta has distinct alpha and beta regions
 - Alpha/beta has mixed alpha-beta structures
- Proteins in the same family have clear common evolutionary origin, and usually have >30% sequence identity
- Proteins in the same superfamily have low sequence identity, but common structural and functional features suggest evolutionary relationships
- Proteins are said to have the same fold if they have the same secondary structures in the same arrangement and with the same topology
 - If 2 proteins have the same fold they do not need to be evolutionary related: it can be a case of converging evolution

Sequence alignment

- It is our only way to compare proteins for which I do not have structures
- A sequence alignment is a continuous stretch of residues of any length
- Sequence comparison can be pairwise or database search
- Database search is an extension of pairwise sequence alignment
- Sequence alignment can be local or global
- A global alignment optimizes pairing over the whole sequences by introducing gaps
 - A global alignment has a length that is at least as long as the longest sequence
- A local alignment stops the alignment if continuing it makes its score lower
 - From a pairwise comparison, I can get many local alignments
- A metric is a set of rules that allow us to define the distance between strings
- The Hamming distance is, for a pair of sequences equal in length, the number of mismatching positions
 - It is used for ungapped alignments
- The Levenshtein or edit distance of 2 strings is the minimal number of edits necessary to change 1 string into the other
 - It is suitable for gapped alignments
 - An edit operation is defined as deletion, insertion or alteration of a single character
- A scoring scheme is a measure of sequence similarity
 - It is a substitution matrix where each possible substitution has a score
 - The matrix is symmetric, so it is often reported only half of it
- Sequence alignment algorithms seek to maximize a scoring function or minimize a dissimilarity measure
- For nucleic acids, there are substitution matrices that only consider match vs mismatch, and matrices that give different scores to transitions and transversions
- For aminoacids, we have the PAM and BLOSUM matrices, and matrices derived from structure alignment
- The PAM matrices were developed by M. Dayhoff and are based on the observed frequencies of mutation of 1 aa into another in aligned proteins of the same family
 - 1 PAM is 1% accept mutation, so 2 sequences 1 PAM apart have 99% sequence identity
 - The matrices were built using closely related sequences 1 PAM apart, so that multiple substitutions were unlikely
- The PAM1 matrix was built by collecting statistics on substitution frequencies in pairwise comparison of sequences 1 PAM apart and correcting for relative aminoacid abundance
 - The score of the mutation $i \rightarrow j$ is the log-odd of the mutation
 - $S = \log \frac{p(i,j)}{p(i)*p(j)}$
 - $p(i,j)$ is the observed $i \rightarrow j$ mutation rate while $p(i)$ and $p(j)$ are the relative aminoacid abundances
 - Note that $p(i)*p(j)$ is the expected mutation rate if all mutations are equally likely, it is a correction factor for aminoacid frequencies
 - Since the score is a really small number, it is usually multiplied by 10
- Other PAM matrices are built as powers of PAM1

- PAM250 is used for comparing sequences with 20% identity
- Conservation is always positively score, but with different scores depending on aa abundance
- The BLOSUM are a family of matrices that also use the log-odds for the substitutions
 - They were produced in the 1990, where there were many more sequences available
 - They are based on ungapped multiple alignments in short regions of related sequences
 - The different matrices were built using alignments with different thresholds of sequence identity
 - Lower matrices are more permissive since are built with sequences that have less than a threshold of sequence identity
- A dotplot is a plot that gives an overview of the similarity between 2 sequences
 - It is also based on scoring schemes
 - Dotlet is a Java tool for dotplot analysis
 - It is useful for finding repeated portions and for finding intron-exon boundaries
- Dynamic programming optimizes the solution of subproblems in order to find a global solution
 - It gives the correct solution provided that all the subproblems are independent, but it is computationally expensive
- Dynamic programming approaches are Needleman-Wunsch (global) and Smith-Waterman (local)
- Global alignment methods (NW) optimize the alignment over the whole sequence, and can include low-similarity regions
- Local alignment methods (SW) can yield multiple alignments from a single comparison
 - Low similarity regions do not affect the alignment score
 - Local alignment is preferred in DB searches
- For database searches, we use methods based on words (K-tuples), also called heuristic
 - Heuristic means approximate, it does not give an optimal solution
 - It also means empirical, not based on theory
- BLAST is an heuristic local alignment method used for database search
 - Originally described by Altschull in 1990 in J. Mol. Bio.
 - It is 1 order of magnitude faster than other heuristic methods
- FASTA is another heuristic algorithm but is no longer used
- An heuristic method is optimized for the expected result, therefore it does not have any intrinsic validity
- An expected result is the result of experimental approaches, which is well accepted in the scientific community
 - It is high quality data
- A heuristic method is not based on theory, while QED is firmly based on theoretical ground
- Whatever is heuristic is at the core data-driven
- In BLAST I chop the query in K-tuples and make a list of words, that I use to scan the DB
 - Word and k-tuples are the same thing
 - A k-tuple is an ordered set of k values
 - At this phase BLAST searches for exact matches of words in the list with DB entries
 - Any of these local alignments can form a maximal segment pair
 - A maximal segment pair (MSP) is defined as the highest scoring pair of identical segments chosen from 2 sequences
 - * It can be of any length, so to maximize the score
 - * It provides a measure of local similarity
 - In biology we care for all conserved regions, not only the best scoring one
 - * To take care of this, a segment pair is defined as locally MSP if its score cannot be improved by extending or shortening both segments
 - BLAST filters for all local MSP that score above a cutoff
 - I want to retrieve from a database all the sequences with MSP score above a cutoff T
 - The greatest advantage of MSP is that we have the mathematical tools to determine its statistical significance
- In BLAST, sequences that score far above the cutoff are almost definitely biologically relevant, while borderline matches can be evaluated considering the biological context
- The behaviour of BLAST can be tweaked with some parameters
 - I can search for exact matches or allow for gaps

- I can choose scoring matrix and gap penalty
- BLAST speeds up DB search by avoiding to spend time in sequences that are unlikely to give high MSP scores
 - Given a fixed word length w , BLAST seeks only segment pairs with a word of score at least T
 - When a match is found, BLAST tries to extend the segment to see if it reaches the desired final cutoff score S
 - The lower the value of T , the more probable that a segment of score $>S$ will contain a word with score $>T$
 - However, the lower the value of T the higher the number of hits, and therefore the execution time
 - Random simulations allowed to determine an optimal T value for various conditions
- The algorithm first makes a list of words that score $>T$ when compared with some word of the query
 - The time of list generation is linearly proportional to the length of the query
- BLAST then tries to extend the MSPs in both directions
- During the extension phase, if the score falls below a certain threshold below the score of the original MSP, it is discarded
 - It loses in accuracy, but in a negligible manner
- Theoretical results on the distribution of MSP scores of random sequences allow the following determination
 - Given a set of probabilities for the occurrence of each residue and a scoring matrix
 - The theory gives the parameters λ and K for evaluating the statistical significance of MSP scores
 - With 2 random sequences of length m and n , the probability of finding an MSP with score equal or better than S is $1 - e^{-y}$, with $y = K * m * n * e^{-\lambda S}$
 - In a similar way, we can calculate the probability of having c MSPs with score greater than S
 - This result is the p-value of the MSP score
- A sequence alignment method uses its algorithm and substitution matrices to give a result that maximizes the score of the alignment
- Sequence alignment methods are less stable than structural ones, more sensitive to length of the sequences and other variables
- The raw score of a sequence alignment is the sum over its length of the score for each match
 - It uses a score substitution matrix to determine the score of each match
 - It can be demonstrated that raw score follows an extreme value distribution
- The bit-score is the Log scaled version of the raw score
 - It is measured in bit, and it is a metric for the search space
 - Each unitary increase in bit score doubles the search space
 - A bit score of 30 means that we expect that score to be observed once in 2^{30} comparisons
 - It is used by BLAST and it uses a formula that is a bit complex
 - * $S' = \frac{\lambda S - \ln(K)}{\ln(2)}$
 - The bit-score S' depends on the parameters λ and K
 - The 2 parameters depend on the substitution matrix and on the gap penalty, and on the size of query and database
 - It is independent on the size of the search space (dimension of the database), because it corrects for it
- The E-value is a correction of the p-value for multiple testing
 - It is the expected number of matches of that score that I expect in a random database
 - It depends on K, λ and the size of the database
- MegaBLAST is an implementation of BLAST optimized for very long and very similar sequences, such as those differing only for sequencing errors
 - It uses a greedy algorithm
- PsiBLAST (position specific iterated)
 - It takes a single protein sequence as input, and compares it to a protein DB with a normal BLAST search
 - Given a threshold, it builds a multiple alignment with all the local alignments above the threshold
 - From the multiple alignment, a profile is built for any local alignment using the query as a base
 - The profile has the same length as the query

- The profile is used again for DB searches using a slight modification of the BLAST algorithm
- The statistical theory developed for BLAST is also valid in profile searches
- The algorithm then iterates the process by building another profile from the alignment of the new hits
- The process is repeated a fixed number of times, or until convergence

Distantly related homologs (30% sequence identity)

- Burkhard Rost is a professor in Munich who first published a graph showing the confidence in sequence alignment as sequence identity against number of residues aligned
 - In this graph, it marks the region where we are confident to have evolutionary relationships
 - The line is the best fit deriving from the data points of structural alignments of all the PDB structures
 - The region below the best fit is where I cannot be confident that the alignment reflects a structural relationship
 - The horizontal asymptote is around 30% sequence identity +/- something, so irrespective of sequence length, under 30% identity we cannot imply structural similarity
 - read paper!
- Also on a statistical standpoint, the alignment is not significant under 30% identity
- Sequence alignment methods are reliable and will give a similar result to structural alignment only when sequence identity is above 30%
- Distantly related homologs are proteins that have the same folding and perform the same function, but have a really different sequence
 - We cannot do sequence alignment with them (!)
 - We can use the multiple sequence alignment (derived from structure) and the HMM of a protein family to model them (!)
- We can have proteins that have the same domains but shuffled in a different order
 - In this case structural alignment is problematic
- Building by homology is the operation of (do)(next time)

Ramachandran plot

- A Ramachandran plot is a bidimensional map of a protein structure where the torsion angles of the backbone are reported
 - Don't say residues, they are in the backbone
- The expected values are determined by measuring torsion angles from a set of well characterized proteins
- The main regions are alpha (A), beta (B), 3-10 helices and left-handed helices (l)
- A good model has at least 90% of the residues in the most allowed regions
- The G factor, for the different angles, measures how unusual a structure is

Building by homology

- The goodness of a protein structure can be determined by comparison with a set of optimal conditions, determined by analysis of the PDB database
- The strongest interaction in proteins are H bonds
 - The electronegative atoms that participate in H bonds are O and N in proteins
 - The main source of H bonding interactions is the backbone
 - The length of an H bond is around 2Å between the 2 electronegative atoms
 - The bond can happen only if the atoms are in plane
 - The strength of an H bond is around 10 Kcal/mol
- Charge-charge particles are really dependent on the environment

- Lennard Jones interactions have an energy around 1 Kcal/mol
 - They are described by the 6-12 potential, since they have a repulsive term (R^{12}) and an attractive term (R^6)
- SS bonds have energy of 30-40 Kcal/mol and a length of 2Å
 - Their presence depends on the redox ambient potential
- A protein family is characterized by different sets of GEO terms
- Given an unknown sequence, I can align it to different protein families and eventually translate the GEO terms of the family to it
 - I cannot go below a threshold of 30% of sequence identity with the family template
- It is one of the main shortcut used for predicting the folding of a protein sequence
- If in my model I have even a small difference in the active site from that of the family, the GEO terms cannot be translated
- If we don't have the structure of the protein and we cannot assign it to a protein family, we don't know anything about it
- If we do have the structure, we can try to compute the function by programs of theoretical chemistry
- Pfam is a DB of protein families that should be used for those sequences that don't find a template in the PDB with sequence alignment
- Protein folding usually starts with seeds of alpha-helices that then elongate and promote the final folding
- We have 3 methods for computing protein structure
 - Building by homology
 - Threading
 - Ab initio
- Which method is better to use depends on the availability of structures that have a sequence identity over a threshold with my sequence
 - Above 30% I can use the concept of protein family (building by homology)
 - Below 30% I need to use threading, fold recognition, machine learning
 - If I have a new folding, I need ab initio or machine learning
- If I get a model, I can understand its validity by checking if it would be stable
- Comparative modelling is a procedure that, starting from a sequence
 - Selects a template by aligning (BLAST) against all the PDB structures
 - Once found a good template, I can use NW (global alignment) to improve my alignment with the target
 - I then use modeller for modelling my sequence on the template
 - The output of modeller is a PDB file containing the model
 - I check with Procheck the plausibility of my model
 - The goodness of my model depends on the goodness of the initial alignment
 - If I am not satisfied I align again and model again, until I am satisfied
- Threading procedures are based on the modelling of my sequence on different folds
 - In the PDB we have folds, that are self-stable and can be abstracted from the protein
 - The main difference among different folds is the secondary structure, hence the topology of my model
 - * In essence, the difference is in the pattern of H bonds
 - I have a scoring function that considers the stability of my model (H bonds, other interactions)
 - * I get a likelihood value for every model
 - I select the best model among the computed ones
 - Different models can better cover different portions of my sequence
- Ab initio minimizes the energy of the system by computing all the pairwise interactions
 - It is feasible only on small sequences
- There is a paper written by the author of the Rosetta method (Sanchez, 2000) that analysed the validity of the different methods
 - If my starting sequence identity is above 60% my model is good for docking and it is comparable to a low quality experimental structure
 - In the 60-30% range we have a rough idea of the organisation of the backbone

- Under 30% we can be lucky, or completely wrong
- The coverage of a local alignment is its length compared to the sequences
- How to select the best template
 - Highest sequence identity
 - Highest coverage
 - Highest template resolution

Exercise for the report

- In the report we can model as many sequences from the homework.txt file as we want, but the first one (B0JDP9) should be annotated in depth
- As a template we should use one that has a title, author (me), abstract
- The protein is a putative laccase from a boletus and it is really poorly annotated
 - Will we confirm this EC number?
- It comes from TrEMBL and it has evidence at the transcript level
- There are some GO terms, but they have been only annotated computationally
- There is a putative signal peptide
 - Should we carry it along in the computation?
 - In the PDB structures we do not have signal peptides
- We perform a BLASTp against the PDB
- What E-threshold do we choose?
 - If it is too low I tend to find very exact but local alignments, if it is too high non-significative matches
 - I do not use filters, I allow gaps and I want 50 hits
 - I leave the auto matrix
 - * It will use blosum62
 - Let start with 0.1
- In the report I would write
 - I used blastp 2.9.0+, E-value 0.1, matrix Auto against uniprotkb_pdb version...
 - In the materials and methods I should specify a reference for blast, the parameters used, the DB version used
- The score reported after BLAST is a bit-score
- I retrieved A0A3F2YLU5, with e-value 0.0 and 62.3% identity
 - There is a small portion missing at N terminal, maybe the signal peptide?
- The second hit (Q12718) is a Swissprot entry so we start from it
 - Identity 62.0%, e-value 0.0
 - Function: lignin degradation and detoxification of lignin derived products
 - * EC 1.10.3.2, curated *1. . . means ocydoreductase
 - This EC number is for a laccase, or urshiol oxidase
 - If I follow the link from the EC number, I go to Enzyme (Expasy)
 - There are cofactors: Cu cation, so there is a metal binding site
 - There are some publications: we should read them
 - It is a secreted protein, so I can expect SS bridges
 - There are many PTMs: SS bonds, glycosilation
 - Since there are glycosilations, I have many residues that have to be conserved for conserving structure
 - * All the glycosilations are N-linked on Asn
 - We have only 1 PDB structure: 1GYC
 - * It is an X-ray with 1.90Å resolution
 - * Crystal structure determination at room temperature of a laccase from trametes versicolor in its oxidised form containing a full complement of copper ions
 - Full complement means 4 Cu++ ions in this case
 - When we want information about an enzyme, we can look in BRENDA

- We should study the problem before attempting to solve it
- In the template we see that 3 Cu++ are in plane, while 1 is further apart
- Whatever we do in our model, the 3 coppers have to be in that exact distances, to the .1 digit
 - This architecture is a funneling system for extracting electrons from the substrate
- Biological motivations have to be included in the report
 - We shouldn't copy-paste, but read the articles and understand
- When a metal ion enters in the structure of a protein it needs to be stabilized by residues
 - Cu++ is most frequently stabilised by His
- The copper ions are numbered and are referred to with a type entry
 - The type refers to the spectrum of the ion
- I should write a table where I report whatever is relevant (position that have to be conserved)
- In the template
- The stabilization of Cu is given by the interaction of the Cu outermost cell with His side chain through the formation of coordination (covalent) bonds
 - Coordination bonds involve sharing 2 electrons
- Positions that need to be conserved (numbers of cu not correct)
 - His84->Cu1
 - His86->Cu2
 - His129->Cu2
 - His131->Cu3
 - His415->Cu4
 - His418->Cu1
 - His420->Cu3
 - His472->Cu3
 - His473->Cu4
 - His474->Cu2
 - His478->Cu4
- These positions are in uniprot, in PDB it is different because of the signal peptide
 - I can alligne with lalign the 2 sequences and see
- The His have to be in that position and they need to have the same torsion angles (χ angles)
 - The χ angle is the relative torsion angle between the lateral side chain and the backbone
- If in the active site the torsion angles are different, I cannot have a functional site
- In order to reduce an O2 molecule I need 4 electrons
- Electrons are funneled and this process is really dependent on the position of the metal ions
- In a redox reaction the acceptor has an higher redox potential of the donor
- Laccases are not so specific
- Before the paper, there was another crystal of a laccase but it was copper depleted
 - The fold was similar to this
 -
- Electrons flow from the lone Cu to the 3 Cu in plane
- In the abstract we need an excuse to justify why we are doing this activity
- There are residues of the gene sequence that do no match the structure
 - It can be sequencing errors, gene variants, due to the expression system
- The abstract should be a few lines
- Introduction can be a few sentences expanding what was said in the abstract
- Experimental procedure should follow the workflow that we did
 - The allignment, with all the parameters and references
 - A reference to modeller
- We should put a picture of the 3d structure
- We have 2 SS bridges to put as a constraint in the model
- The cluster of 4 Cu is called also T2/T3 cluster
 - The 3 Cu are type 3
 - The lone Cu is type 2
- There is a water funnel from the catalytic site to the solvent

- Aligning uniprot and pdb sequences with lalign, I see that the difference is in the signal peptide
 - 20 residues more in the uniprot So these are the PDB positions
 - Lone Cu
 - * Cys453.sg->Cu1(cu1503)
 - 2.19 Å
 - * His395.nd1->Cu1(cu1503)
 - 2.02 Å
 - * His458.nd1->Cu1(cu1503)
 - 2.04 Å
 - Cu triplet
 - * His66.nd1->Cu3(cu1500)
 - 2.15 Å
 - * His109.ne2->Cu3(cu1500)
 - 2.12 Å
 - * His454.ne2->Cu3(cu1500)
 - 2.17 Å
 - * His111->Cu2(cu1501)
 - 2.23 Å
 - * His400.ne2->Cu2(cu1501)
 - 2.12 Å
 - * His452.ne2->Cu2(cu1501)
 - 2.16 Å
 - * His64.ne2->Cu4(cu1502)
 - 2.01 Å
 - * His398.ne2->Cu4(cu1502)
 - 1.97 Å