

QNIDQPTEMTATEGAIVQINCTYQTSGFNGLFWYQQHAGEAPTFLSYNVLDGLEEKGRFSSFL
SKGYSYLLKELQMKDSASYLCAVMDSNYQLIWGAGTKLIIPDIQNPDPAVYQLRDSKSSDKS
LFTDFDSQTNVSQSFKSDSDVYITDKCVLDMRSMDFKNSAVAWSNKSDFACANAFNNSIIPEDT
PSPIAGITQAPTSQILAAGRRTLRCTQDMRHNAMEWYRQDLGLGLRLIHYSNTAGTTGKGEV
GYSVSRANTDDFPLTLASAVPSQTSVYFCASSEAGGNTGELFFGEGSRLTVLEDLKNVFPPEV
FEPSEAEISHTQKATLVCLATGFYPDHVELWWVNGKEVHSGVCTDPQPLKEQPALNDSRYAL
RLRVSATFWQNPRNHFRCQVQFYGLSENDEWTQDRAKPVTQIVSAEAWGRAMRTHSLRYFR
VSDPIHGVPFISVGVDHSHPITTYDSVTRQKEPRAPWMAENLAPDHWEERYTQLLRGWQQMF
ELKRLQRHYNHSGSHTYQRMIGCELLEDGSTTGFLQYAYDGQDFLIFNKDTLSWLAVDNVAHT
AWEANQHELLYQKNWLEEECIAWLKRFLEYGKDQLQRTEPPLVRVNRKETFPGBTALFCKAHG
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MQQWGRLLQTYREWHDPALNEAMWPARPEKQRTVSDYTTIPHSDVYGVSI FEPVGHIPDSVG
FYRLSHTRMARGWAEASVIQTVPKARDQTWEDNESLGYFQVQCRFHNRPNQWFTASVRLRS
AYRSDNLAPQEKLQPQDTCVGSHVEKGNVVWSLEVHDPYFGTALCVLTAKQTHSIEAESPEFV

TRain: T-cell Receptor Automated Immunoinformatics – User's Guide

Austin Seamann & Dario Ghersi



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<https://github.com/Aseamann/TRain>

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1 — Introduction

1.1 Overview of TRain

The TRain suite provides the accumulation and connection of several in-house and well cited bioinformatic tools to gain further utilization of T-cell receptor sequences and structures. TRain consists of five main components: input, modeling, pairing, docking, and analysis (see Figure 1.1). These components are interchangeable with different modeling and docking tools as the connection between each step is through common file types such as FASTA and PDB files. In the current state, TRain takes advantage of the Rosetta suite of programs found at <https://www.rosettacommons.org>.

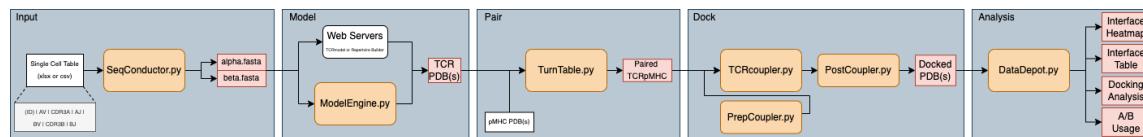


Figure 1.1: Flowchart for the TRain suite: General flow of TRain input to analysis. TRain takes input of single cell T-cell receptor sequencing data to produce full TCR sequences. Full TCR sequences are then submitted to modeling webserver of choice. Resulting PDB file containing TCR 3D structure then gets paired with a MHC and bound peptide to be docked. Docking is conducted with an automated pipeline of Rosetta programs. Resulting TCRpMHC complexes then can be further investigated with analytical tools.

1.2 TRain setup & availability

The code for TRain is available through GitHub at: <https://github.com/Aseemann/TRain>. TRain has several needed Python3 packages and other dependencies. To allow for the flexible of use of TRain , packages and dependencies are laid out for each step and in the quick start guide. Use of a package manager such as Conda (<https://www.anaconda.com/products/individual>) may be beneficial. With the reliance of several different dependencies, the instructions listed in each section may not be

all-inclusive. Thankfully there are lots of valuable resources to find solutions so if you run into an issue, Google away.

1.3 Input

TRain is capable of handling single cell T-cell receptor sequencing output from sources such as (company here). This introduces the first Python program SeqConductor. SeqConductor reads in either a xlsx or csv file containing TCR AV, AJ, BV, and BJ gene segments and CDR3 α and CDR3 β amino acid sequences. This constructs the amino acid sequences for the variable regions of each TCR.

The resulting variable region sequences can then be concatenated with a constant TCR region to produce a full TCR sequence. The primary goal of TRain is to gain further understanding of TCRpMHC interfaces. Thus, the constant region is not an extremely valuable portion but is needed for modeling purposes to avoid alignment errors. The full TCR sequences are then prepared to be passed to the following modeling step.

Resulting fasta files are produced and can either be submitted directly to the suggested modeling suites or automated in the Modeling step.

1.4 Modeling

Currently, four modeling pipelines are readily available through web servers to produce 3D structures of TCRs from submitted alpha and beta chain sequences. These four services being LYRA, TCRmodel1, Repertoire Builder, and TCRBuilder [GP18; Kla+15; Sch+19; 20]. TCRmodel1 has an advantage that it is also available as a local program through the Rosetta suite.

To increase the efficiency of submission to TCRmodel1, the next program, ModelEngine, can utilize multiple CPU cores to rapidly produce models. TCRmodel1 can be ran with either no loop refinement or with loop refinement, impacting the time it takes per model. ModelEngine manages submission and renaming of the resulting output from TCRmodel1.

1.5 Pairing

Resulting modeled TCRs become beneficial when you are able to analyze their theoretical biological function. To do this, the first step is pairing it with a potential antigen. Unlike antibodies, TCRs are specific to a peptide presenting structure known as the major histocompatibility complex (MHC), also known as human leukocyte antigen (HLA). As this tool is capable of analysis of TCRs non-exclusively to homo sapiens, the term MHC will be utilized.

The program TurnTable has several functions to easily pair TCR structure(s) to one or several pMHCs. First, TurnTable centers the TCR to coordinates 0,0,0 and zeroes out all three primary axes of inertia ensuring the interaction interface is pointing down with the alpha chain on the left and beta chain on the right. Then TurnTable positions the TCR's interface in-line but at a distance to the pMHC interface as needed according to the RosettaDock 4.0 input desires [Mar+18]. Along with repositioning the TCR and pMHC, TurnTable trims the TCR chains to just the variable region (if needed), removes the beta-2 microglobulin, and trims the MHC. This trimming process helps reduce run-time of docking steps in the next component of TRain. As a final step, TurnTable renames the resulting PDB's atoms and residues as desired by RosettaDock 4.0. This renaming can be corrected for in the PostCouper program.

1.6 Docking

TCRcoupler is where TCRs are docked to the paired pMHC antigen. TCRcoupler can be preformed on a single PDB file or a directory of PDB files. Following RosettaDock 4.0 procedure, flexible side chain and flexible back bone settings are allowed for the TCR chains [Mar+18]. However, less time-demanding but also less refined docking can be done with rigid settings [Cha+11]. In the guided examples in this manual, a lower number of docking permutations will be utilized but recommended numbers will be provided.

Resulting docked TCRpMHC complexes can be viewed using any protein visualization program. However, to make for better analysis, a few steps should be complete before continuing past docking. PostCoupler takes in resulting PDB files and cleans them of any residual information and most importantly, rematches the numbering of the native PDB files.

To determine the capabilities of this docking approach, crystal structures of TCRpMHC interactions can be "re-docked". To assist in this step, the program PrepCoupler can prepare a native crystal structure PDB to be submitted for comparison in the following analysis step.

1.7 Analysis

With complete crystal/modeled docked TCRpMHC structures DataDepot provides several analytical figures and tables to gain insight to the binding/non-binding interface. This step is not all encompassing of analytical features but can provide quick insight into the docked structures produced. Analysis can be done to look closely at a single interface or compare across several with different tools. All analysis steps are conducted using Python.

2 — Quick Start Guide

2.1 Installs

The code for TRain is available through GitHub at: <https://github.com/Aseemann/TRain>. Download or clone the latest version to your location of choice.

Using git command line:

```
1 git clone https://github.com/Aseemann/TRain
```

Pip installs:

```
1 pip install pandas
2 pip install openpyxl
3 pip3 install biopython
4 pip install scipy
5 pip install -U scikit-learn
6 pip install matplotlib
7 pip install seaborn
```

For modeling and docking, a local installation of Rosetta needs to be installed. For licensing details visit <https://www.rosettacommons.org/software/license-and-download>. Installation instructions can be found at https://new.rosettacommons.org/docs/latest/getting_started/Getting-Started and Rosetta should be built with MPI executables and instructions can be found at https://new.rosettacommons.org/docs/latest/build_documentation/Build-Documentation or follow instructions below. While there is the option to run without MPI, it is not recommended. For more instructions on how to run ModelEngine and for a list of command line options, see chapter 5. If MPI is not installed on the computer you can install using the following (apt installer):

```
1 # Linux
```

```

2 sudo apt install libopenmpi-dev
3 # Or visit: https://www.open-mpi.org/faq/?category=building
4
5 # MacOS
6 xcode-select --install
7 brew install openmpi
8 # Or visit: https://www-lb.open-mpi.org/software/ompi

```

Follow below for general build options of Rosetta for Linux and MacOS systems.

```

1 cd rosetta_src_xx/main/source
2 ./scons.py bin mode=release extras=mpi -j<number_of_processors_to_use>

```

2.2 Input

For our quick start we'll ensure each step is able to be ran. Assuming your working directory is "/TRain", the rest of the commands will direct you fully. The first step is to construct a full TCR protein sequence using the gene segments and CDR3 regions listed.

```

1 cd 01_Input
2 python3 SeqConductor.py Sample_Input/Test_Table_Single.xlsx -f -a

```

The files alpha.fasta and beta.fasta should appear in your working directory. The contents should be identical to the fasta files location in "01_Input/Sample_Output/Quick_Start/" and "02_Model/Sample_Input/Quick_Start/".

2.3 Model

Now we can submit our fasta files for modeling. At this point we will need Rosetta installed.

```

1 cd ..//02_Model
2 python3 ModelEngine.py -a Sample_Input/Quick_Start/alpha_single.fasta
3 -b Sample_Input/Quick_Start/beta_single.fasta

```

The resulting model will be under the directory "Modeled". You can open this PDB file with your PDB file viewer of choice. Only the variable region of the TCR will be modeled. It should match the model found in "02_Model/Sample_Output/Quick_Start/" and "03_Pair/Sample_Input/Quick_Start/".

2.4 Pairing

Our modeled TCR is predicted to be a M1 antigen specific TCR. So we'll pair it with an M1 antigen from PDB model 5ISZ. This step will prepare the two structures for the following docking step.

```

1 cd ..//03_Pair
2 python3 TurnTable.py -t Sample_Input/Quick_Start/ES179M1-01.pdb
3 -p Sample_Input/5isz.pdb

```

The paired TCR and pMHC will now be in the PDB file under the new directory "Paired". The new name of the PDB will start with the TCR name and then the pMHC name.

2.5 Docking

For our quick start guide, we'll attempt a very short docking run just to ensure everything is working properly. There are two examples runs listed so you can determine if the MPI binaries are working on your system, or else you can use Rosetta without MPI. These examples are not recommended for good predictions, to ensure you're utilizing TRain properly, visit chapter 6.

We'll begin by updating our config.ini file or copying it from "02_Model". Then we'll create a new directory to conduct docking. This is done so your output can be organized as several new things will be created to perform each step needed for docking.

```
1 cd .../04_Dock
2 cp .../02_Model/config.ini .
3 mkdir QS_Dock
4 cd QS_Dock
5 cp ..../TCRcoupler.py .
6 cp ..../PDB_Tools_V3.py .
7 cp ..../config.ini .
8 cp ..../Sample_Input/Quick_Start/ES179M1-01_5isz.pdb .
9
10 # Example 1 (w/o MPI)
11 python3 TCRcoupler.py ES179M1-01_5isz.pdb -q -r -a 10 -d 100 -e 10
12
13 # Example 2 (with MPI)
14 python3 TCRcoupler.py ES179M1-01_5isz.pdb -r -a 10 -d 100 -e 10
```

Since we're testing with the rigid docking protocol, you'll find three folders with the "/output_files" directory. Within the folder there will be the "relax", "dock", and "refine" directories. The best scoring refined PDB will be found in the "refine" directory.

We'll now take the final structure and renumber the pMHC to what was present in 5isz.pdb. While entering input for PostCoupler.py with the example below, your input will be unique so follow instructions below.

```
1 cd ../
2 python3 PostCoupler.py QS_Dock/output_files/refine/ES<tab> -c ACDE
3 -r Sample_Input/Quick_Start/5isz.pdb
```

2.6 Analysis

To conduct an analysis of a single docked TCRpMHC complex, we'll begin with both the Rosetta Energy Breakdown Table and Heatmap. Energy Breakdown will provide us with insight of what amino acids are interacting between the TCR and the pMHC.

```
1 cd ..../05_Analysis
2
```

```
3 # Table (output = output.csv)
4 python3 DataDepot.py -t
5 Sample_Input/Quick_Start/ES179M1-01_5isz_Docked.pdb
6 python3 DataDepot.py -t
7 Sample_Input/Quick_Start/ES179M1-01_5isz_Docked.pdb -m
8
9 # Heatmap
10 python3 DataDepot.py -e
11 Sample_Input/Quick_Start/ES179M1-01_5isz_Docked.pdb
12 python3 DataDepot.py -e
13 Sample_Input/Quick_Start/ES179M1-01_5isz_Docked.pdb -m
```

A Busage

```
1 python3 DataDepot.py -a
2 Sample_Input/Quick_Start/ES179M1-01_5isz_Docked.pdb
```

Input Step Installs

Using the SeqConductor program

Input files

Parameters

Output

Under the hood

3 — The Input Step

The input step is handled by the SeqConductor program. The SeqConductor program takes in input from single cell sequencing data of T-cell receptor gene segments names and CDR3 amino acid sequences. The inputted segments are then aligned with the CDR3 amino acid sequence taking priority in final output. Output can be specified for an information table or an alpha and beta fasta file for direct submission to Repertoire Builder or TCRmodel.

3.1 Input Step Installs

SeqConductor executable code can be found in the folder 01_Input. Python packages required for use can be installed as followed:

```
1 pip install pandas  
2 pip install openpyxl
```

3.2 Using the SeqConductor program

3.2.1 Input files

Required input for SeqConductor is a table of single cell sequencing data in the form of TRAV, CDR3 α sequence, TRAJ, TRBV, CDR3 β sequence, TRBJ. By default, TRAV, CDR3 α , TRAJ, TRBV, CDR3 β , TRBJ are respective to columns 1, 2, 3, 4, 5 and 6. While column 0 is reserved for sequence ID. This can be altered with parameters listed below. These tables can be in the format of xlsx or csv files. The program automatically detects based on the file's handle. Regarding xlsx files, sheets names can also be specified if not the primary sheet. An optional input is the reference fasta file of gene family segments. By default, the fasta file "family_seq.fasta" is utilized. This fasta file is pulled results from IMGT/GENE-DB specified for the TCR molecular components of Homo sapiens [GCL05]. While full support isn't guaranteed for other organism, "full_family_seq.fasta" contains

the rest of the organisms that IMGT/GENE-DB has data for. Additionally, if a species alternative to Homo sapiens is desired, manual selection of the constant region is required.

3.2.2 Parameters

The SeqConductor program accepts the following parameters:

Argument	Name	Description	Default
Input			
Single Cell Table		xlsx or csv of single cell t-cell data (Required)	
-s	--sheet	Parameter allows for selection of an alternative sheet name from a submitted xlsx file	0
-a	--append	Append each chain with constant region	False
-c	--columns	List of numbers correlating to the columns containing each segment. Can exclude Seq ID by providing just 6 columns.	0,1,2,3,4,5,6
-r	--organism	Parameter allows you to change organism in use, requires "full_family_seq.fasta" gene family file	homo sapiens
-y	--alpha	Alpha Chain: Constant region alternative	TRAC*01
-z	--beta	Beta Chain: Constant region alternative	TRBC1*01
-g	--genefamily	Parameter allows for the selection of an alternative gene family fasta file	family_seq.fasta
Output			
-t	--information	Parameter outputs a table containing prominent information along with the resulting α & β chain sequences.	True
-f	--fasta	Parameter provides fasta files with resulting α & β chains separated to two fasta files.	False
-m	--omission	Characters to avoid in header ID for fasta file submission comma sep.	
Other			
-v	--verbose	Show alignments being produced	False
-l	--silent	Mute even poor alignments	False

Examples of typical runs:

```

1 cd 01_Input
2 # Standard alpha.fasta & beta.fasta output, just variable regions
3 python3 SeqConductor.py Sample_Input/Test_Table.xlsx -f
4
5 # Information Table output
6 python3 SeqConductor.py Sample_Files/Test_Table.xlsx -i
7
8 # Modeling input: alpha.fasta & beta.fasta output, with variable and constant
9 # region
10 python3 SeqConductor.py Sample_Files/Test_Table.xlsx -f -a

```

```
11 # Modeling input: alpha.fasta & beta.fasta output, with variable and constant  
12 # region but adjusting for Rep. Builder naming  
13 python3 SeqConductor.py Sample_Files/Test_Table.xlsx -f -a --omission +
```

3.2.3 Output

Sample outputs can be found in the sub-directory `Sample_Output/`.

1. alpha.fasta
2. beta.fasta
3. alpha_full.fasta (Appended constant region)
4. beta_full.fasta (Appended constant region)
5. alpha_full_rep.fasta (Removed "+" from Seq. IDs to avoid Repertoire Builder Error)
6. beta_full_rep.fasta (Removed "+" from Seq. IDs to avoid Repertoire Builder Error)
7. Test_Table_Results.csv
8. Test_Table_Results_Full.csv

3.3 Under the hood

The main steps carried out by SeqConductor:

1. Construct dictionary of gene family segments
2. Construct dictionary containing information from submitted table
3. Create full TCR sequences
4. Output:
 - (a) Information Table
 - (b) Fasta files: alpha.fasta & beta.fasta

Alignment of V-gene segment + CDR3 + J-gene segment is conducted in step 3. The CDR region, which from cell sequencing is in full, is always retained while the start/end of each gene segment can be trimmed. All alignments are done with scores of Match = 2.5, Mismatch = -1, Gap = -1.5, and Extend Gap = -0.5. First, the program aligns the TRAV segment with CDR3 α . To perform the alignment, the V-segment sequence is trimmed to the final amino acids with a length of the CDR3 sequence minus 5. In the case that a CDR3 sequence is shorter than 7 amino acids, the last amino acids from the V-segments are pulled equal to the length of the CDR3 sequence. It is common to see very short overlaps in the V-segment + CDR3 overlap. To avoid poor alignments, where the CDR3 is placed in front of the V-segment, a sliding window approach is then used. In the case of a sliding window alignment, the V-segment is shrunk by one amino acid (from the head of seq.) until a good alignment is found or the alignment is less than 2 amino acids long. In the case the alignment is less than 2 amino acids long, the CDR is directly appended to the V-segment and a cautionary message is sent to the console. The V-segment/CDR3 + J-segment overlap is slightly different. In this case, larger overlap is more common. So a single alignment is completed between the V-segment/CDR3 + J-segment with no additional sliding window option. For this alignment, the V-segment/CDR3 is trimmed to the length of the J-segment length. In the case of a poor alignment with several gaps in this method, the J-segment is directly append to the V-segment/CDR3 sequence and a message is sent to the console again. For additional details on performed alignments refer to Figure 3.1

Typical:	
Sliding Window Catch:	Sliding Window Fail (Append):
V-segment: ...SSSQTTDSGVYCAVE	V-segment: ...PSQPGDSAVYFCAAS
CDR: CHVEPYSGTYKYIF	CDR: CVYRNNNARLMF
Initial Alignment:	Initial Alignment:
SGVYCAVE	YFCAAS
.	
CHVEPYSGTYKYIF	CVYRNNNARLMF
Fixed Alignment:	Fixed Alignment:
GVYCAVE	YFCAAS
CHVEPYSGTYKYIF	CVYRNNNARLMF
Final:	Final:
...SSQTTDSGVYFCHVEPYSGTYKYIF	...PSQPGDSAVYFCAASCVYRNNNARLMF

Figure 3.1: SeqConductor **Alignment Examples**: The first alignment example is of a typical alignment of V-segment + CDR3 + J-segment. It is common for the V-segment + CDR3 overlap to be very short (2-5 amino acids). The CDR3 + J-segment overlap is typically longer. The sliding window catch example demonstrates the fall back option if a poor initial alignment is determined. Then the final example of a sliding window fail is where an alignment of length 1 is detected and the second segment is just appended to the first.

Modeling Step Installs

Using the ModelEngine program

Configuration File

Input files

Parameters

Output

Under the hood

4 — The Modeling Step

Many TCR modeling services are already developed and easily available to produce theoretical TCR $\alpha\&\beta$ chain structures. These services include LYRA, TCRmodel, and Repertoire Builder, TCRBuilder [GP18; Kla+15; Sch+19; 20]. TCRmodel and Repertoire Builder offer batch submission which is helpful for generating models of TCR sequences collected. ModelEngine utilizes the only locally available modeling option, TCRmodel. TCRmodel is included in Rosetta distribution and to improve its ease-of-use, ModelEngine allows for multi-processing to rapidly produce more models.

4.1 Modeling Step Installs

ModelEngine only relies on Rosetta to be installed and built. Instructions are the same for what we find in the quick start guide and in the docking step. However, building with MPI is not necessary for running TCRmodel.

For modeling and docking, a local installation of Rosetta needs to be installed. For licensing details visit <https://www.rosettacommons.org/software/license-and-download>. Installation instructions can be found at https://new.rosettacommons.org/docs/latest/getting_started/Getting-Started and Rosetta should be built with MPI executables and instructions can be found at https://new.rosettacommons.org/docs/latest/build_documentation/Build-Documentation or follow instructions below.

Follow below for general build options of Rosetta for Linux and MacOS systems.

1 **cd rosetta_src_xx/main/source**

2 **./scons.py bin mode=release extras=mpi -j<number_of_processors_to_use>**

4.2 Using the ModelEngine program

4.2.1 Configuration File

Config.ini file must be prepared. Point to the location of chromedriver installation. The file is found in the primary directory of TRain.

4.2.2 Input files

Two separate fasta files containing alpha chains in one file and beta chains in the other can be submitted. Headers must match up between alpha and beta chains. SeqConductor will produce these fasta files.

4.2.3 Parameters

The ModelEngine program accepts the following parameters:

Argument	Name	Description	Default
Input			
-a	--alpha	Fasta file containing alpha chain sequences	
-b	--beta	Fasta file containing beta chain sequences	
-r	--refine	Model with CDR3 loop refinement	False
-s	--start	Starting PDB in Fasta file (Alpha)	
Output			
-d	--dir	Change standard output directory for resulting modeled TCRs	Modeled
Other			
-v	--verbose	Readout output from TCRmodel	False
-m	--multi	Split up load to multiple cores	False
-c	--cpus	Number of CPUs allocated	All
-u	--cutoff	Sequence similarity cutoff for templates (int)	100

An example of a typical run:

```

1 cd 02_Model
2
3 # Submission to TCRmodel (Some may fail)
4 python3 ModelEngine.py -a Sample_Input/alpha_full.fasta
5 -b Sample_Input/beta_full.fasta -m

```

4.2.4 Output

Resulting structures that were successful will now be in the download directory Models or in the download directory file name provided. For sequences that didn't produce a successful model, an error list will be printed after completion of run.

4.3 Under the hood

ModelEngine utilizes the TCRmodel which is a component of the Rosetta distribution of programs. ModelEngine determines what script is available to run based on your install of Rosetta. TCR

sequences are pulled from the submitted fasta files and paired with their partnered chains. Sequences are then submitted to the TCRmodel script and outputted to the desired output folder. Multi-processing is handled by the python package, concurrent.futures.ProcessPoolExecutor. After models are produced, the files are renamed according to the header in the fasta files. Models that fail to produce are reported to the user.

Pairing Step Installs

Using the TurnTable program

Input files

Parameters

Output

Under the hood

5 — The Pairing Step

After constructing a modeled TCR structure, it then needs to get paired to a pMHC before the docking steps. TurnTable allows for submission of single or multiple TCR and pMHC PDB files. It then pairs each from the collection. To assist in the ability of utilizing crystal structures versus the modelled TCRs, full TCRpMHC complexes can be submitted and the TCR or pMHC extracted. This process also facilitates the submission of full TCRpMHC crystal structures to be submitted for native structure docking comparison along with swapping of each TCR for each pMHC of crystal structures. To help with efficient docking, TCR chains are trimmed if from a crystal structure, the MHC is trimmed, and the beta-2 microglobulin is removed. Following trimming, the PDB(s) are then renumbered and relabeled as needed for `TCRcoupler` and this can be corrected for after docking with `PostCoupler.py` if you want to return to the native numbering. Returning to native numbering can help assist with ensuring consistency between native crystal structures and the re-docked structures for further analysis. As a final step, the center of the TCR chains are centered to coordinates 0,0,0 with the pMHC below the TCR.

5.1 Pairing Step Installs

The only non-standard dependencies of TurnTable are BioPython, numpy, SciPy, and sklearn. These are needed for the use of `PDB_Tools_V3.py`, which TurnTable utilizes and are requested to be installed in the universal installations. Thus, nothing additional needs to be installed for the pair step.

```
1 pip3 install biopython  
2 pip install scipy  
3 pip install -U scikit-learn
```

5.2 Using the TurnTable program

5.2.1 Input files

There are several input methods for TurnTable . The standard is to supply one TCR and one pMHC, either can be stripped from a complete complex, and pairing will occur between those two structures. Submission of multiple TCRs or pMHC is possible with a folder containing the PDB files, this is checked for automatically. A single directory of TCRpMHC structures can also be submitted and for every TCR and every pMHC to be swapped around resulting with the squared number of inputs. If submitting TCR crystal structure, ensure you utilize `--trimA` and `--trimB` command line options as this is not default.

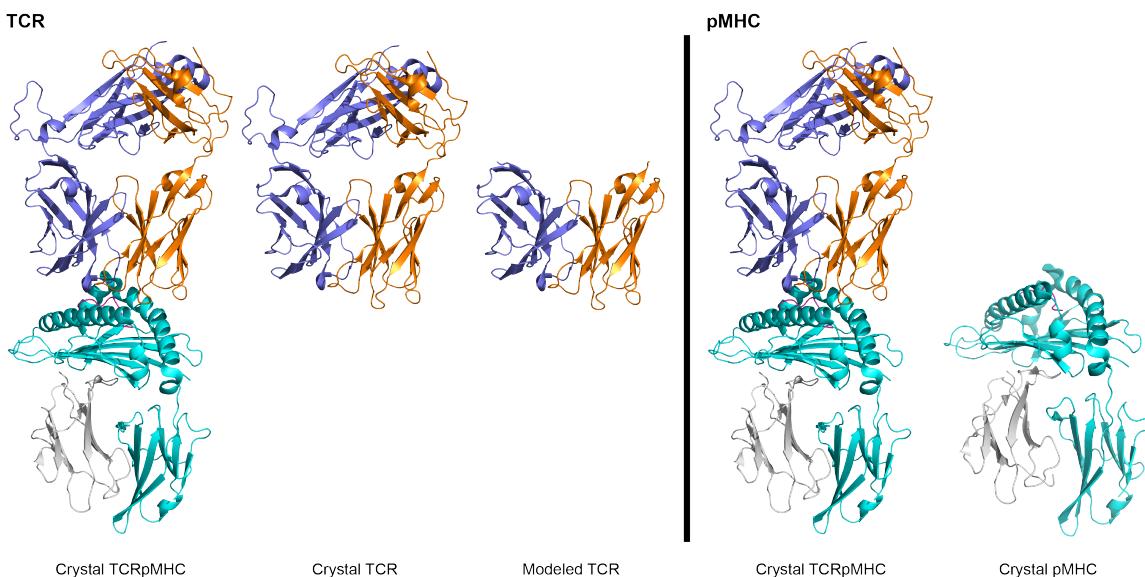


Figure 5.1: **TurnTable Input Options:** Above is a visualization of the potential structures that can be submitted to TurnTable as PDBs. Additionally, with the command line option "-p", a single or multiple full TCRpMHC crystal structures can be submitted.

5.2.2 Parameters

The TurnTable program accepts the following parameters:

Argument	Name	Description	Default
Input			
-t	--tcr	TCR pdb file or folder of TCR PDBs	
-p	--pmhc	pMHC pdb file or folder of pMHC PDBs	
-d	--pdbs	Folder of PDBs and all TCRs and pMHCs will be swapped	
Output			
-a	--trimA	Trim TCR alpha, needed if full crystal structure	False
-b	--trimB	Trim TCR beta, needed if full crystal structure	False
-m	--trimM	Prevent trimming of MHC	False

Examples of typical runs:

```

1 cd 03_Pair
2 # Run_1:
3 python3 TurnTable.py -t Sample_Input/1qrn.pdb -p Sample_Input/1qse.pdb
4 --trimA --trimB
5
6 # Run_2:
7 python3 TurnTable.py -t Sample_Input/1qse.pdb -p Sample_Input --trimA
8 --trimB
9
10 # Run_3:
11 python3 TurnTable.py -t Sample_Input/Modelled -p Sample_Input/1qrn.pdb
12
13 # Run_4:
14 python3 TurnTable.py -d Sample_Input --trimA --trimB

```

5.2.3 Output

Resulting output will create a Paired/ sub-directory containing updated TCRpMHC PDB files. PDB files are named as "TCR_pMHC.pdb". These file are now in a state prepared for docking, see chapter 6.

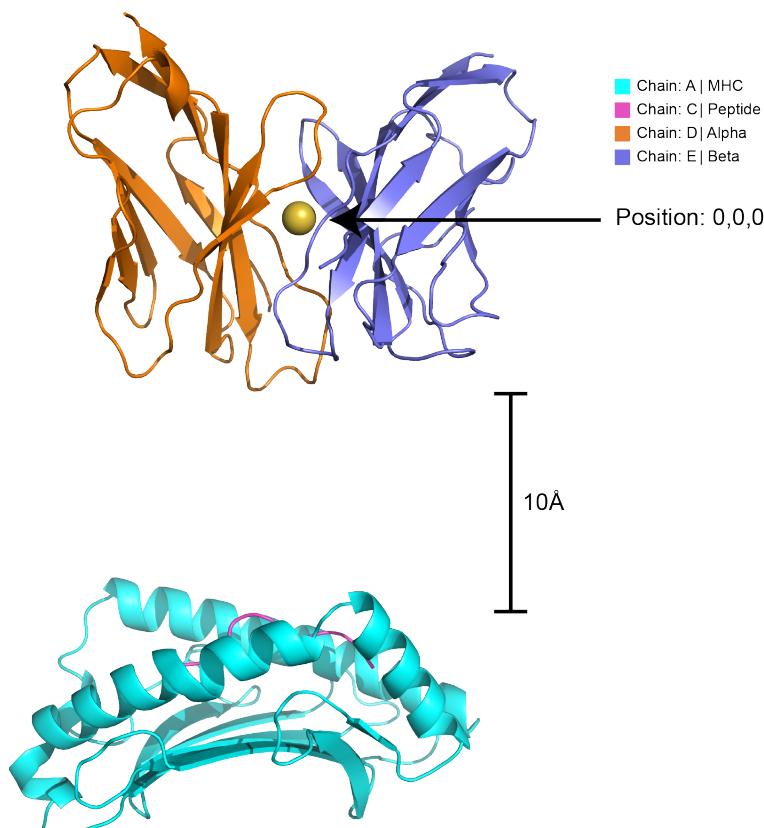


Figure 5.2: **Paired TCRpMHC:** Add new description here.

5.3 Under the hood

The main steps carried out by TurnTable:

1. Determine files versus folders.
2. Create temporary TCR PDB.
3. If crystal structure, clean PDB and split off TCR.
4. Update TCR labels to D and E for alpha and beta respectively.
5. If crystal structure, trim TCR.
6. Align TCR principal axes of inertia along the XYZ planes.
7. Create temporary pMHC PDB.
8. Clean crystal structure and split off pMHC.
9. Superimpose reference to centered temporary TCR file.
10. Superimpose pMHC to reference pMHC.
11. Remove reference structure and save as "TCR Name"_"pMHC Name".pdb

The majority of TurnTable is handled by methods from `PDB_Tools_V3.py`.

Docking Step Installs

Using the PrepCoupler program

Input files

Output

Example Run

Using the TCRcoupler program

Configuration File

Parameters

Flexible Docking

Rigid Docking

Using the PostCoupler program

Parameters

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Example Run

6 — The Docking Step

To gain a structural prediction a TCRpMHC interface, two Rosetta docking protocols are part of the TRain suite. One or several PDBs can be provided for computational docking conducted following the RosettaDock 4.0 protocol [Mar+18] or alternatively a simplified rigid docking protocol following RosettaDock 3.2. Flexible docking allows for movement of sidechains and slight movement of the backbone of the TCR, this allows for potentially better predictions. Docking is a computationally taxing process; If a heavily multi-core computer is not available, restraining to rigid docking may be necessary. Optional parameters and alternative starting positions can allow for additional customization.

6.1 Docking Step Installs

Installed on server under "/opt/rosetta_src_2021.16.61629_bundle".

For docking, a local installation of Rosetta needs to be installed. For licensing details visit <https://www.rosettacommons.org/software/license-and-download>. Installation instructions can be found at https://new.rosettacommons.org/docs/latest/getting_started/Getting-Started and Rosetta must be built with MPI executable and instructions can be found at https://new.rosettacommons.org/docs/latest/build_documentation/Build-Documentation or follow instructions below. While there is the option to run without MPI, it is not recommended. For more instructions on how to run ModelEngine and for a list of command line options, see chapter 5.

If MPI is not installed on the computer you can install using the following (apt installer):

```
1 # Linux
2 sudo apt install libopenmpi-dev
3
4 # MacOS
5 xcode-select --install
6 brew install openmpi
7 # Or visit: https://www-lb.open-mpi.org/software/ompi
```

```
8 # Both
9 pip3 install biopython
10 pip install scipy
11 pip install -U scikit-learn
```

or following instructions at <https://www.open-mpi.org/faq/?category=building>.

Follow below for general build options of Rosetta for most operating systems.

```
1 cd rosetta_src_xx/main/source
2 ./scons.py bin mode=release extras=mpi -j<number_of_processors_to_use>
```

The configuration file for TCRcoupler is inside directory 04_Dock. Modify the configuration file with your preferred text editor writing the location of Rosetta install in line 2 inside the quotations.

6.2 Using the PrepCoupler program

PrepCoupler is a useful program if TurnTable is not necessary for any reason. PrepCoupler prepares the PDB(s) for Rosetta. To do so, several modifications are made. The PDB is renumbered to a continuous count of amino acids versus a new count for each chain. As well as, the chains are labeled to standard TCR PDB chain labeling of MHC: A, Peptide: C, Alpha:D, and Beta:E. With the removal of the beta-2 microglobulin (chain: B) for more efficient docking as it is not a component of the interface. Then to further enhance efficiency, the MHC chain is trimmed to just the two alpha helices and the back beta pleated sheet. The $\alpha\&\beta$ chains are also trimmed to contain only the variable region. This program however does not separate the TCR from the pMHC. This program should also be ran on native structure being submitted for docking analysis.

6.2.1 Input files

Provide any TCR PDB file or folder of TCR PDB files.

6.2.2 Output

TCR PDB file with updates to comply with Rosetta applications including: proper order of chains, updated numbering, updated chain labels, removal of unneeded data.

6.2.3 Example Run

```
1 cd 04_Dock
2 # Run 1:
3 python3 PrepCoupler.py Sample_Files/1ao7.pdb
4
5 # Run 2:
6 python3 PrepCoupler.py Sample_Files/PDB_Dir/
```

6.3 Using the TCRcoupler program

TCRcoupler is an automation of several Rosetta applications to generate a docked TCRpMHC complex. Depending on the computational resources available, use of optional parameters may be necessary. Things to reduce run time include: changing from flexible to rigid docking, decrease number of relaxation steps, decrease number of docking permutations, decrease number of refinement runs, or increase core count.

To ensure TCRcoupler run smoothly a few things should be ensured. TCRcoupler relies on the mpi complied version of Rosetta. This allows TCRcoupler to unitize multiple cores to increase efficiency of runs. By default, TCRcoupler will request all cores available on the machine but can be changed with command line argument (see section 6.1.2). Rosetta requires a specific numbering scheme for the structure and chain order within the PDB. To avoid numbering and chain order issues, utilize TurnTable (refer to chapter 5).

6.3.1 Configuration File

Config.ini file must be prepared. Point to the location of Rosetta installation (refer to chapter 2). Separate from 02_Model and 05_Analysis Config.ini but can be copied/pasted.

6.3.2 Parameters

The TCRcoupler program accepts the following parameters:

Argument	Name	Description	Default
Input			
pdb		PDB file or folder of PDBs for docking	
-n	--native	Native structure folder or file to run optional comparison to crystal structure, pdbs have to be in folder and match numbering of submitted pdbs for batch submission.	
Standard Options			
-l	--linux	Changes to Linux runnable program	True
-m	--mac	Changes to MacOS runnable program	False
-c	--cores	Max number of cpu cores provided	All
-q	--nompi	Run Rosetta without mpi, not recommended for large runs	False
Docking Options			
-f	--flexible	Initializes flexible docking	True
-r	--rigid	Initializes rigid docking	False
-p	--pmhc	(Flex) Number of pmhc relax runs	100
-x	--xml	(Flex) Number of xml relax runs for TCR	40
-b	--bb	(Flex) Number of back bone rub runs for TCR	30
-s	--fast	(Flex) Number of fast relax runs performed	30
-a	--relax	(Rigid) Number of relax runs performed	100
-d	--docking	(Both) Number of docking runs performed	10000
-e	--refine	(Both) Number of refinement runs, post dock	100

6.3.3 Flexible Docking

Input files

PDB(s) submitted for flexible docking must be numbered properly and the alpha and beta chain must come after the MHC and peptide or resulting errors may occur. If PDBs submitted have not been processed through TurnTable then PrepCoupler should be run. PDBs provided as native structures should also be run through PrepCoupler. Flexible docking also requires PDB_Tools_V3.py to be located in the same directory as TCRcoupler.

Output

Docking generates several output files including: several flag files, split TCR and pMHC PDB files, input_files and output_files directories and sub-directories, several intermediate PDB files, and ensemble list files. To help reduce storage utilization, TCRcoupler automatically deletes PDBs produced that are not the highest scoring. Automatic removal of PDBs can be inhibited by command line parameter. For results, enter into the output_files directory and within /Refine/ the remaining PDB will be the best scoring docked structure.

Example Run

Setup:

Before we start the run, use your preferred text editor and modify config.ini to your Rosetta installation.

```

1 (Driver)
2 rosetta_loc="/opt/rosetta_src_2021.16.61629_bundle"
```

For an example run, create a new directory in 04_Dock for our run. Then copy TCRcoupler.py, PDB_Tools_V3.py, config.ini, and Sample_Files/2nx5_2nx5.pdb to our new folder.

```

1 cd 04_Dock
2 mkdir Run_1
3 cp TCRcoupler.py Run_1/
4 cp PDB_Tools_V3.py Run_1/
5 cp config.ini Run_1/
6 cp Sample_Files/2nx5_2nx5.pdb Run_1/
7 cd Run_1
```

Now let's do a flexible docking run. For this run, we're going to allocate 100 CPU cores.

```

1 python3 TCRcoupler.py 2nx5_2nx5.pdb -f -c 100
```

As an alternative, let's submit a folder of PDBs. Here's the entire process. Nohup and allow us to run in background

```

1 cd 04_Dock
2 mkdir Run_1
3 cp TCRcoupler.py Run_2/
4 cp PDB_Tools_V3.py Run_2/
5 cp config.ini Run_2/
6 cp -r Sample_Files/Multi_Run Run_2/
7 cd Run_2
8 nohup python3 TCRcoupler.py Multi_Run -f -c 100 &
```

6.3.4 Rigid Docking

Input files

PDB(s) submitted for rigid docking must be numbered properly and the alpha and beta chain must come after the MHC and peptide or resulting errors may occur. If PDBs submitted have not been processed through TurnTable then PrepCoupler should be ran. PDBs provided as native structures should also be ran through PrepCoupler.

Output

Rigid docking will produce less resulting files and directories. The produced item will include: three flag files, a time.txt file, several intermediate PDB files, and output_files directory. Just like with flexible docking, intermediate PDB files will be removed unless requested by user not to. Results can also be found in the output_files directory and within /Refine/ the remaining PDB will be the best scoring docked structure.

Example Run

Rigid docking follows in line with flexible docking but with just the replacement parameter of -f with -r. Keep in mind, a directory of PDBs can also be submitted for rigid docking.

```

1 cd 04_Dock
2 mkdir Run_3
3 cp TCRcoupler.py Run_3/
4 cp config.ini Run_3/
5 cp -r Sample_Files/2nx5_2nx5.pdb
6 cd Run_3
7
8 python3 TCRcoupler.py Multi_Run -r -c 100

```

6.4 Using the PostCoupler program

6.4.1 Parameters

The PostCoupler program accepts the following parameters:

Argument	Name	Description	Default
Input			
pdb		PDB file being renumbered	
-r	--reference	Reference PDB file being used to match numbering	
-c	--chains	Chains that will be renumbered from reference PDB	All
-u	--custom	Custom numbering for smallest chain e.g. 9,11,2,4,5 Has to match number of amino acids to numbers provided	
Output			
-n	--name	(Optional) Customized name for output file	

6.4.2 Input files

PDB being submitted would be the docked structure. This was renumbered to the required scheme for Rosetta applications. Assumes chain labeling is identical.

6.4.3 Output

Resulting PDB with either "_orinum.pdb" appending PDB file provided or with custom name provided.

6.4.4 Example Run

Let's try to examples. One with a redocked structure where both the TCR and pMHC can use the same reference. In the second, we'll used a TCR and pMHC from two separate structures and only renumber from their respective reference.

```
1 cd 04_Dock
2 # Run 1:
3 python3 PostCoupler.py Sample_Files/1qrn_1qrn_docked.pdb
4 -r Sample_Files/1qrn.pdb -n 1qrn_1qrn_updated.pdb
5
6 # Run 2:
7 python3 PostCoupler.py Sample_Files/1qrn_1qse.pdb -r 1qse.pdb -c AC
8
9 # Run 3:
10 python3 PostCoupler.py Sample_Files/1qrn_1qse.pdb -r 1qrn.pdb -c DE
```

Analysis Step Installs

Using the DataDepot program

- Configuration File
- Energy Breakdown
- ABusage
- Native Structure Comparison

7 — The Analysis Step

The analysis step is an accumulation of Python methods that allow for quick visual insight. All of these methods are encompassed in DataDepot . Some of these methods still rely on Rosetta to collect even further information from the structures produced. Methods that require a Rosetta installation will be signified and the configuration file must be updated, see more information below.

7.1 Analysis Step Installs

Several decencies are needed for DataDepot and can be installed using pip. For more instructions on how to run ModelEngineand for a list of command line options, see chapter 7.

```
1 pip3 install biopython
2 pip install scipy
3 pip install -U scikit-learn
4 pip install pandas
5 pip install matplotlib
6 pip install seaborn
```

7.2 Using the DataDepot program

DataDepot assumes that TCRs are labeled A = MHC, C = Peptide, D = Alpha, and E = Beta. If labeling does not match, PrepCoupler can be used from chapter 6.

7.2.1 Configuration File

Config.ini file must be prepared if conducting Energy Breakdown and Native Structure Comparison. Point to the location of Rosetta installation (refer to chapter 2).

7.2.2 Energy Breakdown

Rosetta's application Residue Energy Breakdown provides details of residue-residue interactions occurring within a PDB file. This information can provide more insight than just distance value cutoffs for interactions occurring at the interface of a TCRpMHC complex. DataDepot provides two forms to view the interactions happening at the interface of the TCRpMHC complex. These two forms are in a simple table and in a heatmap.

For both, you can submit either a PDB file or an already complete energy breakdown table. If a PDB is provided, Energy Breakdown is ran and the resulting .out file is converted to a .csv. If a energy breakdown table is submitted .out and .tsv files are converted to a .csv. The resulting .csv file of either is then processed to either produce the table or heatmap.

Parameters

Energy Breakdown parameters:

```
-t --table      Energy breakdown csv input for table
-e --heatmap    Energy breakdown csv input for heatmap
-m --mac        Changes rosetta from Linux to MacOS version      default=False
```

Table

The Energy Breakdown table provides a list of interactions occurring between the alpha and beta chains of the TCR to the MHC or peptide. Both attractive and repulsive energy values are shown.

Example Run

```
1 05_Analysis
2 # Run 1:
3 python3 DataDepot.py --table Sample_Input/sample.pdb
4
5 # Run 2:
6 python3 DataDepot.py --table Sample_Input/energy_breakdown_sample.out
```

Heatmap

The Energy Breakdown heatmap provides similar information as the table. However, the heatmap makes it easier to get a visual reference of interactions occurring at the interface. Only attractive energy values are displayed in the heatmap.

Example Run

```
1 05_Analysis
2 # Run 1:
3 python3 DataDepot.py --heatmap Sample_Input/sample.pdb
4
5 # Run 2:
6 python3 DataDepot.py --heatmap Sample_Input/energy_breakdown_sample.out
```

7.2.3 ABusage

ABusage calculates interface scores for Alpha to pMHC and Beta to pMHC utilizing the Rosetta application InterfaceAnalyzer. The program is ran twice, once for the alpha chain and another for

the beta chain. From the output of InterfaceAnalyzer for both, the delta G separated value is pulled. This provides us with an energy based value for the interactions occurring between Alpha to the pMHC and Beta to the MHC. The output is AB_Usage.csv, which is a table containing all delta G separated scores for each Alpha and Beta chain.

Parameters

ABusage parameters:

- a --ab Submit PDB for ab_usage interface scores
- m --mac Changes rosetta from Linux to MacOS version default=False

Example Run

```
1 05_Analysis
2 # Run 1:
3 python3 DataDepot.py --ab Sample_Input/sample.pdb
4
5 # Run 2:
6 python3 DataDepot.py --ab Sample_Input/Multi_PDBs
```

7.2.4 Native Structure Comparison

TCRcoupler allows you to submit a native crystal structure along with a PDB being submitted for docking. This can be useful to compare a crystal structure of a TCRpMHC complex to a re-docking attempt or compare against slightly mutated submitted chains. Submitting a native structures adds additional columns to the score files produced during docking and refinement.

Parameters

Native Structure Comparison parameters:

- s --sc Score file produced from docking or refinement (or dir of .sc)
- x --xaxis X axis for native structure comparison
- y --yaxis Y axis for native structure comparison

Example Run

```
1 05_Analysis
2 # Run 1:
3 python3 DataDepot.py --sc Sample_Input/1qrn_1qrn.sc -x l_sc -y Fnat
4
5 # Run 2:
6 python3 DataDepot.py --sc Sample_Input/Score_Files -x motif_dock -y Fnat
7
8 # Run 3:
9 python3 DataDepot.py --sc Sample_Input/Score_w_RMSD.sc -x total_score
10 -y all_rmsd
```

Axis Options:

1. I_sc
2. motif_dock
3. total_score
4. Fnat
5. ca_rmsd
6. all_rmsd

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