```
1. Fix
```

```
coord_lookup = {
    c['index']: (c['x'] / 10.0, c['y'] / 10.0, c['z'] / 10.0)
    for c in atom_coords
}
```

This means that the code is now correctly identify the distance as nm

- 2. The ITP files need the following fix:
- a. resid: make it all res
- b. atom: make it all C1, C2, ...
- 3. The Gro files need the following fix:
- a. have the first column be 1 res for all
- 4. More fix the the ITP file: Add to the bead connection 2 more column:
- a. b0 value: distance between 2 beads based on the distance formula
- b. k value: leave it as 20000 for all column

Code fixing:

Fix an issue in 6-ring part where C=N is assigned as TC5

add another section between section C and D that does the following:

for every unmapped inner atom that is not C or O, check to see if it has a non-ring connection that is of length 1 and the atom is C, if it is, use the pick key where the element is the inner element and bond order is 1 and kind is T then add it to both of the atoms

This is to account for some of the inner atoms that is not C or O

Fix an issue with 5-bead mapping where it would throw an error every time.

Add more bracket handling for case of [2H]

```
# Bracket handling: "[ ... ]"
if ch == '[':
    # Find the matching ']'
```

```
j = smiles.find(']', i + 1)

if j == -1:
    raise ValueError(f"Unmatched '[' at position {i}")

# Extract the content inside brackets

inside = smiles[i + 1 : j]

# Strip any non-letter character, keep only A–Z or a–z

letters_only = "".join(c for c in inside if c.isalpha())

# Emit each letter as its own token

for letter in letters_only:
    tokens.append(letter)

# Advance i to character after ']'

i = j + 1

continue
```

Fix to the dictionary:

notice how I have a lot of duplicate here, it overlaps one another I can list all of the key-value pair first, so that all of the key and value pairs are saved even if the keys are the same, then loop through that array one by one to add the key-value pairs to the dictionary, but whenever a key overlap, you add a + and check if it still overlap until all keys are unique and the dictionary will be unique

THIS SECTION IS LISTING NEW BEADS:

```
("P6?", [11, 2, "S(C)(=O)(=O)(C)", 0, ""]),

("C2?", [11, 2, "Ge(C)(C)(C)(C)", 0, ""]),

("C2?", [11, 2, "Pb(C)(C)(C)(C)", 0, ""]),

("C2?", [11, 2, "Si(C)(C)(C)(C)", 0, ""]),
```

```
("C2?", [11, 2, "Sn(C)(C)(C)(C)", 0, ""]),

("P2?", [11, 1, "C(O)(=O)(CO)", 0, ""]),

("SC6?", [11, 1, "S(=O)(=O)(C)", 0, ""]),

("P2?", [11, 1, "C(O)(=O)(CN)", 0, ""]),

("SX4e?", [11, 1, "C(Cl)(F)(F)", 1, ""]),

("X4e?", [11, 1, "C(OC)(F)(F)", 1, ""]),

("SX4e?", [11, 1, "C(O)(F)(F)", 1, ""]),

("X4e?", [11, 1, "C(=C)(F)(F)", 1, ""]),

("X4e?", [11, 1, "C(=C)(F)(F)", 1, ""]),

("X4e?", [11, 1, "C(=O)(CF)(N)", 1, ""]),
```

("X2?", [11, 1, "C(F)(Cl)(Cl)", 0, ""]),

("X2?", [11, 1, "C(CCl)(Cl)(Cl)", 0, ""]),

("X2?", [11, 1, "C(=CCl)(Cl)(Cl)",0, ""]),

("SX2?", [11, 1, "C(C)(Cl)(Cl)", 0, ""]),

("SX2?", [11, 1, "C(C)(Cl)(CCl)", 0, ""]),

("SX2?", [11, 1, "C(=C)(Cl)(Cl)", 0, ""]),

("X1?", [11, 1, "C(Br)(Cl)(Br)", 0, ""]),

("X1?", [11, 1, "C(Br)(Br)(Br)", 0, ""]),

("X1?", [11, 1, "C(=CBr)(Br)(Br)",0, ""]),

("X2?", [11, 1, "C(Cl)(Cl)(Br)", 0, ""]),

("SP2?", [11, 1, "C(C)(=O)(=O)", 0, ""]),

("N5a?", [11, 1, "C(C)(C=O)(=C)", 0, ""]),

("N6?", [11, 1, "C(=C)(C)(CO)", 0, ""]),

("P4?", [11, 1, "C(O)(C)(CO)", 0, ""]),

 $("SN4?",\ [11,1,"N(O)(C)(C)",\quad 0,""]),$

("SP4?", [11, 1, "C(O)(=O)(=O)", 0, ""]),

```
("P6?", [11, 1, "C(CN)(=O)(N)", 0, ""]),
```

("P6?",
$$[11, 1, "C(N)(=O)(NN)", 0, ""]$$
),

("SP5?",
$$[11, 1, "C(N)(=N)(N)", 0, ""]$$
),

```
("SP6?", [11, 0, "O=S=O", 0, ""]),
```

```
("SC2", [7, 0, "CCC",
                        1, ""]),
("SX4e",[7, 0, "FCF",
                         1, ""]),
("SC6", [7, 0, "CCS",
                         2, ""]),
("SX3", [7, 0, "CCCl",
                         2, ""]),
("SX3", [7, 0, "CICC",
                          2, ""]),
                          2, ""]),
("SX4e",[7, 0, "CCF",
("X1", [7, 0, "CCI", 2, ""]),
                          2, ""]),
("SX2", [7, 0, "CCBr",
("SX2", [7, 0, "BrCC",
                         2, ""]),
("TC6", [7, 0, "CS",
                       2, ""]),
("TX1", [7, 0, "CI", 2, ""]),
("TX2", [7, 0, "CBr", 2, ""]),
("TX2", [7, 0, "BrC", 2, ""]),
("TX4e",[7, 0, "CF", 2, ""]),
("X1", [7, 2, "C(Br)(Br)(Br)(Br)", 0, "."]),
("X2", [7, 2, "C(Cl)(Cl)(Cl)(Cl)", 0, "."]),
("X3", [7, 2, "C(F)(F)(F)(F)", 0, "."]),
("C2", [7, 2, "C(C)(C)(C)(C)", 0, ""]),
("X3", [7, 2, "C(C)(C)(C)(Cl)", 0, ""]),
("X2", [7, 2, "C(C)(C)(C)(Br)", 0, ""]),
("X1", [7, 2, "C(C)(C)(C)(I)", 0, ""]),
```

This current part is very limited in what it can do so let's fix it:

```
# CASE 3: 4 edge atoms.
elif num_edges == 4:
    # Find the center atom that has 4 inner connections.
```

```
center local = None
    for i, atom in enumerate(section):
        if len(atom[4]) == 4:
            center local = i
            break
    if center local is None:
        raise ValueError("Non-ring section with 4 edges does not have
an atom with 4 inner connections.")
    # Build array4: for each inner connection of the center atom,
trace to the final edge atom.
    # start by adding the central atom's global index.
    array4 = [section[center local][0]]
    for (nbr, ) in section[center local][4]:
        final edge local = get final edge(section, center local, nbr)
        # Only add if the final atom is an edge and its type is 'F'
        if final edge local is not None and
section[final edge local][5] and section[final edge local][1] == 'F':
            array4.append(section[final edge local][0])
    # Ensure exactly 4 branch edge atoms were found.
    if len(array4) != 4:
        raise ValueError("Non-ring section cannot be mapped: expected
4 branch edge atoms, found {}.".format(len(array4)))
    # Assign the bead "SX4e" with a random tag to all atoms in array4.
    rstr = generate random string()
    for idx in array4:
        final[idx] = "SX4e" + rstr
    # Build array5: the list of atoms still unmapped.
    array5 = [atom[0] for atom in section if final[atom[0]] == ""]
    # If exactly 2 atoms remain and their types are C and O, assign
bead "TP1d" with a random tag.
    if len(array5) == 2:
        types = [next(a for a in section if a[0] == idx)[1].upper()
for idx in array5]
        if sorted(types) == ['C', '0']:
```

```
rstr2 = generate_random_string()
    for idx in array5:
        final[idx] = "TP1d" + rstr2
        return final
    else:
        raise ValueError("Non-ring section cannot be mapped:
remaining atoms are not C and O (found: {}).".format(types))
    else:
        raise ValueError("Non-ring section cannot be mapped:
unexpected number of unmapped atoms in 4-edge mapping (found {} in array5).".format(len(array5)))
```

currently it only accounts for 1 specific case that is C(CO)(F)(F)(F), which is not what we want, so let's break it down into 2 parts:

part 1: if the amount of atoms is 6: we will do the following:

find the center atom (the only atom that has 4 inner connections)

there should now be 4 path, and 1 will have 2 atoms and the rest will have 1 atoms now we should break this section into 2 parts,

the first part is the path with the 2 atoms,

we will change both of the edge of the two atoms to true

remove the connection between the atom that is connected to the center and the center atom

now make those two atoms its separate section and update mapping

run this function again on this section

the rest are the center atom connected to the other 3 singular path

make this part its own section and disconnect the center connection with the other path now update mapping and run the function again on this section

part 2: if the amount of atoms is 5: we will do the following:

find the center atom (the only atom that has 4 inner connections)

there should now be 4 path, and all 4 path will have only 1 atoms

we will do the same as if there are 3 edges, by put the center node and the each branches into a bracket and then look into the dictionary to find the bead then throw an error stating the center and the branches if it cannot find it

```
# CASE 2: 3 edge atoms.
elif num edges == 3:
    # Find the atom with 3 inner connections.
   center local = None
    for i, atom in enumerate(section):
        if len(atom[4]) == 3:
            center local = i
            break
    if center local is None:
        raise ValueError("Non-ring section with 3 edges does not have
an atom with 3 inner connections.")
    # Trace each branch from the center atom.
    branch paths = []
    for (nbr, _) in section[center_local][4]:
        branch_str = trace_branch(section, center_local, nbr)
        branch paths.append(branch str)
    # 1) Try section 7 matching
    import re
    candidate keys = []
    for key, val in martini dict.items():
        if val[0] == 7 and val[1] == 1 and "(" in val[2]:
            prefix, remainder = val[2].split("(", 1)
            if prefix.strip() != section[center_local][1]:
                continue
            branch_segments = re.findall(r'\setminus(([^{\wedge}]+)\setminus)', val[2])
            if len(branch_segments) != len(branch_paths):
                continue
            # order-independent match
            unmatched = branch segments.copy()
            matched all = True
            for bp in branch paths:
                for bs in list(unmatched):
```

```
if bp == bs:
                         unmatched.remove(bs)
                         break
                else:
                     matched all = False
                     break
            if matched all:
                candidate keys.append(key)
    candidate keys = list(set(candidate keys))
    # 2) Fallback to section 11 if needed
    if not candidate keys:
        for key, val in martini dict.items():
            if val[0] == 11 and val[1] == 1 and "(" in val[2]:
                prefix, remainder = val[2].split("(", 1)
                if prefix.strip() != section[center local][1]:
                     continue
                branch segments = re.findall(r'\setminus(([^{\wedge}]+)\setminus)', val[2])
                if len(branch segments) != len(branch paths):
                     continue
                unmatched = branch segments.copy()
                matched all = True
                for bp in branch paths:
                     for bs in list(unmatched):
                         if bp == bs:
                             unmatched.remove(bs)
                             break
                     else:
                         matched all = False
                         break
                if matched all:
                     candidate keys.append(key)
        if candidate keys:
            warnings.warn(
                f"Warning: falling back to section 11 for 3-edge
mapping (center: {section[center_local][1]} and branches:
{branch paths})",
                UserWarning
            )
```

```
candidate keys = list(set(candidate keys))
    # 3) Commit or error
    if len(candidate keys) == 1:
        rstr = generate random string()
        for atom in section:
            final[atom[0]] = candidate keys[0] + rstr
        return final
    elif not candidate keys:
        raise ValueError(
            f"Non-ring section cannot be mapped: no candidate bead
found for 3-edge mapping (center: {section[center local][1]} and
branches: {branch paths})."
    else:
        raise ValueError(
            f"Non-ring section cannot be mapped: ambiguous candidate
keys for 3-edge mapping (center: {section[center local][1]} and
branches: {branch paths})."
Here is the example for 3 edge bead mapping,
however in this case for 4 edge beads, to make the distinction, we
will check in the section where val[1] = 2 instead, the rest is the
same
then the error throw is for 4-edge mapping (center: ... identical)
After everything, we should have the correct bead mapping of every 4
edge 1-bead mappable beads, sometimes the mapping will have 1 more
sections due to split
more fixing:
For the part that has 6 total atoms:
fix this part only. we only change the edge status for the atom that
is connected to the center atom on the branch path = 2 side
so only that one specific atom we will change the edge status
```

Next is the connection:

we will only remove the connection between the center atom and that one atom that we just change the edge status

the other way around, remove the connection to the center atom of that new edge atom $\,$

we need to change mapping so that it will correctly display the two section as 2 different sections

we can run the rest accordingly

NOW THAT IT WORKS, TIME TO ADD MANY MORE BEADs, these are 1 center and 4 branches.