arboreto/core.py

def clean:
Z. 221: returns a tuple of (matrix, names) equal to the specified ones minus the target_gene_name if the target happens to be one of the transcription factors. If not, the specified (tf_matrix, tf_names) is returned verbatim.

Dann:
```
>> Regressor =
SKLEARN_REGRESSOR_FACTORY[regressor_type](random_state=seed,**regressor_kwargs)
>> regressor.fit(tf_matrix, target_gene_expression)
```