

Script Templating for EXOSIMS

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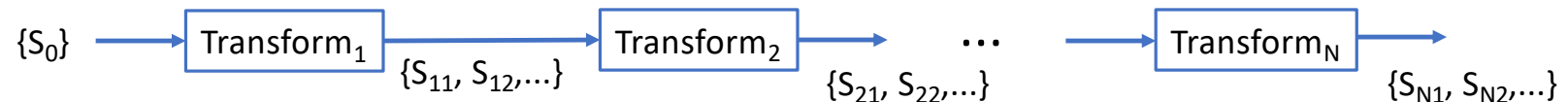
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Goal

- Support generation of a family of derived scripts using one valid script as a starting point.
- Scenario: We have one script that works. We want to do parameter optimization or sensitivity studies on the basis of that script.
- Two worthwhile ideas here: compositional script transforms, and naming conventions.
- Thanks to: Dean Keithly for discussions and prior work (“makeSimilarScripts.py”)

Basic Idea

- System takes one script as input, and at each of N stages, transforms that script into a set of scripts (script = dictionary).
- Envision the initial script as a one-script set. Then the transformation process looks like:



- At each stage, each input script gets turned in to one or more output scripts.
- All output scripts after a given stage are pooled, and given as input to the next stage.

Three Kinds of Transform

1. Update (1 input, 1 output):

- The transform contains a dictionary of values. Update the values in the input dictionary, with those in the transform dictionary.
- $T = \{ "dMagLim": 23 \}$ -> set dMagLim in all input scripts to 23.

2. Sequence (1 input, M outputs): **<== In practice, this is the most used.**

- The transform contains a dictionary of values that are vectors. For each element in the vector, output a new script with that value.
- $T = \{ "dMagLim": [23, 24, 25] \}$ -> make 3 output scripts, one with each value.

3. Cross product (1 input, M x P x ... outputs):

- Transform contains a dictionary of (several) vectors, and all combinations of their elements are used to create output scripts.
- $T = \{ "dMagLim": [23, 24, 25], "minComp": [0, 0.1] \}$ -> 6 output scripts are generated, with each combination of values.

Compositional

- The transforms can be composed as many times as desired.
- For instance, an original script can be left intact and one or more updates can be applied to it – transforming that one script into a different (single) script.
- Then a sequence of values can be plugged in to a different element in the script.
- As an example, two sequence transforms are equivalent to a cross-product (Cartesian product) transform that has two target elements.

Naming

- *Naming sounds trivial but it is important to the system function.*
- We have to say which kind of transform we intend.
 - We use the “xform_type” attribute, right in the transform.
- We have to name the resulting script.
 - We use a “xform_name” attribute, also in the transform.
 - It uses the Python format language, so you can do clever things.
 - E.g.: xform_name = “c1={coeffs[2]:.2f}” -> use the %.f format on the third element of the coeffs array in the dictionary as this fragment of the name.
- The names are *chained*, same as the transforms: names accumulate by *concatenation* in sensible ways as the transforms are performed.

Example (1)

We want to iterate over 3 components of a four-element coefficient vector.

Start out with simple update, to reset the mission life and set up $\text{coeffs}[3] = 0.5$, which will not change.

```
[  
  {  
    "xform_type": "update",  
    "xform_name": "",  
    "missionLife": 3.0,  
    "coeffs": [1, 1, 1, 0.5]  
  },  
  ...  
]
```

← this is the first of several chained transforms

Example (2, cont.)

Next, make a sequence over 6 choices for coeffs[0]. We go from 1 script input to 6 scripts output. Output filename example is “c1=0.10”.

```
{
  "xform_type": "sequence",
  "xform_name": "c1={coeffs[0]:.2f}",
  "xform_action": {"coeffs": "masked"},
  "coeffs": [[0.05, NaN, NaN, NaN],
             [0.2, NaN, NaN, NaN],
             [0.4, NaN, NaN, NaN],
             [0.6, NaN, NaN, NaN],
             [0.8, NaN, NaN, NaN],
             [1.0, NaN, NaN, NaN]
            ]
},
```

← masked = NaNs do not over-ride extant values

Example (3)

Now, 6 further choices for coeffs[1]. Six scripts input, 36 output. Output filename example is “c1=0.10_c2=0.80” because names accumulate by concatenation.

```
{
  "xform_type": "sequence",
  "xform_name": "c2={coeffs[1]:.2f}",
  "xform_action": {"coeffs": "masked"},
  "coeffs": [[NaN, 0.05, NaN, NaN],
             [NaN, 0.2, NaN, NaN],
             [NaN, 0.4, NaN, NaN],
             [NaN, 0.6, NaN, NaN],
             [NaN, 0.8, NaN, NaN],
             [NaN, 1.0, NaN, NaN]
            ]
},
```

Example (4)

6 choices for coeffs[2]. 36 in, 216 out.

Output filename example is “c1=0.10_c2=0.80_c3=1.00”

Note: Chaining all previous scripts gives a complete sweep, in one file.

```
{
    "xform_type": "sequence",
    "xform_name": "c3={coeffs[2]:.2f}",
    "xform_action": {"coeffs": "masked"},
    "coeffs": [[NaN, NaN, 0.05, NaN],
               [NaN, NaN, 0.2, NaN],
               [NaN, NaN, 0.4, NaN],
               [NaN, NaN, 0.6, NaN],
               [NaN, NaN, 0.8, NaN],
               [NaN, NaN, 1.0, NaN]
    ]
}]
```


this is the last of the
chain of transforms



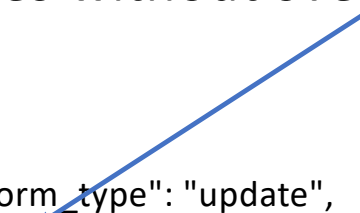
More On Naming

- We also found it useful to extend the name syntax a bit.
- The driving need was nested parameters, especially modules. We wanted to be able to *update submodules* without *over-writing* all other choices.

```
{  
  "xform_type": "update",  
  "+modules": {  
    "SimulatedUniverse": "SAG13Universe",  
    "SurveyEnsemble": "IPClusterEnsemble"  
  }  
},
```



```
{  
  "xform_type": "update",  
  "modules": {  
    "SimulatedUniverse": "SAG13Universe",  
    "SurveyEnsemble": "IPClusterEnsemble"  
  }  
},
```



- “+” means “go inside and update” (for dictionaries) and “add to end” (for lists, e.g. scienceInstruments).

Realization: A Python script

```
# json-xform: Transform an EXOSIMS JSON script into a set of such scripts.
#
# Usage:
#  json-xform [-v] [-o FILE] SCRIPT XSCRIPT ...
#
# where:
#  SCRIPT is the JSON script used by EXOSIMS
#  XSCRIPT is a JSON script giving the transform
# and, optionally:
#  -o FILE to specify where files should go; FILE must
#    have one %s to receive a file index.
#  -v for some verbose output
```

Remarks

- I implemented a relative mode for all operations. It is kind of like “masked”, in that it interprets the given values specially. In this case, as multipliers rather than as absolute values.
- This could use some kind of filter operation, so that some scripts could be eliminated. This would seem to require a programmatic interface (a predicate that would indicate what should be filtered), which I didn’t see a clean/general way to do in JSON.
- In practice, we used the “update” and “sequence” transforms the most. We would typically use an offline procedure to generate a sequence of parameter values (sometimes nonuniform spacing was best), and then make the sequence into an input to the “json-xform” script.