

ADDITIONAL FILE 1: Pseudocode for conversion from event interaction graph to metabolic interaction graph (Figure 3B-b1 and 3B-b2) used in MINR module development.

INPUT: Pairs metabolic event

OUTPUT: The metabolic interaction network

```
metabolic_events = Module1.extract_metabolic_events(texts)
```

```
# Initializing the metabolic interaction network
```

```
# Querying each event arguments.
```

```
foreach metabolic_event_ in metabolic_event_pairs_:
```

```
    if type_of(metabolic_event) is "Positive_regulation":
```

```
        skip() # Skipping regulation node.
```

```
#Initializing node for the metabolic interaction reconstruction.
```

```
substrates = [] #List of substrate nodes
```

```
products = [] #List of product nodes
```

```
enzymes = [] #List of enzymes nodes
```

```
theme_nodes = get_neighbor_by_edge_type(eventnode, "Theme")
```

```
product_nodes = get_neighbor_by_edge_type(eventnode, "Product")
```

```
cause_nodes = get_neighbor_by_edge_type(eventnode, "Cause")
```

```
positive_regulation_node = get_neighbor_by_node_type(eventnode, "positive_regulation")
```

```
#Adding a proxy node for if enzyme was not specified.
```

```
if enzymes is empty:
```

```
    proxy_node = create_proxy_node()
```

```
#Adding enzyme node
```

```
if exists(cause_nodes):
```

```
    extends(enzymes, cause_nodes)
```

```
if exists(positive_regulation_node):
```

```
    cause_nodes = get_neighbor_by_edge_type(positive_regulation_node, "Cause")
```

```
    extends(enzymes, cause_nodes)
```

```
#Adding the substrate and the product nodes.
```

```
if type_of(eventnode) is metabolic_conversion:
```

```
    extends(substrates, theme_nodes)
```

```
if type_of(eventnode) is metabolic_consummption:
```

```
    extends(substrates, theme_nodes)
```

```
if type_of(eventnode) is metabolic_production:
```

```
    extends(products, theme_nodes)
```

```
#Building a metabolic reaction (Substrate -> Enzyme -> Product).
```

```
foreach substrate in substrates:
```

```
    connect_from_to(substrate, enzyme)
```

```
foreach product in products:
```

```
    connect_from_to(enzyme, product)
```

```
#Add these reaction into the metabolic_interaction_network.
```

```
append(metabolic_interaction_network, substrate, enzyme, product)
```

```
return metabolic_interaction_network
```