

# WormBase Reimplementation

Part II: Configuration  
13 February 2008

# Configuration

**Very flexible**

- ✓ site-wide
- ✓ per-page (view level)
- ✓ per-class (model level)

# Formats

## YAML

```
pages :  
  gene :  
    widget_order :  
      - [ identification, location, expression,  
function, gene_ontology, genetics, homology,  
references, similarities ]  
    widgets :  
      identification :  
        - [ description, ncbi_kogs, species,  
other_sequences, ncbi, gene_models, cloned_by ]
```

## POP

```
antibody => {  
  widget_order => [qw/identification expression_patterns references/],  
  widgets     => { identification => [  
    qw/name common_name other_name summary/]}
```

## Apache

```
<pages>  
  <antibody>
```

# Sample Configuration

```
pages :
```

```
gene :
```

```
widget_order :
```

```
    - [ identification, references ]
```

```
widgets :
```

```
    identification :
```

```
        - [ description, ncbi_kogs, species ]
```

# Why?

free stuff:  
actions  
model methods  
template selection  
view formatting

# Each page is an action

pages :

**gene** :

widget\_order :

- [ identification, references ]

WormBase::Controller::Gene;

sub gene { AceDB->fetch(Gene => @\_ ) }

**eg: /gene/\*/**

# Each widget is an action

```
pages :
```

```
gene :
```

```
widgets :
```

```
identification :
```

```
- [ description, ncbi_kogs, species ]
```

```
WormBase::Controller::Gene;
```

```
sub identification( );
```

**eg: /gene/\*/identification**

# Each field is an action

```
pages :
```

```
gene :
```

```
widgets :
```

```
identification :
```

```
    - [ description, ncbi_kogs, species ]
```

```
WormBase::Controller::Gene;
```

```
sub species( );
```

**eg: /gene/\*/species**

# Config and models align

```
pages :  
  
    gene :  
  
        widgets :  
  
            identification :  
  
                - [ description, ncbi_kogs, species ]  
  
WormBase::Model::Gene;  
  
sub description()  
  
    my ($self, $gene) = @_;  
  
    return $object->Description;  
  
);
```

# Config maps to views...

```
pages :
```

```
    gene :
```

```
        widgets :
```

```
            identification :
```

```
                - [ description, ncbi_kogs, species ]
```

```
--
```

```
description.tt2
```

```
[% description %]
```

# Future Calls

- I. Introduction
- II. Documentation and configuration
- III. Anatomy of a model
- IV. Controllers: dynamic actions, root actions
- V. Views: design decisions, flexibility