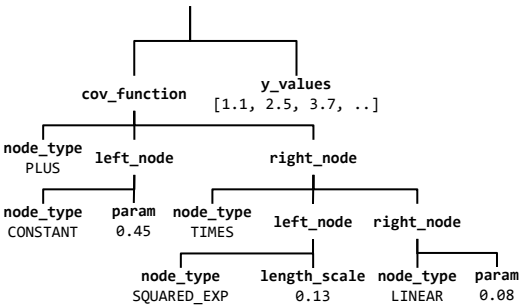
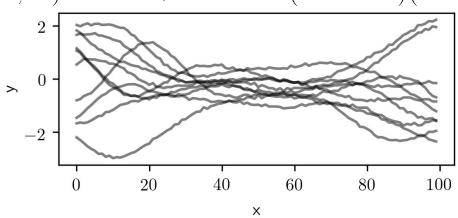
```
@gen function p(x_values::Vector)
    cov_function ~ cov_function_prior()
    cov_matrix = compute_cov_matrix(cov_function, x_values)
    n = length(xs)
    y_values ~ mvnormal(zeros(n), cov_matrix .+ 0.01 * I(n))
end

@gen function cov_function_prior()
    node_type ~ categorical(production_rule_probabilities))
    if node_type == CONSTANT
        param ~ uniform(0, 1)
        return ConstantNode(param)
    elseif node_type == LINEAR
        param ~ uniform(0, 1)
        return LinearNode(param)
    elseif node_type == SQUARED_EXP
        length_scale ~ uniform(0, 1)
        return SquaredExponentialNode(length_scale)
    elseif node_type == PERIODIC
        ..
    elseif node_type == PLUS
        left_node ~ cov_function_prior()
        right_node ~ cov_function_prior()
        return PlusNode(left_node, right_node)
    elseif node_type == TIMES
        left_node ~ cov_function_prior()
        right_node ~ cov_function_prior()
        return TimesNode(left_node, right_node)
    end
end
```

(a) A Gaussian process generative model **p** that uses a PCFG-based prior on a combinatorial space of covariance functions, expressed in a Gen probabilistic modeling language.



(b) An execution trace of the generative model **p** from (a). Each random choice has a unique address in a hierarchical address space that is based on the tree of function calls.

$$k(x, x') = 0.45 + e^{-\frac{(x-x')^2}{0.13}}(x - 0.08)(x' - 0.08)$$



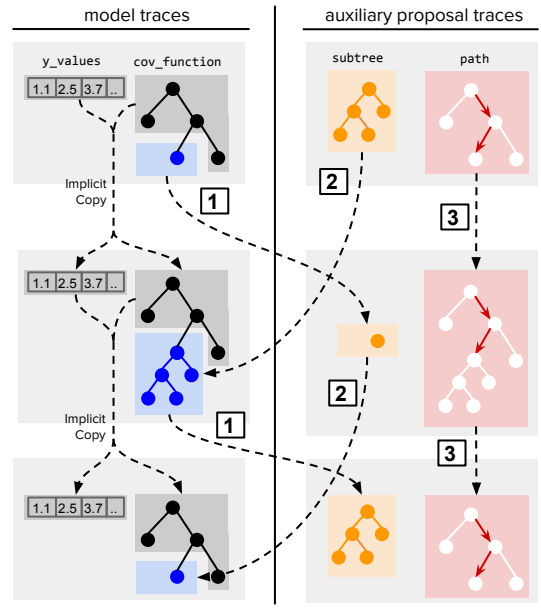
(c) The covariance function represented by the trace in (c), and several samples from the resulting Gaussian process.

```
@gen function q(trace)
    prev_cov_function = trace[:cov_function]
    path ~ walk_tree(prev_cov_function, (:cov_function,))
    subtree ~ cov_function_prior()
    return path
end

@gen function walk_tree(node::Node, path)
    if isa(node, LeafNode)
        done ~ bernoulli(1)
        return path
    elseif ({done} ~ bernoulli(0.5))
        return path
    elseif ({:recurse_left} ~ bernoulli(0.5))
        path = (path..., :left_node)
        return ({:left} ~ walk_tree(node.left, path))
    else
        path = (path..., :right_node)
        return ({:right} ~ walk_tree(node.right, path))
    end
end
```

(d) Auxiliary proposal distribution **q**, which proposes a new subtree in the covariance function, expressed in a Gen probabilistic modeling language.

```
@trace_bijection h from (p_in, q_in) to (p_out, q_out) begin
    path = @proposal_return_value()
    model_subtree_address = foldr(=>, path))
    @copy(p_in, model_subtree_address, q_out, :subtree)
    @copy(q_in, :subtree, p_out, model_subtree_address)
    @copy(q_in, :path, q_out, :path)
end
```

(e) An involution **h**, which swaps the previous and newly proposed subtrees.



(f) Schematic showing the involution **h** applied twice. The first application replaces a subtree with one node with a subtree with 5 nodes. The second application reverts the change.