

START

```
READ:
  signature_genes
  expression_matrix
COMPUTE:
  cell_labels = randomly assigned cell_types for each cell
  prob = a matrix of probabilities to assign each cell to each cell_type
  FOR cells from each cell_type :
    distribution_parameters[cells] = {u1,u2,v1,v2}
    #mean and variations of signature/non-signature gene expressions
  ENDFOR
```

Initialize model

```
WHILE iteration < limit:
  iteration += 1
  FOR cells from each cell_type:
    prob[cells] = EstimateLikelihood(prob[cells],
    distribution_parameters[cells])
  ENDFOR
```

E step

Probability estimation for
cell type assignment

```
FOR cells from each cell_type:
  distribution_parameters=EstimateFromLikelihood(
  prob[cells],
  expression_matrix[cells],
  signature_genes[cells])
ENDFOR
cell_labels = cell_type with the max prob for each cell
```

M step

Optimizing parameters of
the gene expression distribution

No

```
IF FOR n=1: convergence_n:
  all (difference(cell_labels[iteration] - cell_labels[iteration - n]) < convergence_rate)
```

Stop rules

Yes

```
return cell_labels
BREAK
ENDIF
ENDWHILE
```

Final model

END