

```
<< myPadRight.m;  
<< cellerator.m;  
<< kMech_Rev.m;  
Off[General::"spell"];  
Off[General::"spell"];
```

myPadRight Version 0.3 for Cellerator Loaded.

Cellerator™ 1.4.6 (30-July-2004) loaded 8-Nov-2004 15:38
using *Mathematica* Version 5.0 for Microsoft Windows (June 11, 2003)

kMech is loaded

```

(* Start mRNA Splicing Simulation *)
(* NE1: RNA polymerase; NEs: spliceosome; NEd: degradation enzymes *)

mRNASplicing = Union[
  Enz[{DNA, NTP}  $\rightleftharpoons$  {premrRNA, DNA}, BiBi[kf1, kr2, kcat3]],
  {{premrRNA + NEs  $\rightleftharpoons$  $Complex$NEs$premrRNA$, kf4, kr5}},
  {{$Complex$NEs$premrRNA$  $\rightarrow$  NEs + mRNA, kcat6}},
  {{premrRNA  $\rightleftharpoons$  NMP, kf7, kr8, kcat9}},
  {{$Complex$NEs$premrRNA$  $\rightleftharpoons$  NMP, kf10, kr11, kcat12}},
  {{mRNA  $\rightleftharpoons$  NMP, kf13, kr14, kcat15}}
]

{{$Complex$NE1$DNA$NTP$  $\rightarrow$  DNA + NE1 + premrRNA, kcat3},
{$Complex$NEs$premrRNA$  $\rightarrow$  mRNA + NEs, kcat6}, {DNA + NE1 + NTP  $\rightleftharpoons$  $Complex$NE1$DNA$NTP$, kf1, kr2},
{NEs + premrRNA  $\rightleftharpoons$  $Complex$NEs$premrRNA$, kf4, kr5}, {mRNA  $\rightleftharpoons$  NMP, kf13, kr14, kcat15},
{premrRNA  $\rightleftharpoons$  NMP, kf7, kr8, kcat9}, {{$Complex$NEs$premrRNA$  $\rightleftharpoons$  NMP, kf10, kr11, kcat12}}

```

```

{myODEs,myVars}=interpret[mRNAsplcing]

{{DNA'[t] ==
  -kf1 DNA[t] NE1[t] NTP[t] + kcat3 $Complex$NE1$DNA$NTP$[t] + kr2 $Complex$NE1$DNA$NTP$[t],
 mRNA'[t] == -kf13 mRNA[t] NED[t] + kr14 $Complex$mRNA$NED$[t] + kcat6 $Complex$NEs$premRNA$[t],
 NE1'[t] ==
  -kf1 DNA[t] NE1[t] NTP[t] + kcat3 $Complex$NE1$DNA$NTP$[t] + kr2 $Complex$NE1$DNA$NTP$[t],
 NED'[t] == -kf13 mRNA[t] NED[t] - kf7 NED[t] premRNA[t] + kcat15 $Complex$mRNA$NED$[t] +
  kr14 $Complex$mRNA$NED$[t] - kf10 NED[t] $Complex$NEs$premRNA$[t] +
  kcat9 $Complex$premRNA$NED$[t] + kr8 $Complex$premRNA$NED$[t] +
  kcat12 $Complex$$Complex$NEs$premRNA$$NED$[t] + kr11 $Complex$$Complex$NEs$premRNA$$NED$[t],
 NEs'[t] == -kf4 NEs[t] premRNA[t] + kcat6 $Complex$NEs$premRNA$[t] + kr5 $Complex$NEs$premRNA$[t],
 NMP'[t] == kcat15 $Complex$mRNA$NED$[t] + kcat9 $Complex$premRNA$NED$[t] +
  kcat12 $Complex$$Complex$NEs$premRNA$$NED$[t],
 NTP'[t] == -kf1 DNA[t] NE1[t] NTP[t] + kr2 $Complex$NE1$DNA$NTP$[t],
 premRNA'[t] == -kf7 NED[t] premRNA[t] - kf4 NEs[t] premRNA[t] + kcat3 $Complex$NE1$DNA$NTP$[t] +
  kr5 $Complex$NEs$premRNA$[t] + kr8 $Complex$premRNA$NED$[t], $Complex$mRNA$NED$'[t] ==
  kf13 mRNA[t] NED[t] - kcat15 $Complex$mRNA$NED$[t] - kr14 $Complex$mRNA$NED$[t],
 $Complex$NE1$DNA$NTP$'[t] == kf1 DNA[t] NE1[t] NTP[t] - kcat3 $Complex$NE1$DNA$NTP$[t] -
  kr2 $Complex$NE1$DNA$NTP$[t], $Complex$NEs$premRNA$'[t] ==
  kf4 NEs[t] premRNA[t] - kcat6 $Complex$NEs$premRNA$[t] - kr5 $Complex$NEs$premRNA$[t] -
  kf10 NED[t] $Complex$NEs$premRNA$[t] + kr11 $Complex$$Complex$NEs$premRNA$$NED$[t],
 $Complex$premRNA$NED$'[t] == kf7 NED[t] premRNA[t] - kcat9 $Complex$premRNA$NED$[t] -
  kr8 $Complex$premRNA$NED$[t], $Complex$$Complex$NEs$premRNA$$NED$'[t] ==
  kf10 NED[t] $Complex$NEs$premRNA$[t] - kcat12 $Complex$$Complex$NEs$premRNA$$NED$[t] -
  kr11 $Complex$$Complex$NEs$premRNA$$NED$[t]},
 {DNA, mRNA, NE1, NED, NEs, NMP, NTP, premRNA, $Complex$mRNA$NED$,
 $Complex$NE1$DNA$NTP$, $Complex$NEs$premRNA$,
 $Complex$premRNA$NED$, $Complex$$Complex$NEs$premRNA$$NED$}}

```

```
Lamda = 1;

myKs = {

  KmNE1$DNA = 40; (*2;*) KmNE1$NTP = 1000; kcat3 = 0.1; (*0.6;*)
  kf1 → Kf2S [KmNE1$DNA, KmNE1$NTP, kcat3, Lamda],
  kr2 → Kr [kcat3, Lamda],

  KmNEs$premrna = 3.5; (*15;*) kcat6 = 0.03; (*0.1;*)
  kf4 → Kf [KmNEs$premrna, kcat6, Lamda],
  kr5 → Kr [kcat6, Lamda],

  KmNEd$premrna = 2000000 (*10 1*); kcat9 = 30000 (*3000*);
  kf7 → Kf [KmNEd$premrna, kcat9, Lamda],
  kr8 → Kr [kcat9, Lamda],

  KmNEd$Complex$NEs$premrna = 30000000; kcat12 = 30000;
  kf10 → Kf [KmNEd$Complex$NEs$premrna, kcat12, Lamda],
  kr11 → Kr [kcat12, Lamda],

  KmNEd$mRNA = 30000000; (* 20 X KmNEd$premrna *) kcat15 = 30000;
  kf13 → Kf [KmNEd$mRNA, kcat15, Lamda],
  kr14 → Kr [kcat15, Lamda]
}

{kf1 → 2.5 × 10-6, kr2 → 0, kf4 → 0.00857143, kr5 → 0,
 kf7 → 0.015, kr8 → 0, kf10 → 0.001, kr11 → 0, kf13 → 0.001, kr14 → 0}
```

```

myICs = {
  DNA[0] == 12,
  NTP[0] == 25000,
  premRNA[0] == 0,
  mRNA[0] == 0,
  NMP[0] == 0,

  NE1[0] == 0.025, (*0.003,*)
  NEs[0] == 5, (*0.006,*)
  NEd[0] == 3.5, (*1 0.2,*)

  $Complex$NE1$DNA$NTP$[0] == 0,
  $Complex$NEs$premRNA$[0] == 0,
  $Complex$premRNA$NEd$[0] == 0,
  $Complex$$Complex$NEs$premRNA$$NEd$[0] == 0,
  $Complex$mRNA$NEd$[0] == 0
};

```

```

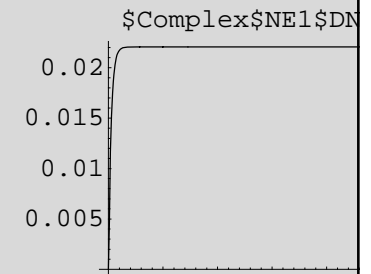
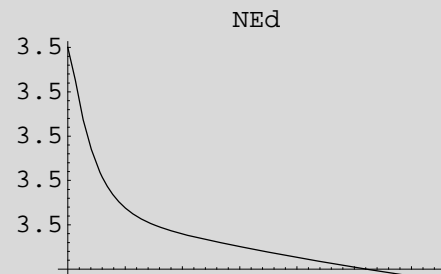
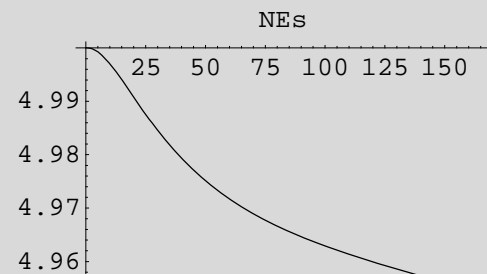
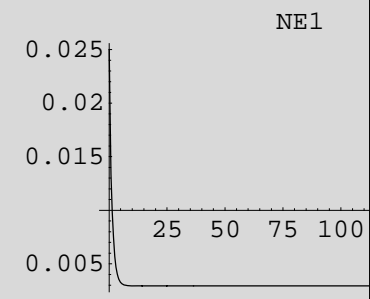
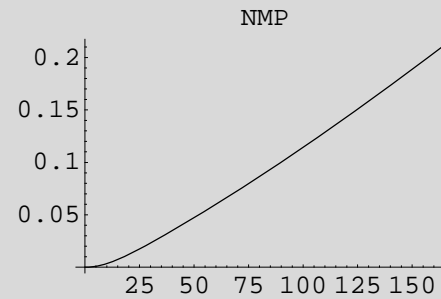
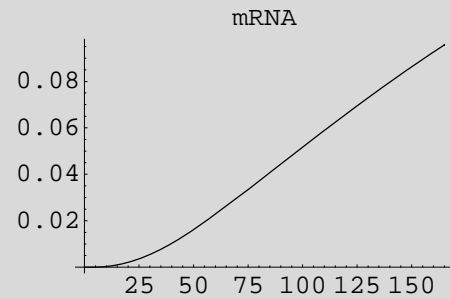
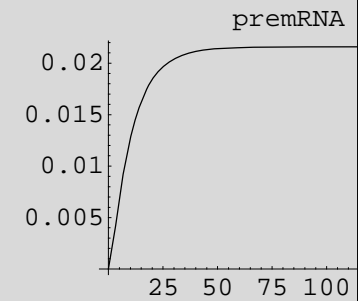
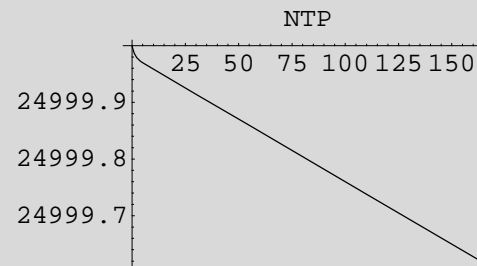
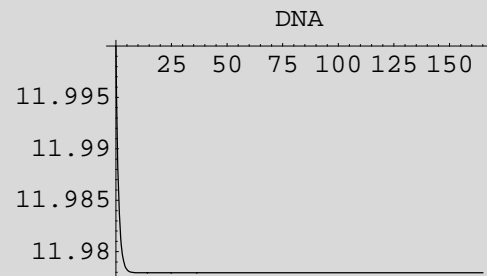
tmax = 165;
mySolution = NDSolve[Join[myODEs /. myKs, myICs], myVars, {t, 0, tmax}, MaxSteps -> 3000]

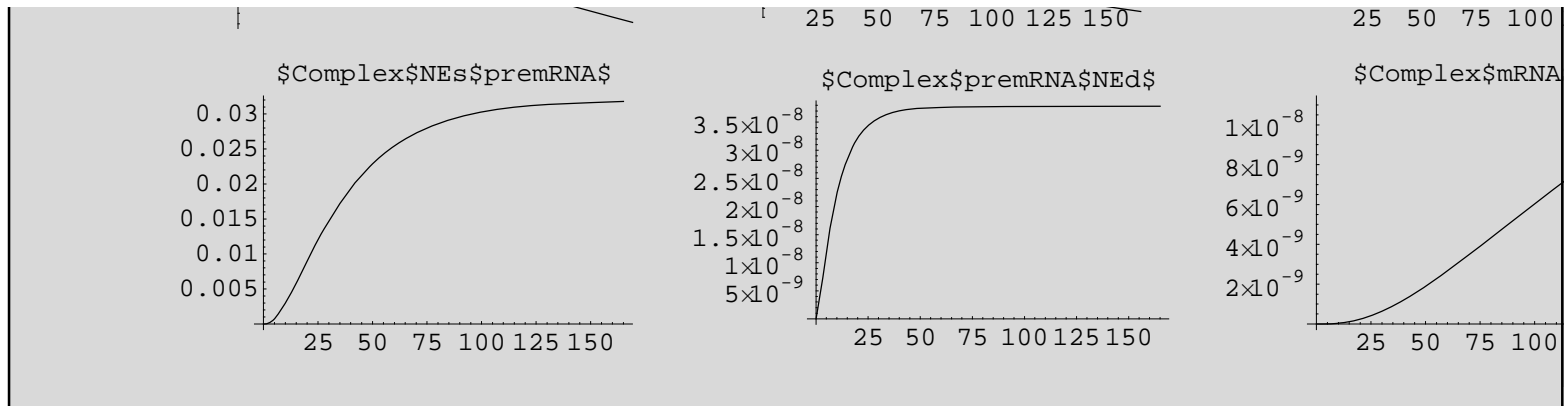
{{DNA -> InterpolatingFunction[{{0., 165.}}, <>],
 mRNA -> InterpolatingFunction[{{0., 165.}}, <>], NE1 -> InterpolatingFunction[{{0., 165.}}, <>],
 NEd -> InterpolatingFunction[{{0., 165.}}, <>], NEs -> InterpolatingFunction[{{0., 165.}}, <>],
 NMP -> InterpolatingFunction[{{0., 165.}}, <>], NTP -> InterpolatingFunction[{{0., 165.}}, <>],
 premRNA -> InterpolatingFunction[{{0., 165.}}, <>],
 $Complex$mRNA$NEd$ -> InterpolatingFunction[{{0., 165.}}, <>],
 $Complex$NE1$DNA$NTP$ -> InterpolatingFunction[{{0., 165.}}, <>],
 $Complex$NEs$premRNA$ -> InterpolatingFunction[{{0., 165.}}, <>],
 $Complex$premRNA$NEd$ -> InterpolatingFunction[{{0., 165.}}, <>],
 $Complex$$Complex$NEs$premRNA$$NEd$ -> InterpolatingFunction[{{0., 165.}}, <>]}}

```

```
orderedVars={DNA,NTP,premRNA,mRNA,NMP,NE1,NEs,NEd,$Complex$NE1$DNA$NTP$,
$Complex$NEs$premRNA$, $Complex$premRNA$NEd$, $Complex$mRNA$NEd$};
```

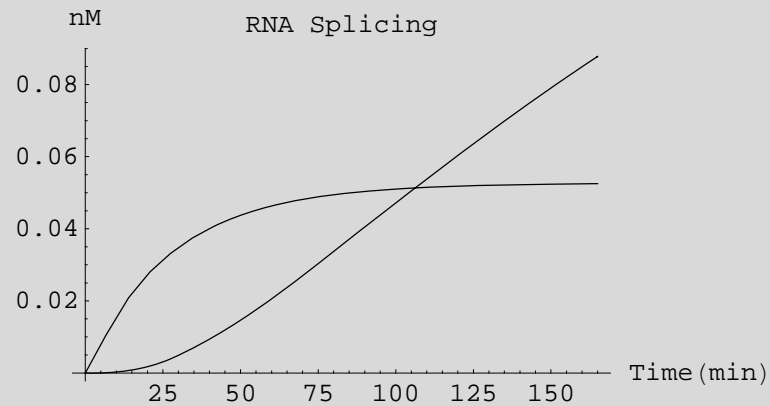
```
Show[GraphicsArray[
  Partition[
    Map[Plot[#[t]/.mySolution,{t,0,tmax},PlotLabel->#,
      PlotRange->All,DisplayFunction->Identity]&,orderedVars],3]
  ]
];
```



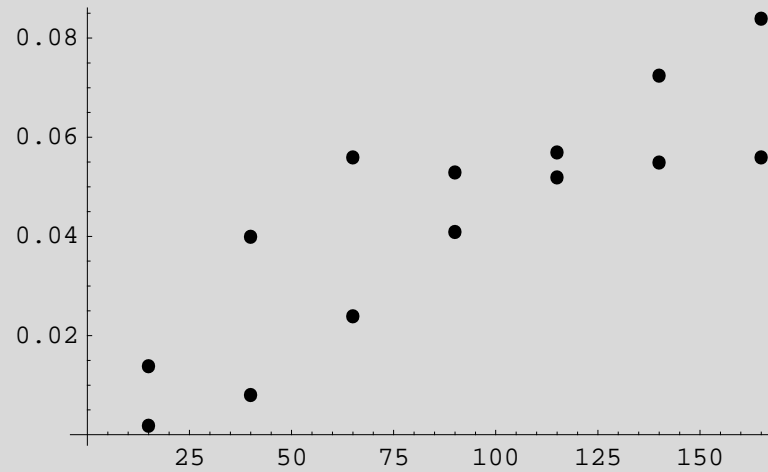


```
totalPremRNA[t_] = premRNA[t] + $Complex$NEs$premRNA$[t] + $Complex$premRNA$NEd$[t];
```

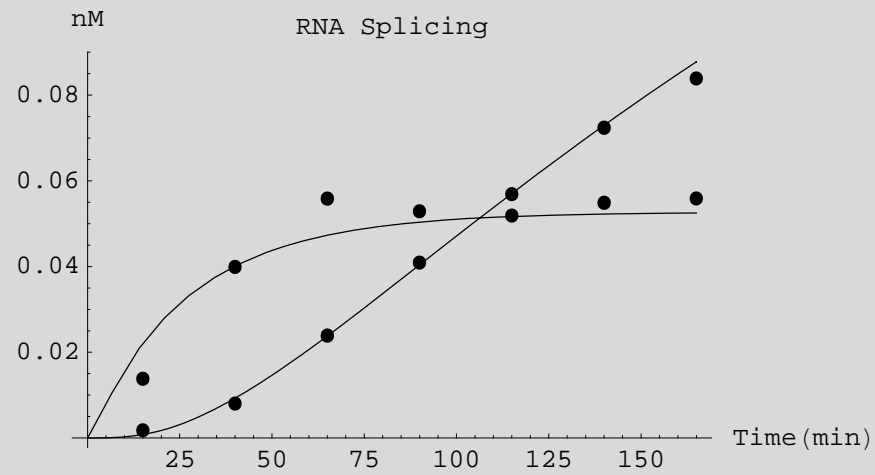
```
P1 = Plot[mRNA[t] /. mySolution, {t, 0, tmax}, PlotRange -> All, DisplayFunction -> Identity];
P2 = Plot[totalPremRNA[t] /. mySolution,
  {t, 0, tmax}, PlotRange -> All, DisplayFunction -> Identity];
Show[P1, P2, AxesLabel -> {"Time (min)", nM}, PlotLabel -> "RNA Splicing",
  DisplayFunction -> $DisplayFunction];
```



```
P3 = ListPlot[{  
  
  (* Time points (min): 15,40,65,90,115,140,165 *)  
  (* mRNA concentration (nM) *)  
  {15, 0.0019}, {40, 0.0081},  
  {65, 0.024}, {90, 0.041}, {115, 0.057}, {140, 0.0725}, {165, 0.084},  
  
  (* pre-mRNA concentration (nM) *)  
  {15, 0.0139}, {40, 0.04}, {65, 0.056}, {90, 0.053}, {115, 0.052}, {140, 0.055}, {165, 0.056}  
  
}, Prolog -> AbsolutePointSize[5]];
```




```
Show[P3, P1, P2, AxesLabel -> {"Time (min)", nM},  
PlotLabel -> "RNA Splicing", DisplayFunction -> $DisplayFunction];
```

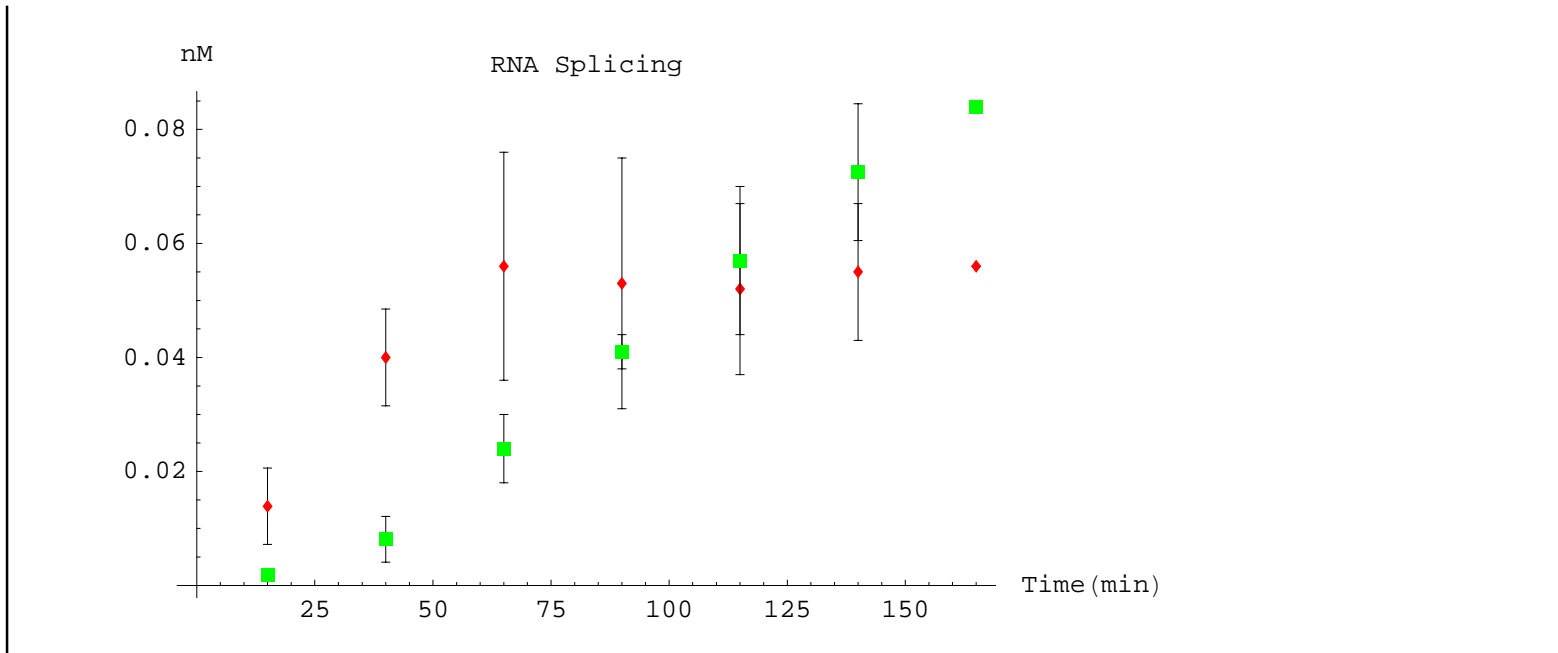


```
<< Graphics`MultipleListPlot`

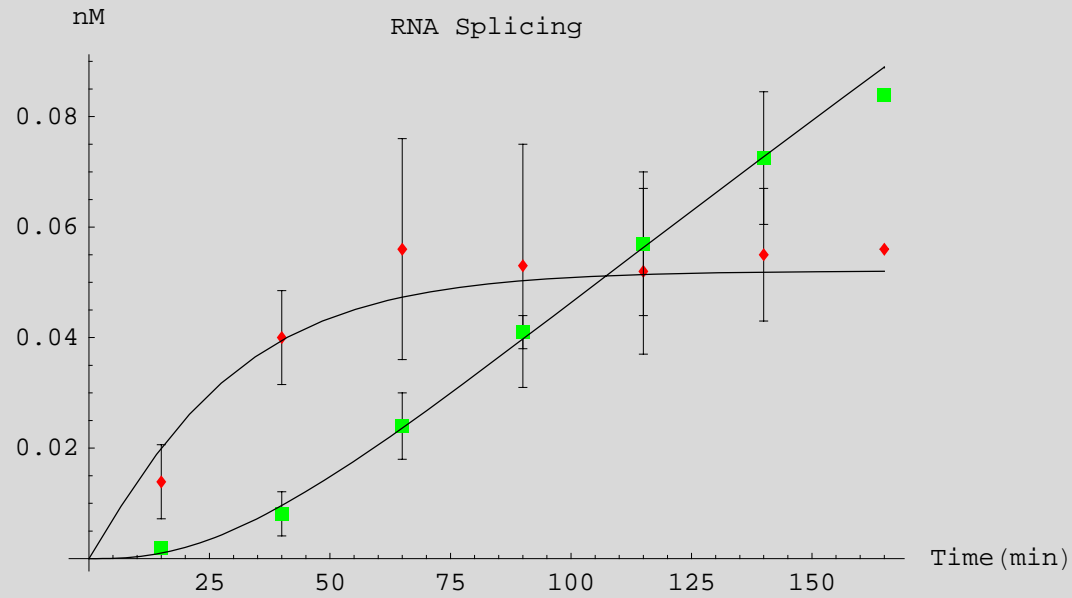
(* mRNA concentration (nM) *)
mRNA = {
  {{15, 0.0019}, ErrorBar[0.001]},
  {{40, 0.0081}, ErrorBar[0.004]},
  {{65, 0.024}, ErrorBar[0.006]},
  {{90, 0.041}, ErrorBar[0.003]},
  {{115, 0.057}, ErrorBar[0.013]},
  {{140, 0.0725}, ErrorBar[0.012]},
  {{165, 0.084}, ErrorBar[0.0]}
};

(* pre-mRNA concentration (nM) *)
premRNA = {
  {{15, 0.0139}, ErrorBar[0.0067]},
  {{40, 0.04}, ErrorBar[0.0085]},
  {{65, 0.056}, ErrorBar[0.02]},
  {{90, 0.053}, ErrorBar[0.022]},
  {{115, 0.052}, ErrorBar[0.015]},
  {{140, 0.055}, ErrorBar[0.012]},
  {{165, 0.056}, ErrorBar[0.0]}
};

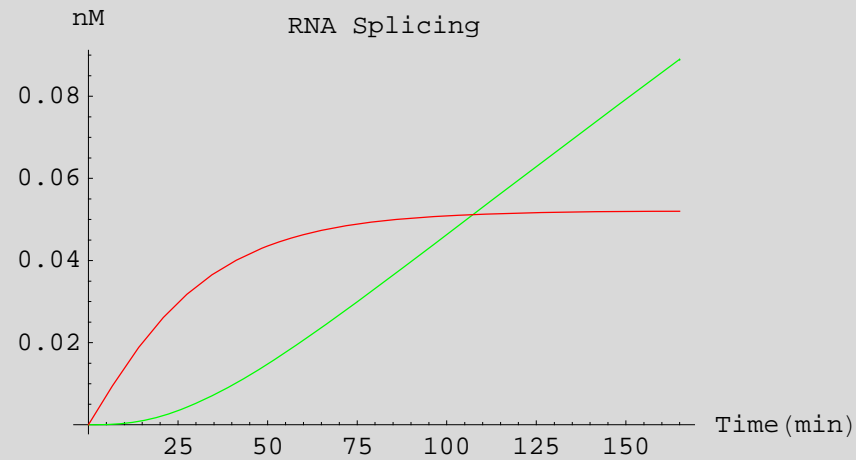
P5 = MultipleListPlot[premRNA, mRNA,
  AxesLabel → {"Time (min)", nM}, PlotLabel → "RNA Splicing",
  SymbolShape → {PlotSymbol[Diamond], PlotSymbol[Box]},
  SymbolStyle → {RGBColor[1, 0, 0], RGBColor[0, 1, 0]}
];
```

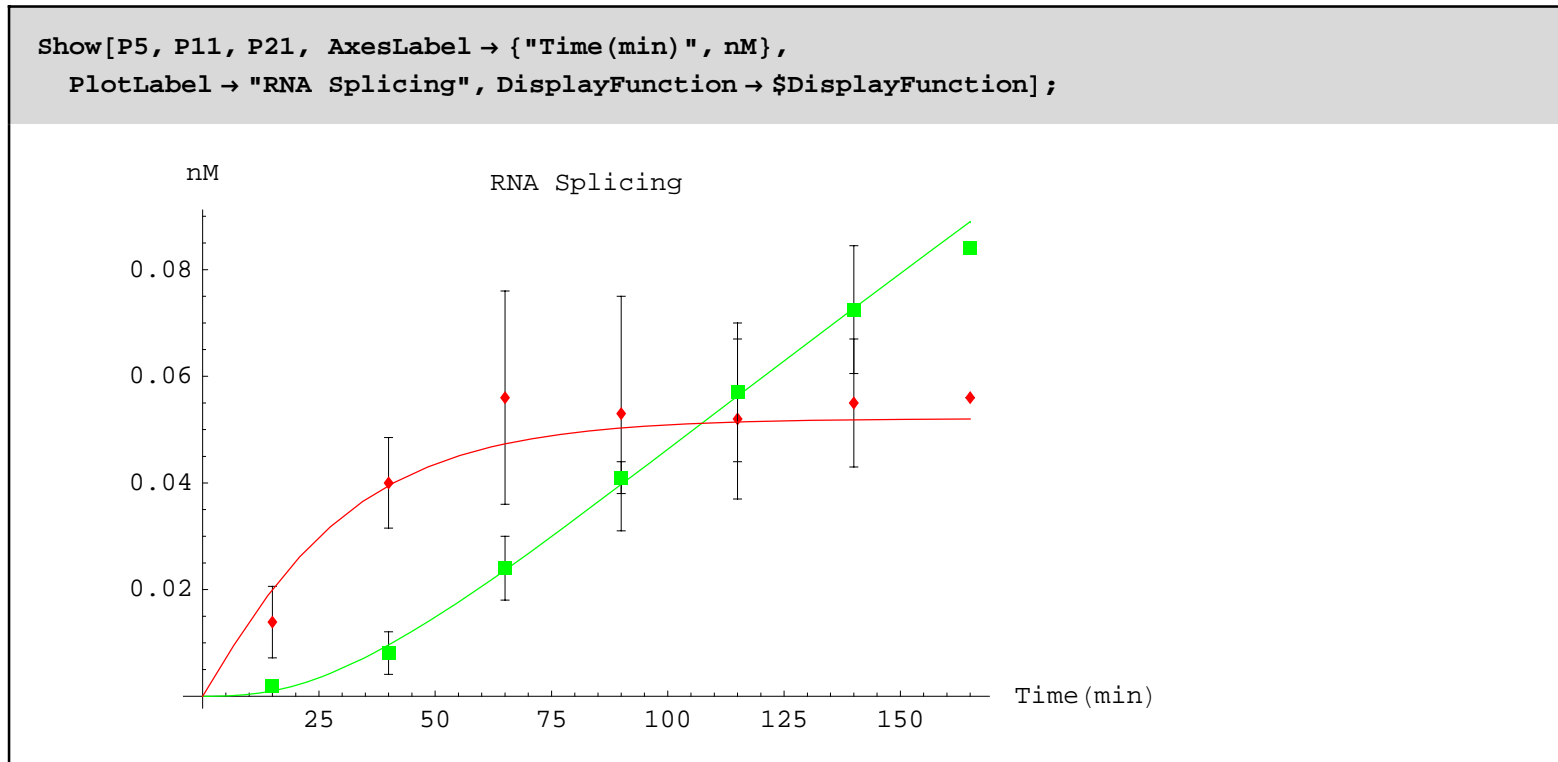


```
Show[P5, P1, P2, AxesLabel -> {"Time (min)", nM},  
PlotLabel -> "RNA Splicing", DisplayFunction -> $DisplayFunction];
```

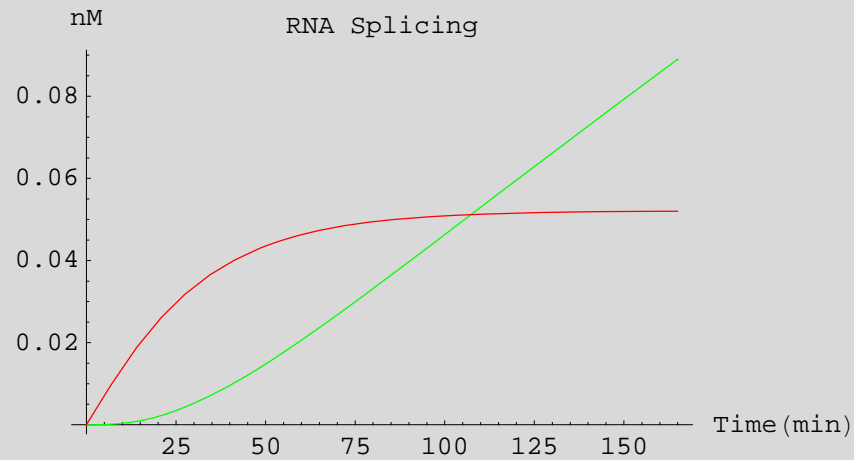


```
(* KmNES$premRNA=1; KmNED$premRNA=50 *)  
  
P11 = Plot[mRNA[t] /. mySolution, {t, 0, tmax},  
  PlotRange -> All, PlotStyle -> {RGBColor[0, 1, 0]}, DisplayFunction -> Identity];  
P21 = Plot[totalPremRNA[t] /. mySolution, {t, 0, tmax}, PlotRange -> All,  
  PlotStyle -> {RGBColor[1, 0, 0]}, DisplayFunction -> Identity];  
Show[P11, P21, AxesLabel -> {"Time (min)", nM}, PlotLabel -> "RNA Splicing",  
  DisplayFunction -> $DisplayFunction];
```

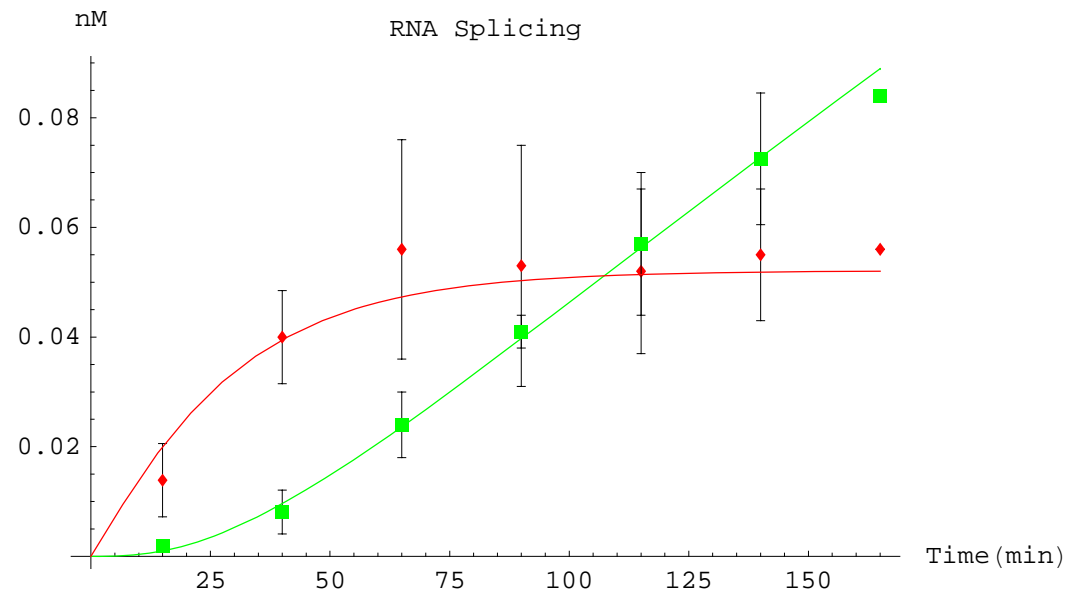




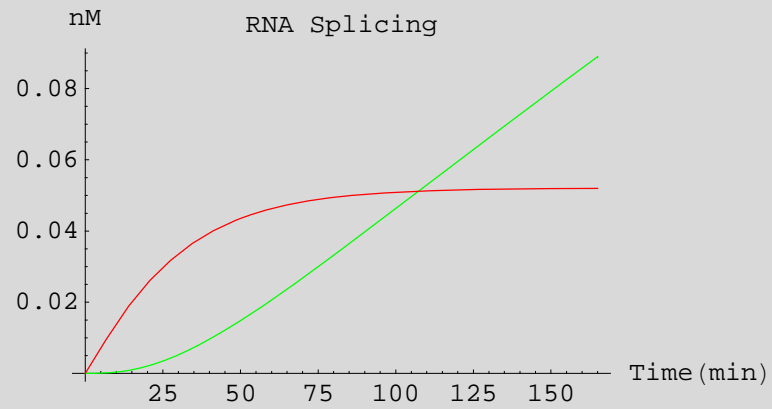
```
(* KmNEs$premRNA=10; KmNEd$premRNA=50 *)  
  
P110 = Plot[mRNA[t] /. mySolution, {t, 0, tmax},  
  PlotRange -> All, PlotStyle -> {RGBColor[0, 1, 0]}, DisplayFunction -> Identity];  
P210 = Plot[totalPremRNA[t] /. mySolution, {t, 0, tmax}, PlotRange -> All,  
  PlotStyle -> {RGBColor[1, 0, 0]}, DisplayFunction -> Identity];  
Show[P110, P210, AxesLabel -> {"Time (min)", nM}, PlotLabel -> "RNA Splicing",  
  DisplayFunction -> $DisplayFunction];
```

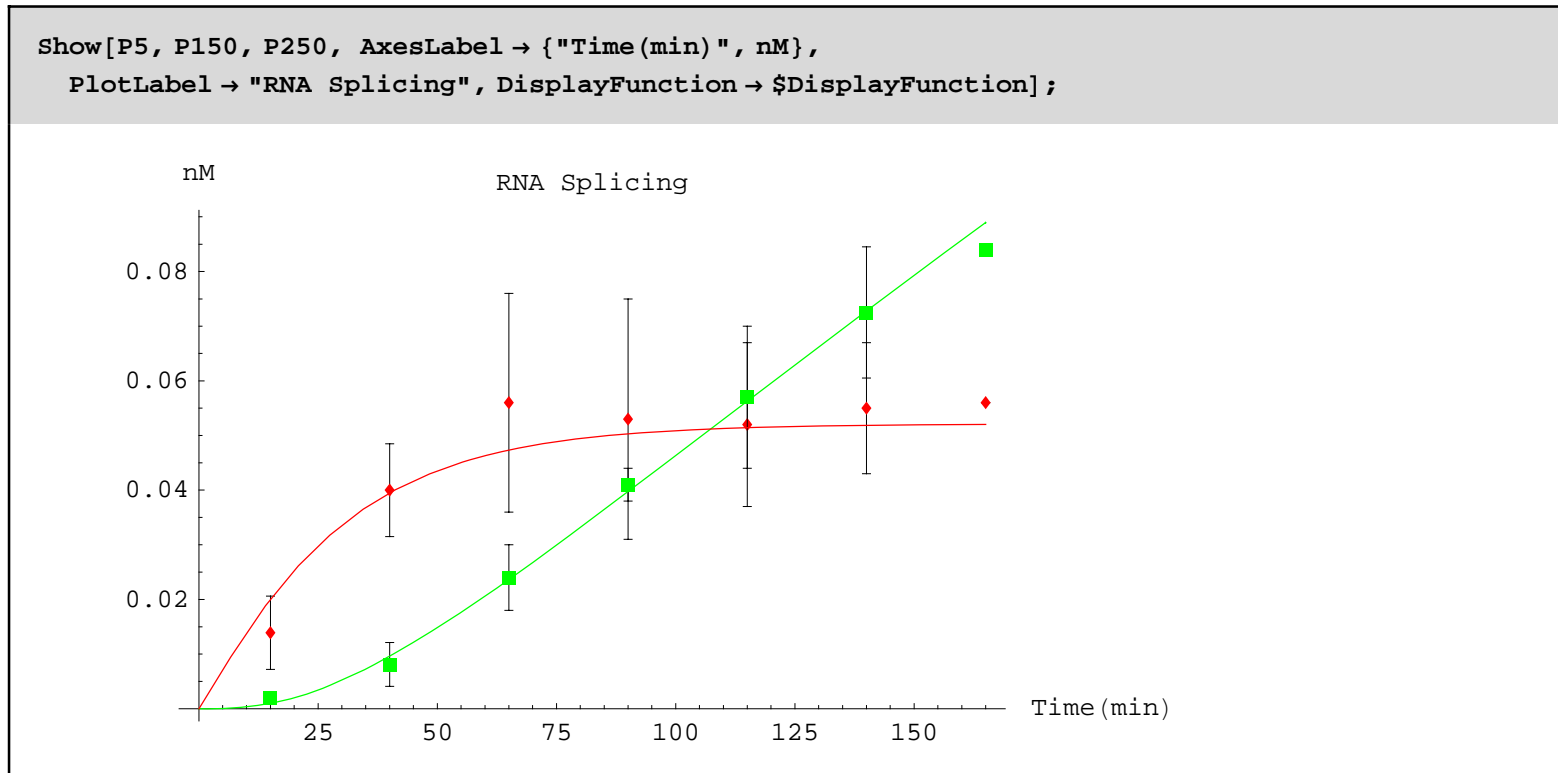


```
Show[P5, P110, P210, AxesLabel -> {"Time (min)", nM},  
PlotLabel -> "RNA Splicing", DisplayFunction -> $DisplayFunction];
```




```
(* KmNEs$premRNA=50; KmNEd$premRNA=50 *)  
  
P150 = Plot[mRNA[t] /. mySolution, {t, 0, tmax},  
  PlotRange -> All, PlotStyle -> {RGBColor[0, 1, 0]}, DisplayFunction -> Identity];  
P250 = Plot[totalPremRNA[t] /. mySolution, {t, 0, tmax}, PlotRange -> All,  
  PlotStyle -> {RGBColor[1, 0, 0]}, DisplayFunction -> Identity];  
Show[P150, P250, AxesLabel -> {"Time (min)", nM}, PlotLabel -> "RNA Splicing",  
  DisplayFunction -> $DisplayFunction];
```





```
<< Statistics`ContinuousDistributions`  
<< Graphics`MultipleListPlot`  
<< myPadRight.m;  
<< cellerator.m;  
<< kMech_Rev.m;  
Off[General::"spell"];  
Off[General::"spell"];
```

myPadRight Version 0.3 for Cellerator Loaded.

Cellerator™ Version 1.0 update 3.1002, loaded at Feb. 4, 2004, 00:45:44
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Technology. U.S. Government Sponsorship Acknowledged. All rights reserved.
Patent Pending (USPTO App 09993291).
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Cellerator™ 1.0 update 3.1002 load (using *Mathematica* Version 4.2
for Microsoft Windows (June 5, 2002)) complete at February 4, 2004 00:45:46

kMech is loaded

```

(* Start mRNA Splicing Simulation *)
(* NE1: RNA polymerase; NES: spliceosome; NEd: degradation enzymes *)

mRNASplicing = Union[
  Enz[NE1{DNA, NTP} ⇌ {premrRNA, DNA}, BiBi[kf1, kr2, kcat3]],
  {{premrRNA + NES ⇌ $Complex$NES$premrRNA$, kf4, kr5}},
  {{$Complex$NES$premrRNA$ → NES + mRNA, kcat6}},
  {{premrRNANEd ⇌ NMP, kf7, kr8, kcat9}},
  {{$Complex$NES$premrRNA$ ⇌ NMP, kf10, kr11, kcat12}},
  {{mRNANEd ⇌ NMP, kf13, kr14, kcat15}}
]

{{$Complex$NE1$DNA$NTP$ → DNA + NE1 + premrRNA, kcat3},
 {$Complex$NES$premrRNA$ → mRNA + NES, kcat6}, {DNA + NE1 + NTP ⇌ $Complex$NE1$DNA$NTP$, kf1, kr2},
 {NES + premrRNA ⇌ $Complex$NES$premrRNA$, kf4, kr5}, {mRNANEd ⇌ NMP, kf13, kr14, kcat15},
 {premrRNANEd ⇌ NMP, kf7, kr8, kcat9}, {{$Complex$NES$premrRNA$ ⇌ NMP, kf10, kr11, kcat12}}

```

interpret[mRNASplcing]

```
{ {DNA'[t] == -kf1 DNA[t] NE1[t] NTP[t] + kcat3 $Complex$NE1$DNA$NTP$[t] + kr2 $Complex$NE1$DNA$NTP$[t],
  mRNA'[t] == -kf13 mRNA[t] NEd[t] + kr14 $Complex$mRNA$NEd$[t] + kcat6 $Complex$NEs$premRNA$[t],
  NE1'[t] == -kf1 DNA[t] NE1[t] NTP[t] + kcat3 $Complex$NE1$DNA$NTP$[t] + kr2 $Complex$NE1$DNA$NTP$[t],
  NEd'[t] == -kf13 mRNA[t] NEd[t] - kf7 NEd[t] premRNA[t] + kcat15 $Complex$mRNA$NEd$[t] +
    kr14 $Complex$mRNA$NEd$[t] - kf10 NEd[t] $Complex$NEs$premRNA$[t] +
    kcat9 $Complex$premRNA$NEd$[t] + kr8 $Complex$premRNA$NEd$[t] +
    kcat12 $Complex$$Complex$NEs$premRNA$$NEd$[t] + kr11 $Complex$$Complex$NEs$premRNA$$NEd$[t],
  NEs'[t] == -kf4 NEs[t] premRNA[t] + kcat6 $Complex$NEs$premRNA$[t] + kr5 $Complex$NEs$premRNA$[t],
  NMP'[t] == kcat15 $Complex$mRNA$NEd$[t] +
    kcat9 $Complex$premRNA$NEd$[t] + kcat12 $Complex$$Complex$NEs$premRNA$$NEd$[t],
  NTP'[t] == -kf1 DNA[t] NE1[t] NTP[t] + kr2 $Complex$NE1$DNA$NTP$[t],
  premRNA'[t] == -kf7 NEd[t] premRNA[t] - kf4 NEs[t] premRNA[t] +
    kcat3 $Complex$NE1$DNA$NTP$[t] + kr5 $Complex$NEs$premRNA$[t] + kr8 $Complex$premRNA$NEd$[t],
  $Complex$mRNA$NEd$'[t] == kf13 mRNA[t] NEd[t] - kcat15 $Complex$mRNA$NEd$[t] -
    kr14 $Complex$mRNA$NEd$[t], $Complex$NE1$DNA$NTP$'[t] ==
    kf1 DNA[t] NE1[t] NTP[t] - kcat3 $Complex$NE1$DNA$NTP$[t] - kr2 $Complex$NE1$DNA$NTP$[t],
  $Complex$NEs$premRNA$'[t] == kf4 NEs[t] premRNA[t] - kcat6 $Complex$NEs$premRNA$[t] -
    kr5 $Complex$NEs$premRNA$[t] - kf10 NEd[t] $Complex$NEs$premRNA$[t] +
    kr11 $Complex$$Complex$NEs$premRNA$$NEd$[t], $Complex$premRNA$NEd$'[t] ==
    kf7 NEd[t] premRNA[t] - kcat9 $Complex$premRNA$NEd$[t] - kr8 $Complex$premRNA$NEd$[t],
  $Complex$$Complex$NEs$premRNA$$NEd$'[t] == kf10 NEd[t] $Complex$NEs$premRNA$[t] -
    kcat12 $Complex$$Complex$NEs$premRNA$$NEd$[t] - kr11 $Complex$$Complex$NEs$premRNA$$NEd$[t] },
{DNA, mRNA, NE1, NEd, NEs, NMP, NTP, premRNA, $Complex$mRNA$NEd$, $Complex$NE1$DNA$NTP$,
  $Complex$NEs$premRNA$, $Complex$premRNA$NEd$, $Complex$$Complex$NEs$premRNA$$NEd$}
```

```
graphList1 = {};
```

```
graphList2 = {};
```

```
For[iter = 1, iter < 100,
```

```

{myODEs, myVars} =
{{DNA'[t] == -kf1 DNA[t] NE1[t] NTP[t] + kcat3 $Complex$NE1$DNA$NTP$[t] + kr2 $Complex$NE1$DNA$NTP$[t],
 mRNA'[t] == -kf13 mRNA[t] NED[t] + kr14 $Complex$mRNA$NED$[t] +
  kcat6 $Complex$NEs$premRNA$[t] + Random[NormalDistribution[0, 0.00001]],

 NE1'[t] == -kf1 DNA[t] NE1[t] NTP[t] + kcat3 $Complex$NE1$DNA$NTP$[t] + kr2 $Complex$NE1$DNA$NTP$[t],
 NED'[t] == -kf13 mRNA[t] NED[t] - kf7 NED[t] premRNA[t] + kcat15 $Complex$mRNA$NED$[t] +
  kr14 $Complex$mRNA$NED$[t] - kf10 NED[t] $Complex$NEs$premRNA$[t] +
  kcat9 $Complex$premRNA$NED$[t] + kr8 $Complex$premRNA$NED$[t] +
  kcat12 $Complex$$Complex$NEs$premRNA$$NED$[t] + kr11 $Complex$$Complex$NEs$premRNA$$NED$[t],
 NES'[t] == -kf4 NES[t] premRNA[t] + kcat6 $Complex$NEs$premRNA$[t] + kr5 $Complex$NEs$premRNA$[t],
 NMP'[t] == kcat15 $Complex$mRNA$NED$[t] + kcat9 $Complex$premRNA$NED$[t] +
  kcat12 $Complex$$Complex$NEs$premRNA$$NED$[t],
 NTP'[t] == -kf1 DNA[t] NE1[t] NTP[t] + kr2 $Complex$NE1$DNA$NTP$[t],
 premRNA'[t] == -kf7 NED[t] premRNA[t] - kf4 NES[t] premRNA[t] +
  kcat3 $Complex$NE1$DNA$NTP$[t] + kr5 $Complex$NEs$premRNA$[t] +
  kr8 $Complex$premRNA$NED$[t] + Random[NormalDistribution[0, 0.00001]],

 $Complex$mRNA$NED$'[t] == kf13 mRNA[t] NED[t] -
  kcat15 $Complex$mRNA$NED$[t] - kr14 $Complex$mRNA$NED$[t], $Complex$NE1$DNA$NTP$'[t] ==
  kf1 DNA[t] NE1[t] NTP[t] - kcat3 $Complex$NE1$DNA$NTP$[t] - kr2 $Complex$NE1$DNA$NTP$[t],
 $Complex$NEs$premRNA$'[t] == kf4 NES[t] premRNA[t] - kcat6 $Complex$NEs$premRNA$[t] -
  kr5 $Complex$NEs$premRNA$[t] - kf10 NED[t] $Complex$NEs$premRNA$[t] +
  kr11 $Complex$$Complex$NEs$premRNA$$NED$[t], $Complex$premRNA$NED$'[t] ==
  kf7 NED[t] premRNA[t] - kcat9 $Complex$premRNA$NED$[t] - kr8 $Complex$premRNA$NED$[t],
 $Complex$$Complex$NEs$premRNA$$NED$'[t] == kf10 NED[t] $Complex$NEs$premRNA$[t] -
  kcat12 $Complex$$Complex$NEs$premRNA$$NED$[t] - kr11 $Complex$$Complex$NEs$premRNA$$NED$[t]},
{DNA, mRNA, NE1, NED, NES, NMP, NTP, premRNA, $Complex$mRNA$NED$, $Complex$NE1$DNA$NTP$,
 $Complex$NEs$premRNA$, $Complex$premRNA$NED$, $Complex$$Complex$NEs$premRNA$$NED$}};

Lamda = 1;

```

```
myKs = {

  KmNE1$DNA = 2; KmNE1$NTP = 1000; kcat3 = Random[NormalDistribution[0.6, 0.05]];
  kf1 → Kf2S[KmNE1$DNA, KmNE1$NTP, kcat3, Lamda],
  kr2 → Kr[kcat3, Lamda],

  KmNEs$premRNA = 1; kcat6 = Random[NormalDistribution[140, 15]];
  kf4 → Kf[KmNEs$premRNA, kcat6, Lamda],
  kr5 → Kr[kcat6, Lamda],

  KmNEd$premRNA = 50; kcat9 = 10;
  kf7 → Kf[KmNEd$premRNA, kcat9, Lamda],
  kr8 → Kr[kcat9, Lamda],

  KmNEd$Complex$NEs$premRNA = 1000; kcat12 = 10;
  kf10 → Kf[KmNEd$Complex$NEs$premRNA, kcat12, Lamda],
  kr11 → Kr[kcat12, Lamda],

  KmNEd$mRNA = 50; kcat15 = 10;
  kf13 → Kf[KmNEd$mRNA, kcat15, Lamda],
  kr14 → Kr[kcat15, Lamda]
};

myICs = {
  DNA[0] == 12,
  NTP[0] == 25000,
  premRNA[0] == 0,
  mRNA[0] == 0,
  NMP[0] == 0,

  NE1[0] == 0.001,
```

```
NEs[0] == 0.0002,  
NEd[0] == 0.02,  
  
$Complex$NE1$DNA$NTP$[0] == 0,  
$Complex$NEs$premRNA$[0] == 0,  
$Complex$premRNA$NEd$[0] == 0,  
$Complex$$Complex$NEs$premRNA$$NEd$[0] == 0,  
$Complex$mRNA$NEd$[0] == 0  
};  
  
tmax = 150;  
mySolution = NDSolve[Join[myODEs /. myKs, myICs], myVars, {t, 0, tmax}, MaxSteps -> 3000];  
  
graphList1 = Join[graphList1,  
  {Plot[mRNA[t] /. mySolution, {t, 0, tmax}, PlotRange -> All, DisplayFunction -> Identity]}];  
  
totalPremRNA[t_] = premRNA[t] + $Complex$NEs$premRNA$[t] + $Complex$premRNA$NEd$[t];  
graphList2 = Join[graphList2,  
  {Plot[totalPremRNA[t] /. mySolution, {t, 0, tmax}, PlotRange -> All, DisplayFunction -> Identity]}];  
  
iter++];  
  
(* mRNA concentration (nM) *)  
mRNA = {  
  {{15, 0.0013}, ErrorBar[0.0012]},  
  {{40, 0.0051}, ErrorBar[0.0027]},  
  {{65, 0.0155}, ErrorBar[0.0029]},  
  {{90, 0.0262}, ErrorBar[0.0037]},  
  {{115, 0.0360}, ErrorBar[0.0072]},  
  {{140, 0.0461}, ErrorBar[0.0025]}  
};
```

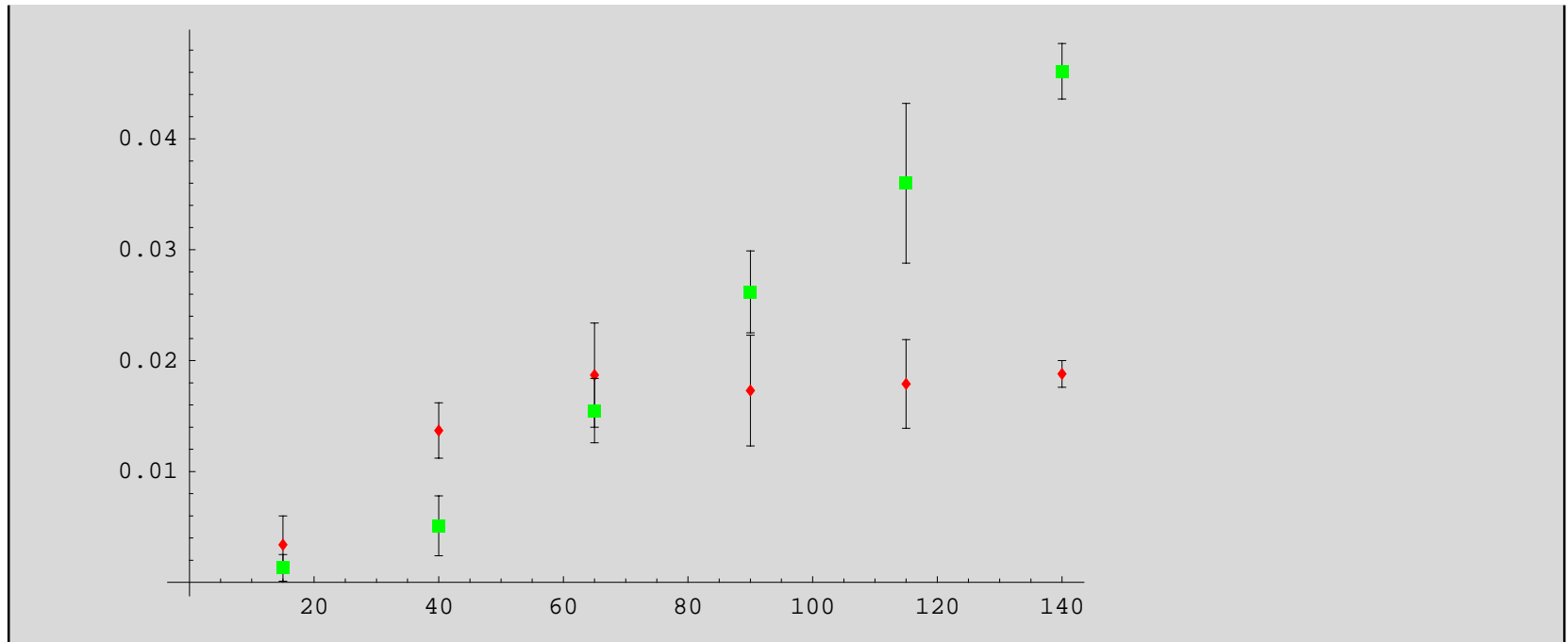


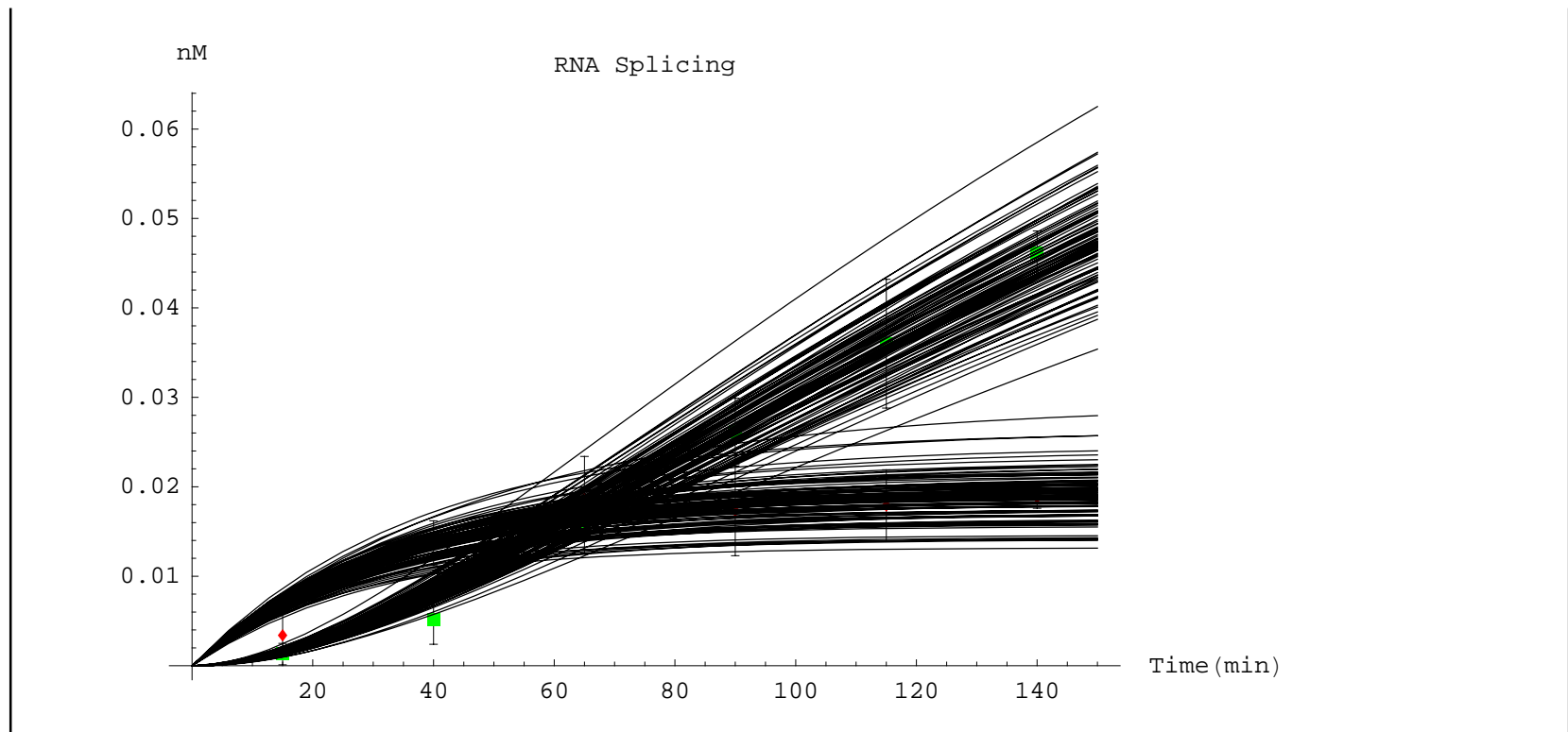
```
(* pre-mRNA concentration (nM) *)
premRNA = {
  {{15, 0.0034}, ErrorBar[0.0026]},
  {{40, 0.0137}, ErrorBar[0.0025]},
  {{65, 0.0187}, ErrorBar[0.0047]},
  {{90, 0.0173}, ErrorBar[0.0050]},
  {{115, 0.0179}, ErrorBar[0.0040]},
  {{140, 0.0188}, ErrorBar[0.0012]}
};

DataPlot = MultipleListPlot[premRNA, mRNA,
  SymbolShape -> {PlotSymbol[Diamond], PlotSymbol[Box]},
  SymbolStyle -> {RGBColor[1, 0, 0], RGBColor[0, 1, 0]}
];

Show[DataPlot, graphList1, graphList2, AxesLabel -> {"Time (min)", nM},
  PlotLabel -> "RNA Splicing", DisplayFunction -> $DisplayFunction];

Clear[graphList1, graphList2]
```





myODEs

```

{DNA'[t] == -kf1 DNA[t] NE1[t] NTP[t] + 0.386444 $Complex$NE1$DNA$NTP$[t] + kr2 $Complex$NE1$DNA$NTP$[t],
 mRNA'[t] ==
  0.000012116 - kf13 mRNA[t] Ned[t] + kr14 $Complex$mRNA$Ned$[t] + 105.435 $Complex$NEs$premRNA$[t],
 NE1'[t] == -kf1 DNA[t] NE1[t] NTP[t] + 0.386444 $Complex$NE1$DNA$NTP$[t] + kr2 $Complex$NE1$DNA$NTP$[t],
 Ned'[t] == -kf13 mRNA[t] Ned[t] - kf7 Ned[t] premRNA[t] + 10 $Complex$mRNA$Ned$[t] +
  kr14 $Complex$mRNA$Ned$[t] - kf10 Ned[t] $Complex$NEs$premRNA$[t] +
  10 $Complex$premRNA$Ned$[t] + kr8 $Complex$premRNA$Ned$[t] +
  10 $Complex$$Complex$NEs$premRNA$$Ned$[t] + kr11 $Complex$$Complex$NEs$premRNA$$Ned$[t],
 Nes'[t] == -kf4 Nes[t] premRNA[t] + 105.435 $Complex$NEs$premRNA$[t] + kr5 $Complex$NEs$premRNA$[t],
 NMP'[t] ==
  10 $Complex$mRNA$Ned$[t] + 10 $Complex$premRNA$Ned$[t] + 10 $Complex$$Complex$NEs$premRNA$$Ned$[t],
 NTP'[t] == -kf1 DNA[t] NE1[t] NTP[t] + kr2 $Complex$NE1$DNA$NTP$[t],
 premRNA'[t] == 8.74921 × 10-7 - kf7 Ned[t] premRNA[t] - kf4 Nes[t] premRNA[t] +
  0.386444 $Complex$NE1$DNA$NTP$[t] + kr5 $Complex$NEs$premRNA$[t] + kr8 $Complex$premRNA$Ned$[t],
 $Complex$mRNA$Ned$'[t] == kf13 mRNA[t] Ned[t] - 10 $Complex$mRNA$Ned$[t] - kr14 $Complex$mRNA$Ned$[t],
 $Complex$NE1$DNA$NTP$'[t] ==
  kf1 DNA[t] NE1[t] NTP[t] - 0.386444 $Complex$NE1$DNA$NTP$[t] - kr2 $Complex$NE1$DNA$NTP$[t],
 $Complex$NEs$premRNA$'[t] == kf4 Nes[t] premRNA[t] - 105.435 $Complex$NEs$premRNA$[t] -
  kr5 $Complex$NEs$premRNA$[t] - kf10 Ned[t] $Complex$NEs$premRNA$[t] +
  kr11 $Complex$$Complex$NEs$premRNA$$Ned$[t], $Complex$premRNA$Ned$'[t] ==
  kf7 Ned[t] premRNA[t] - 10 $Complex$premRNA$Ned$[t] - kr8 $Complex$premRNA$Ned$[t],
 $Complex$$Complex$NEs$premRNA$$Ned$'[t] == kf10 Ned[t] $Complex$NEs$premRNA$[t] -
  10 $Complex$$Complex$NEs$premRNA$$Ned$[t] - kr11 $Complex$$Complex$NEs$premRNA$$Ned$[t]}

```