Workflow Support runbook:

Workflow tools down
This runbook aims to explain the procedures to follow if the workflow tools stop working/begin running very slowly.

When experiencing problems with workflow, errors will normally begin to come into the workflow support email inbox and can look like this:

Workflow runs off two separate nodes, which are load-balanced. The email above tells us that bmclon04 is in trouble, but we should check the health of both nodes as routine:
1. Mechanical tests

Try to reproduce slow loading behaviour/loss of service.

Go to any MS in workflow and try a few pages:

http://production.biomedcentral.com/editor/manuscript/history/5305604856207074

Observe loading behaviour.

Now, bypass load balancer and go to each node directly, checking the same pages as before:

http://b03.production.biomedcentral.com/editor/manuscript/history/5305604856207074

http://b04.production.biomedcentral.com/editor/manuscript/history/5305604856207074

Is one node behaving normally but the other no?
2. Technical tests: Server response times

Check RUOK for both nodes:

http://b03.production.biomedcentral.com/ruok.asp?verbose=true
http://b04.production.biomedcentral.com/ruok.asp?verbose=true

These RUOK links tell us some important info:

<table>
<thead>
<tr>
<th>all ado disks msjava wars name</th>
<th>message</th>
<th>value</th>
<th>/ms OK?</th>
</tr>
</thead>
<tbody>
<tr>
<td>COMPUTERNAME</td>
<td>BMCLON04</td>
<td>True</td>
<td></td>
</tr>
<tr>
<td>LOCAL_ADDR</td>
<td>172.18.8.140</td>
<td>True</td>
<td></td>
</tr>
<tr>
<td>host</td>
<td>b04.production.biomedcentral.com</td>
<td>True</td>
<td></td>
</tr>
<tr>
<td>C: free space/MB</td>
<td>OK</td>
<td>35416</td>
<td>True</td>
</tr>
<tr>
<td>/editor</td>
<td>YES</td>
<td>200</td>
<td>16</td>
</tr>
<tr>
<td>com_sub tier</td>
<td>COM component</td>
<td>OK</td>
<td>True</td>
</tr>
<tr>
<td>DataTool.DataTool</td>
<td>COM component</td>
<td>OK</td>
<td>True</td>
</tr>
<tr>
<td>ADO</td>
<td>Genome Biology</td>
<td>16</td>
<td>True</td>
</tr>
<tr>
<td>maintenance</td>
<td>Paused flag file present False</td>
<td></td>
<td>True</td>
</tr>
<tr>
<td>RUOK</td>
<td>YES</td>
<td>32</td>
<td></td>
</tr>
</tbody>
</table>

If any aspect of the server fails the test, the ‘OK?’ result will be ‘False’ and therefore, RUOK will return a ‘False’ response, which means the node is not happy. Sometimes, the /editor application hangs, which means RUOK fails. A Tomcat restart will be needed.

Slow/laggy loading may be observed from the server response times (/ms). Note that in the image above, t/ms for RUOK is 32. If you see this suddenly hitting >1000/2000 you will notice workflow slowing down, going into loading circles.

IF RUOK RETURNS A VALUE OF ‘FALSE’, THE NODE WILL AUTOMATICALLY BE SKIPPED BY THE LOAD BALANCER, ROUTING ALL REQUESTS TO THE REMAINING NODE.
3. Technical tests: database connection leaks

Check to see if DB connections are leaking in SPLUNK:

sourcetype=jmx_monitor host=BMCLON03 ctr=ORACLE_CONN_ACTIVE | timechart max(val) by inst

sourcetype=jmx_monitor host=BMCLON04 ctr=ORACLE_CONN_ACTIVE | timechart max(val) by inst

Once you have run this query, filter the results down to ‘Last 24 hours’ and then jump to the last page of results. If connections become close to 50, workflow will begin to slow down as DB connections are used up. At 50 connections, all available connections are exhausted and workflow will fail on that node:
4. Technical tests: access spikes

Check OpenNMS to see if there is clear evidence of spiking and ‘click-drag’ the graph to narrow down the time frame:

http://opennms.biomedcentral.com/opennms/KSC/customView.htm?type=custom&report=43

So we can see here, from ~13:10 to 13:50 we see some clear spiking
5. Technical tests: Check logs for errors

Check Tomcat logs for errors using BareTail. Logs are here:

\\bmclon03\LOGS\TOMCAT
\\bmclon04\LOGS\TOMCAT